

SEQUENCE LISTING

<110> Forsyth, R. Allyn
Ohlsen, Kari L.
Zyskind, Judith W.

<120> Genes identified as required for
proliferation of E. coli

<130> ELITRA.009A

<150> US 60/173005

<151> 1999-12-23

<160> 481

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 142

<212> DNA

<213> Escherichia coli

<400> 1

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<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(154)

<223> n = A,T,C or G

<400> 2

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tcacgagtta ccggcccaaa aatacgcgta ccgataggct gctcgctgtt gttgttcacg 120
aagaacacaa gcattaccat cgaagcgaat gaca                                     154
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<210> 3

<211> 140

<212> DNA

<213> Escherichia coli

<400> 3

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attaccatcg aagcgaatga                                     140
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[illegible]

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<211> 255
<212> DNA
<213> Escherichia coli
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<210> 6
<211> 395
<212> DNA
<213> Escherichia coli
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<210> 7
<211> 280
<212> DNA
<213> Escherichia coli
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<210> 8
<211> 363
<212> DNA
<213> Escherichia coli
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gcactggagg caaccgcatt aatcaacgtg aaatacgact aataacaagc aagacgagca 180
agtggctaata aataaaaaaat aacaagggtg ctgcatttcc ccctcatgat gaggggggctt 240
tttttagcga tgataaaaaaa tctcaccgtc gtaggcttta atgattttac cgtcgggtgct 300
gctgatcaac acgtacgcgc caccatata ggtccagtgc gtcccggcat caggcgcgagg 360
cag 363

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<210> 9
<211> 295
<212> DNA
<213> Escherichia coli

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<400> 9
ttacagatac aacgggtttca attccgataa cagccagtta ctacgtctac gatacaaaaca 60
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aagcaagacg agcaagtggc taataataaa aaataacaag gtgtctgcat tccccctca 180
tgatgagggg gcttttttta gcgatgataa aaaatctcac cgtcgtaggc tttaatgatt 240
ttaccgtcgg tgtcgtctgat caacacgtac gcgccacca tataggtcca gtgcg 295

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<210> 10
<211> 161
<212> DNA
<213> Escherichia coli

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<400> 10
acgactaata acaagcaaga cgagcaagtg gctaataata aaaaataaca aggtgtctgc 60
atttccccct catgatgagg gggctttttt tagcgatgat aaaaaatctc accgtcgtag 120
gctttaatga ttttaccgtc ggtgtcgtct atcaacacgt a 161

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<210> 11
<211> 290
<212> DNA
<213> Escherichia coli

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<400> 11
tgcggcgaag tcaaaactta cagatacaac ggtttcaatt ccgataacag ccagttacta 60
cgtctacgat acaaacaaag ttaaatctgg cgcaactggag gcaaccgcat taatcaacgt 120
gaaatacgac taataacaag caagacgagc aagtggctaa taataaaaaa taacaagggtg 180
tctgcatttc cccctcatga tgaggggggt ttttttagcg atgataaaaa atctcaccgt 240
cgtaggcttt aatgatttta ccgtcgggtg cgctgatcaa cacgtacgcg 290

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<210> 12
<211> 137
<212> DNA
<213> Escherichia coli

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<400> 12
ctgggttttag cttttgcttc gtaaacacgt aataaaaacgt cctcacacaa tatgaggacg 60
ccgaatttta gggcgatgcc gaaaagggtg caagaaatat acaacgatcc cgccatcacc 120
aggccatctg gctgggg 137

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<210> 13
<211> 275
<212> DNA
<213> Escherichia coli

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<400> 13
cgtcatgtac gtgcagtttg gtcgtacgct tgatgaattt accgtagatc ggggtgtttca 60

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caaaacgttc gatagcaaca acaatggatt tctccatttt gtcgctaaca acgcgacctt 120
gcagagtacg gattttatcg gtcattacgc acccgcccttc tcgttcagta aagtcttaac 180
gcgtgcgaca tcgcgacgca cttgcttcaa cagggtgagac tggttcagct ggccacttgc 240
agcctgcata cgcaggttga actgctcacg cagca 275

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<210> 14
<211> 239
<212> DNA
<213> Escherichia coli

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<400> 14
tgtcggtaaa caatgacaat ttgagacaga gtgaaaggtc agatttgagg agtaatgcac 60
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ttactcacia tgtatcaggg aaatataact taccgggaga tgtaatatgt ttaatttttc 180
aaatcgaaat ttaaaatatt gtgccggagg catctctggc acattgggca attacggca 239

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<210> 15
<211> 114
<212> DNA
<213> Escherichia coli

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<400> 15
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ttgtcacttc ggcattgata gacttcgacg caagagtgtt cgactcgcgg ttga 114

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<210> 16
<211> 290
<212> DNA
<213> Escherichia coli

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<400> 16
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gctgacatac tgatgcaaaa tcttttagat actcatgatt ttcgaacgca taaatgcaca 120
agaatttata ataaatttct gcgtccggtt tattaccctt ttcattggttag tcgaatgcat 180
atgcatatat tctatcaagg atatcaggag ttaaaccatg tagtaatgcc agattttctc 240
ctttcgataa tgcgtgtttt agttgatttg cccattcatc actattattg 290

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<210> 17
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<212> DNA
<213> Escherichia coli

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<220>
<221> misc_feature
<222> (1)...(444)
<223> n = A,T,C or G

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agaatttata ataaatttct gcgtccggtt tattaccctt ttcattggttag tcgaatgcat 180
atgcatatat tctatcaagg atatcaggag ttaaaccatg tagtaatgcc agattttctc 240
ctttcgataa tgcgtgtttt agttgatttg cccattcatc actattantg aatatttcaa 300
ttgtttctgt gtcataata ttctctgng atgtgnctcg ngatgccnaa cnattatttg 360
antgactcat ngnnattntt atatnnatcc nntnntaant natnantntn aagccngcnt 420
tgcttatggg ntantntnat ttat 444

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<210> 18
 <211> 250
 <212> DNA
 <213> Escherichia coli

<400> 18
 cgctggaaaa aacctaataa attcatctta ttccccctac gagaacccta tttggctcgt 60
 ttcaagccgt atttttattt tgctgcaaatt tgtactgccg atgttctgta atcagattgt 120
 tagatcatct gctacagagt gtgtgaaaat ttaattcgta tgcgaaatta aacgcgtgtc 180
 ttttgtgagt tttgtcacca aatatcgta ttatcactcc cttttactgg ctaaaccaga 240
 aaacttattt 250

<210> 19
 <211> 237
 <212> DNA
 <213> Escherichia coli

<400> 19
 gtattacaac aagaatacag tgctaaaaaa agaatgtacc tgaagatagt cttcattttt 60
 actccaatgt ttctttattg ttatggtttg cgctgttttt gtttgattt cgtagtaaat 120
 atccactaac acatggctca taagtgtacc agatgtaaca ctcaatgcag gatcgatttt 180
 ttgcattcgg gtgctaaatt tccaggatga accattcatg tcatccgaca ttactgg 237

<210> 20
 <211> 237
 <212> DNA
 <213> Escherichia coli

<400> 20
 catcatcaca gcggcagcca tgtacagcag atccatattc aggtttttcca tgacagtctc 60
 cagtttgttt cagttaaaac gtagtagtgt tggtaaatta atgttcttca gacgccatcg 120
 acagatagac gatcgtcaga accatgaaga tgaaggcttg cagcgtaatg atcaggatgt 180
 ggaaaatggc ccacggcaca ttcaggatcc actgtgacca ccacggcaac agaccag 237

<210> 21
 <211> 139
 <212> DNA
 <213> Escherichia coli

<400> 21
 cccgcgacgt tatccgctg taggcatcgt catgacgtaa acggcgatcg gcggtataac 60
 ggttgatcat cgaatccatg ttgccagcag taacaccgaa aaacagattc ggtttaccga 120
 gacgcataaa gtcgtcttt 139

<210> 22
 <211> 211
 <212> DNA
 <213> Escherichia coli

<400> 22
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 cgacgagtaa agtactcaaa cggcgcgctc cacacatgca ccagtcgggt gaacgggaag 120
 agcaggaaga tggtcattcc caacaccaga tgcaggcgga agacgaacgc tacgccgttg 180
 agcatctctg acgatccacc acggaagtga a 211

<210> 23
 <211> 154

<212> DNA
<213> Escherichia coli

<400> 23
cacgacggat tttcgctgcc atgattcgct ccttagagta cttctggtgc cagagagata 60
attttcatga acttctcact acgaagctca cgagttaccc ggccccaaaa tacgcgtacc 120
gataggctgc tcgctgttgt tggtcagaag aaca 154

<210> 24
<211> 160
<212> DNA
<213> Escherichia coli

<400> 24
acttcgtcat cacgacggat tttcgctgcc atgattcgct ccttagagta cttctggtgc 60
cagagagata attttcatga acttctcact acgaagctca cgagttaccg gccccaaaat 120
acgcgtaccg ataggctgct cgctgttgtt gttcagaaga 160

<210> 25
<211> 244
<212> DNA
<213> Escherichia coli

<400> 25
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ggttaacacg ataacttcgt catcacgacg gattttcgct gccatgattc gctccttaga 120
gtacttctgg tgccagagag ataattttca tgaacttctc actacgaagc tcacgagtta 180
ccggcccaaa aatacgcgta ccgataggct gctcgctggt gttgttcaga agaacacaag 240
catt 244

<210> 26
<211> 108
<212> DNA
<213> Escherichia coli

<400> 26
tgttcgatct cgaaacttac acctttctca gccagcacaa tgcggacctg atggctatag 60
atgtcagtag gaccggaaaa cagcgtcatt acccgaacgt ttgttggc 108

<210> 27
<211> 369
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(369)
<223> n = A,T,C or G

<400> 27
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cgtgagtcct gaatgcgatt atttaccgga ttaatttcaa acatggctctg atttctttta 120
ttgagctagt caaaatgcgg tgataagagc gggattgtac ccaatccacg ctctttttta 180
tagagaagat gacgctaaat tggccagata ttgtcgatga taatttgcag gctgcgggtc 240
cacgaaactc gttgatatcg agcttataag ccagttgcac ttngcgcacc cgttatccgg 300
ccagagggcg gtatcgacat taaaagcaat accatccagc agtggaccgc cgcccagaccg 360
gttcgacca 369

<210> 28
 <211> 457
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(457)
 <223> n = A,T,C or G

<400> 28
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 tttcaaacaT ggtctgattt cttttattga gctagtcaaa atgcggtgat aagagcggga 120
 ttgtacccaa tccacgtctt tttttataga gaagatgacg ctaaattggc cagatattgt 180
 cgatgataat ttgcaggctg cggttgccgc gaaactcgtt gatatcgagc ttataagcca 240
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 catccagcag tggaccgccg ccgaccggtt cgaccatnac cttcaaataga cgttcgcccc 360
 ccagccgctg ttgcancaga cggaaatgac cgtcaaacag cggctccggg aacatctgcc 420
 cccacggggc agcatcgcgC agcagctgcg ccacttc 457

<210> 29
 <211> 729
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(729)
 <223> n = A,T,C or G

<400> 29
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 taatttgTtc gagctttatt gaacacattg ccaacacatt aaatttagga gtgggtgtaca 120
 actaaacctg cagccaagga tgtatagtga gcgaagccct atcaggcctt tttggtcagt 180
 agataagatt gatcttcgtt gatagaattt acttacacca gctgttacat taagataatt 240
 ttttggtggg agaatgataa gatcttacgt aacaatttga ttttaatggg gccgataata 300
 ggagtcgaac ctacgacctt cgcattacga atgcgctgct ctaccaactg agctatatcg 360
 gccctgaaag gacatgttca cgaacgtgaa tcacgggtgga caagggtaaa actaaccggg 420
 cgatgcgtca atggccttgt gaatcaaata gctacttttg catcaccggg ttttatTTac 480
 gcacgaatgg tgtaatcacc aatgccgatc cacttgtaag tggTcaagt cttncagccc 540
 cattgggcca cgcgccgtgg agtttttgtg tgcttaccgg cactttcgca cccagaccaa 600
 actggccgcc gtcggtaaaa cgcgtagagg cgttacgtaa acagcggacg aatccacttc 660
 gtnacaaaac gcttggcgtt ggcataatcg gggtcangat cgcaatcgga gtgtttgtgtg 720
 cccgggttn 729

<210> 30
 <211> 305
 <212> DNA
 <213> Escherichia coli

<400> 30
 agccattgtc cggagaatTT tcgtctttct cgaggggtatt atctgaaagt aactcttctg 60
 agctagagtc ttctatgttt aaatccatag tataattaat ttgggggacg accagataag 120
 cattttcttt ggtattttca taatcttcaa tgattatata cgatgtaatc atatattttt 180
 tctgatgaga attctttcat ctctgttaat ttaattctgt tcaagcaatt gatgattttc 240
 gatgagcttt tatatatTTc ttttgTTaat tcatttttcta atttatctgt aagagttgcc 300

cttgg

305

<210> 31
<211> 425
<212> DNA
<213> Escherichia coli

<400> 31
agggtactgg cgagggtatc gagaaacgcc agactgatac ccataaaaaa gagaataaagg 60
taaaccatcc agcttaatag ctgattaata acttttaacg cagcttggtg gcgaagcgga 120
atgaggtaac ccacaatcag gggaaccaga atgattaaca gccagaaaaa catgaaaacc 180
cagtccttgc aaagatgaag tcgaaatgcg cgatgacaca ctactgaaag cggaaggacg 240
agtaaagttg caattaaaag gaaatgttat gcataaggag cagtagagta ttcgttttca 300
tttaaagata ttcttgcgct ttaattacaa actgcaccga tgttggtggc gtcaaaatcg 360
ccgaggcggt ccctgaaggc cggggcagcc cacatggatg tgggctgagg gcgcgtttta 420
caggg 425

<210> 32
<211> 381
<212> DNA
<213> Escherichia coli

<400> 32
aaaagagaat aaggtaaacc atccagctta atagctgatt aataactttt aacgcagctt 60
gttgcggaag cggaatgagg taaccacaaa tcaggggaac cagaatgatt aacagcccag 120
aaaacatgaa aaccagctcc ttgcaaatgaa gaagtcgaaa tgcgcgatga cacactactg 180
aaagcggaag gacgagtaaa gttgcaatta aaaggaaatg ttatgcataa ggagcagtag 240
agtattcggt ttcatTTaaa gatattcttg cgctttaatt acaaactgca ccgatgttgg 300
tggcgtcaaa atcgccgagg cgttccctga aggccggggc agcccacatg gatgtgggct 360
gagggcgcggt ttacagggga t 381

<210> 33
<211> 329
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(329)
<223> n = A,T,C or G

<400> 33
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gaggtgctta aacgaaaaaac cccgcccggt ttgcccgggc ggggttttgg aatcgtgtgt 120
tgttccagtc cctacggcgc attgccgacg accaccaoca cagcacgac gaccactgcg 180
gcggaatggc gcagttggta gtagttttgc gttgagcatg gaagtagtca ttggggacct 240
tgttggtttt gtgtttaaca atatTTatac aagcacagct ttacagggga gacaatggaa 300
aatttttcag caagggaaaa ttgaggggn 329

<210> 34
<211> 442
<212> DNA
<213> Escherichia coli

<400> 34
gatgttgtgc ccgaacttgc catgtccag tccttttctt ctgggccgac tttccgggag 60
gtgcttaaac gaaaaacccc gcccggttg cgccggcggg gttttggaat cgtgtgttgt 120

tccagtcacct	acggcgccatt	gccgacgacc	accaccacac	gcacgacgac	cactgcggcg	180
gatggcgag	ttggtagtag	ttttgcgtt	agcatggaag	tagtcattgg	ggaccttggt	240
ggttttgtgt	ttacaatat	ttatacaagc	acagctttac	aggggagaca	atggaaaatt	300
tttcagcaag	ggaaaattga	ggggttgatc	acgtttttga	ctgaattgca	gataacaaaa	360
aaccccgccg	gagcgaggtt	tcgtcagtcg	cctgcggctg	gtaaccgcaa	agcacactgt	420
attatgtcaa	cactgaaagt	at				442

<210> 35

<211> 272

<212> DNA

<213> Escherichia coli

<400> 35

cgattatagg	gctgaccaa	tacatggata	gataatatgc	catccccca	ggcagtcac	60
gtaaaaagag	catatacaag	gagaatagaa	cacctacagc	tgtaataaga	taaacataat	120
gttttactct	attaacacct	acgatgaatg	cataagagat	gataaccata	aagacaattt	180
gcttaccagt	attcagtata	attgcaaaga	tgaatacaat	aaaaacaagt	aaagtaaagt	240
ttttacttac	ctttgtatta	gtaaattttt	ta			272

<210> 36

<211> 255

<212> DNA

<213> Escherichia coli

<400> 36

tgcgattacg	gcatgcttat	gatcaggaat	gttaatgcct	gctatacggg	ccactatgca	60
ctcctactat	ttaatatgta	cgttccatgc	tgaaaagccc	gttttcagga	tactcaaagt	120
gaaacgcaca	gacatacaaa	agattggctg	gctaattctag	ccagctcaac	ccaactttgc	180
aagaaaaata	tgcgaaaaaa	tcagccttgg	cgctgtttat	gcttcggctc	ggcactgcaa	240
atcacacgga	tgaca					255

<210> 37

<211> 389

<212> DNA

<213> Escherichia coli

<400> 37

aacgtaaaac	tttacgtaaa	ttaacatggt	taacattttat	gccactattg	tttgtaaatt	60
catatttcgt	aatgcttctg	aatttttcgt	gtgatggttt	taaatactat	ggtgtttact	120
cttgagggga	cggcctattt	ataaaatacg	gacatttcaa	taaatgcccg	tataaacaga	180
gtatgattct	ggctggctcg	tgagtatcaa	tgttgaccg	aatgtgaacg	aataaataat	240
tcgtttat	taccacccat	tctcttttcg	attcgttgct	tgtacgcgta	gatgctacgg	300
atatccatat	ccagaacttc	agcaatctga	tatggattat	aaccagaaac	catatacccc	360
attatggtga	attccatctg	agttaatgt				389

<210> 38

<211> 178

<212> DNA

<213> Escherichia coli

<400> 38

gtggtagga	tctttatagt	tacgctcggc	ggcatccatc	gggatacctg	cggcattttc	60
tttggaacaa	ccgatttcag	aattgtgttt	gtttggatga	acctgaatgg	agagtggctg	120
tgctgcgc	aatactttga	acaggaaagg	cagttcgcca	aagcgtttgg	caacggcc	178

<210> 39

<211> 191

<212> DNA
<213> Escherichia coli

<400> 39
tcgcaaggaa aggcgtcagc gcaaaaacca gctccggctt gtggtttagga tctttatagt 60
tacgctcggc ggcattccatc gggatacctg cggcattttc tttggcaaaa ccgatttcag 120
aattgtgttt gtttgatga acctgaatgg agagtggctg tgctgcgcac aatactttga 180
acaggaaagg c 191

<210> 40
<211> 158
<212> DNA
<213> Escherichia coli

<400> 40
ccggcttgtg gttaggatct ttatagttac gctcggcggc atccatcggg atacctgcgg 60
cattttcttt ggcaaaaccg atttcagaat tgtgtttgtt tggatgaacc tgaatggaga 120
gtggctgtgc tgcgcataat actttgaaca gaaaaggc 158

<210> 41
<211> 184
<212> DNA
<213> Escherichia coli

<400> 41
tcgaagaatt taacggaggg taaaaaaacc gacgcacact ggcgtcggct ctggcaggat 60
gtttcgtaat tagatagcca ccggcgcttt aatgcccga tgcggatcgt agccttcaat 120
ctcaaagtct tcgaaacggt agtcgaagat ggattcgggt ttacgtttga taatcaactt 180
cggc 184

<210> 42
<211> 122
<212> DNA
<213> Escherichia coli

<400> 42
gtagaagttc aaattacgaa cctgaatttt actcggggca gtttcaacca tactcattgc 60
aatcttttcc tcatcgtgcc tgatgcactt cgctaatacag gcttaccgta ggccggatca 120
gg 122

<210> 43
<211> 163
<212> DNA
<213> Escherichia coli

<400> 43
taaattccgc gtatagcgtg ggcgcttttg ctccggctgc ttcgacgagg tccgcaagag 60
aagtcgcttc ataaccgtgt tgccagaaca atttcatggc cttatcaagc gcggcatccc 120
tgtcgaacac ttttggggcg ccacggcttt tttttacaca ttg 163

<210> 44
<211> 161
<212> DNA
<213> Escherichia coli

<400> 44
gcaaattgtt tcgtaattca ggagaaatgg caaataaagc attaaaaatt tgaatgcttt 60

gtgtaataaa aaagcagaca ggcgacggag tgaccactcc gtcgctttac aaagagagga 120
 aaatcatagg ttgccggtgt agtgccagcg taaataacgc a 161

<210> 45
 <211> 251
 <212> DNA
 <213> Escherichia coli

<400> 45
 ggctgtaacg gtaaagccct caccgaagcg agggcttgaa ggagaagggg tatgatgcga 60
 cttgtcatca tactgattgt actgttactc ataagtttca gcgcttatta acagtcagtc 120
 tcaggggagg agcaatcctc ccttaccctt actcactaaa ttaggtcaaa gaatcaacga 180
 tgtcaatcag ggcgatgcgg ttgtatcgcc cttaccactc ccagactttc gacgggtgtaa 240
 ccaccgcagg a 251

<210> 46
 <211> 286
 <212> DNA
 <213> Escherichia coli

<400> 46
 caccgaagcg agggcttgaa ggagaagggg tatgatgcga cttgtcatca tactgattgt 60
 actgttactc ataagtttca gcgcttatta acagtcagtc tcaggggagg agcaatcctc 120
 ccttaccctt actcactaaa ttaggtcaaa gaatcaacga tgtcaatcag ggcgatgcgg 180
 gtgtatcgcc cttaccactc ccagactttc gacgggtgtaa ccaccgcagg aagagggata 240
 tcccactctt caacggggag tttttccacc aactgacaat catgcg 286

<210> 47
 <211> 180
 <212> DNA
 <213> Escherichia coli

<400> 47
 ccggggctga cgtgggcat aatcgggtcg ccaggaatag ggcggcagca tttcgcaaag 60
 gtgatcagca cgccatcggc acctttaatg ggcagatgtc cgtggctttg ggttgccggg 120
 ggaatggagg cgtcccatg ttgcagattt ttcgcgacca ccacgctcat tgcgttacca 180

<210> 48
 <211> 254
 <212> DNA
 <213> Escherichia coli

<400> 48
 tgtcgagcat acgcggcagc gccgactcgg aagatgaagt ccccagtaca atcagcagtt 60
 cttcacggat gtagcggata aatttgaaga tactgaaacc agtcgcttta gcgattgaac 120
 ccaataccag caccacaaac aggatacagg taatgtagaa acagataatc agctgcccc 180
 gttgcaccag tgtgccgacg ccgtatttac cgatggtaaa cgccattgcc ccgaacgcac 240
 caataggtgc caga 254

<210> 49
 <211> 300
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature

[illegible]

```
<400> 53
aaatagaccg gcatactttc gtgcggcagc ataatcaaca gtacgagcgc agcgggtacta 60
atgataaagg tgtagcatag atattttactt ggcgatttca ggatcttadc tgaaatcatg 120
ccaccaatcg gtccaccaat cattttcaga caqt 154
```

<210> 54
 <211> 191
 <212> DNA
 <213> Escherichia coli

<400> 54
 tccttagtca ggtactgacg tacttttaaaa tcgctgtcca ggttgtcagc gaattctttg 60
 gtgttcgcaa accaggtaga gttccatggt tttacaatac ccaggcgaat accattagga 120
 tgtactttct gacccattgc tagtctccag agtctcagcg atcggacaca accacagtga 180
 tgtggctggg g 191

<210> 55
 <211> 190
 <212> DNA
 <213> Escherichia coli

<400> 55
 gctgggtgcc gttttccatg ccagtggggc gacgcgcggc aaggcactat ccggcaaggg 60
 ttgcgcttca tcagccataa tccggcgaat gatccacgcc gcccccgacg acattaaagg 120
 ccgttcaagc agcggatcgt caggctgtaa gcgcaatttg cctgccttgc cgtggcgagc 180
 aaacgcggta 190

<210> 56
 <211> 402
 <212> DNA
 <213> Escherichia coli

<400> 56
 aaaaaatgaa attcctcttt gacggggcaa tagcgatatt ggccatTTTT ttagcgcaac 60
 atttgcgga aattcccttc tccatacagg tgtagtgcac cgaccgcgac cacatatcgc 120
 cccggcgga tggcgcgtaa tttatccgc caggcgagat ttcgctgatg catcagcaca 180
 tcgtacagcg actgactgaa cgtattgggc agcgttatat cattatTTTg cggcggtgca 240
 ttcagccacc agctcatcat ttgttgcagc aaccgtgcgt tggatgcca gtgggtcagc 300
 gtatcgcca gcagcgccag tcctttgtca gggagctgga gcaacatggc aatctggttt 360
 tcagcccctt ccagttcaat cacgggttta tgttgttgc tc 402

<210> 57
 <211> 595
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(595)
 <223> n = A,T,C or G

<400> 57
 aattaatcag agcaacggta aaacaatgaa agtgtaaaaa acacttttgc gccattatg 60
 gagaaaaaaa gaaaatttga tggagagtga tgagagaata ttacaacacg atgattttgc 120
 agagattatg aagaactata ccgatgact ggtgataaat aaagcaaata accaggatta 180
 atctgtatta atttataaga aagcaactta ataccgcgag aatgatttct gcgggtaagt 240
 attagcttat ttttctgagc attaatcccg cgcgtaatcc caacgctacc aacggattag 300
 ggaataacac atactctaca tcatgggtta cggtaaaacg ttcctctccg tcctgcgcca 360
 gcaatgttcc tttctcaaac ggcataaaat tcagcgtgtc acttgccata tgcatttctga 420
 aggacggcga gtggcgagta atttgcgaaa ccacccgata acggagcggc ggtgttctca 480
 cgataccgac actctcacca gatagcagcg cagcaattgc gctggcagtt actgcaaact 540
 ggcgaagatc gttttgcccc aagggaacg ctttgccaag ttncagccgt acang 595

<210> 58
 <211> 250
 <212> DNA
 <213> Escherichia coli

<400> 58
 gaaactcagt ggaatggggg agccgcaata gcgaacatgt tccatgccgc caataatctg 60
 tgcgcggtga atatgcccga gcgcgatgta gtcggctggg ggaaagtgtt gtgccggaaa 120
 cgcgccagc gtgccaatat aaatgtcacg cagggcgta cttttactgg ccccccacgg 180
 cgttaaatgt cccgtggcga tgatgggcag aggtgatcg ccgcgcagtt tgcaggcatc 240
 ggcatagtgt 250

<210> 59
 <211> 236
 <212> DNA
 <213> Escherichia coli

<400> 59
 aaaggttcgg caaaagccat aaccttttcg tcagctttgg ccggataagg gacacattgc 60
 gacgtttcga ccattttata acgggtaaaa ccaccatcaa catgaggaa atacatggca 120
 ctgccaaaaa aacgcatac tgtacactga ttctcgttat gttcaatgca gtatttgag 180
 tgaccgcacg gtttagacg attaatggct accgtttgcc cttcatgtaa ttctga 236

<210> 60
 <211> 92
 <212> DNA
 <213> Escherichia coli

<400> 60
 gaagagatgt tcaggttttc gttatcggca atggtatcga acttgatatt ctcatattc 60
 tcgtcaggcg tggagtacgc cgccgcacg aa 92

<210> 61
 <211> 62
 <212> DNA
 <213> Escherichia coli

<400> 61
 tgtcgacatt cagcatttc ggtattcgt cgccgagggc aaatgtacag gttgaggagg 60
 tg 62

<210> 62
 <211> 72
 <212> DNA
 <213> Escherichia coli

<400> 62
 acttatcaaa ccatttttcc gttcaccgg aggtctgcac ctgagcgatg gtgtcatcca 60
 tcagctttt ga 72

<210> 63
 <211> 66
 <212> DNA
 <213> Escherichia coli

<400> 63

gcaacttgnt ggacagggca aaaaattcct gcctgggctg ccgnatctgn g 531

<210> 68
<211> 102
<212> DNA
<213> Escherichia coli

<400> 68
agcgccggtta acgcccgtta aatgttctcg ttccgcttcc cgatcgttat tcaacaggct 60
gcgtaccgta gcggcatatt tcttccctgc ttcacgcca tc 102

<210> 69
<211> 167
<212> DNA
<213> Escherichia coli

<400> 69
aaaactcacc ttttttggtg ttatccctca attaccacaa gtaaaaggag ataaaccgac 60
aatgacctag acgtaattat gtaaaaatac tgatgttcgt cactgactat ttccgatatt 120
cagctgttga aaaatcaaaa aactggaaaa ataattttaa atatcat 167

<210> 70
<211> 83
<212> DNA
<213> Escherichia coli

<400> 70
gccacgcca gcataaacag cgggatcgag ccttcaatcg gtacgcccag tacacctttc 60
accatcagca ccagcgataa tcc 83

<210> 71
<211> 103
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(103)
<223> n = A,T,C or G

<400> 71
gccnggcggg aaccgacatg ttccactct acgcccgtg gcgcggtttt catttttgcg 60
cacctgatag ccgcacgatt gcagatcaac aacgcctttt ttg 103

<210> 72
<211> 121
<212> DNA
<213> Escherichia coli

<400> 72
tagcttcttc cacattgtcg aactgaacgt ccagacgggtg tttagaaacg ttgatgctcg 60
ggattttttc cgcaccacag caaacgcgcg ccatggctgc aacggtttct gacggatact 120
g 121

<210> 73
<211> 163
<212> DNA

<213> Escherichia coli

<400> 73

```
tagttattgg ctgttttgag aatgtaatct tccaactgct tataactctt cagatgcaat 60
aatccgagaa tcacatgcaa tttattcata aattcgtggg atcgttcacg aagtgcgtca 120
gcatagtga ccagaccgtc gagtcgctgc atcagtttac gta 163
```

<210> 74

<211> 106

<212> DNA

<213> Escherichia coli

<400> 74

```
aaaaccatga ggttattatg gccgatttga ggagggaaaag agtaagagca gtttggttaa 60
tgtacaacga cgattctccc accggggcgcg ttttaaagcg acggtg 106
```

<210> 75

<211> 319

<212> DNA

<213> Escherichia coli

<400> 75

```
ctggagattg agtagatatt cttgttcaga atgtatcagc ccgatgggtc tacgattctt 60
aagccacgaa gagttcagat agtacaacgg catgtctctt ttgactatct ggcaaccggg 120
cagtgtgttc tctcacgcat cacaaaagca gcaggcataa aaaaaccgcg ttgcgcgggt 180
ttttcacaaa gtttcagcaa attggcgatt aagccagttt gttgatctgt gcagtcaggt 240
tagccttatg acgtgcagct ttgtttttgt ggatcaaacc tttagcagcc tgacgggtcca 300
cgatcggttg catttcggt 319
```

<210> 76

<211> 237

<212> DNA

<213> Escherichia coli

<400> 76

```
cgaaccaacg acccccacca tgtcaagggtg gtgctctaac caactgagct atgaacgcaa 60
cgttgtaggt gacaacgggg acgaatatta gcggcagagt gggaagggtg caagaggcaa 120
aacgtaattt tctgcgctat ttcgaccgtt tgcagagctt ttaagcaaatt tggctatatt 180
ttgttgattt gcaagggtga tttttattca ggatcgcatt tacatctgat acaaccc 237
```

<210> 77

<211> 241

<212> DNA

<213> Escherichia coli

<400> 77

```
tgtgacagag tggttatcgt taatcaggca aagagggaaa aacatattat ttaaaccatt 60
atagcgcata aaatatcctt ataattaaca agaaagaaaa ggcatattct ctgcattatc 120
attttctacg actgtcaaaa atcgctcatt ttttaatgag tttatttggt taatattatg 180
ggaaaagggtg atgcatttgg gagaggaaga gtattccccg gtcagacgac cggggaaggg 240
g 241
```

<210> 78

<211> 89

<212> DNA

<213> Escherichia coli

<210> 84
 <211> 632
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(632)
 <223> n = A,T,C or G

<400> 84
 tnnccannnnc nnnnnnnnnn nnnnnnnncn ntncctagan tntcnangtc tncnncnncn 60
 tnnccnnncc cttcnnnncc nnnnnanangn nnnnncccc cnnncccnnt tttgttttgg 120
 aaantccgtt tcaggaanag cttctgaatc ccganccgntt gataactgnn ggccagagtc 180
 ataatgcgca ccaataataa tcagcgggcc atcggcagga ccataatcag caacaatgnn 240
 nnggtagggg ccacccgtaa tggggaccgt cctgcgaggt aactctggca ccgctactga 300
 caaagacctc ttttatatat tctgcgggac ctattcagat tatcaatatt gtcnggcact 360
 acgtggatgc acaagtttgt gtaagataac gaactgnttt ttctaattgc tcaggacttt 420
 gcgtgtcggg gccgttgacg gtaatgcatt gaccaggggt tggtaaaaaa taatcatagg 480
 gagtaaaaac acaataataa taataaaagc caagattatt tttttcatat gcaaaaattat 540
 taatgggggt gcgtttggtg aatcattatn ttgctatggg tttcgatatt gngattttta 600
 ttaaagatta agcangggat tataccaaaa ga 632

<210> 85
 <211> 161
 <212> DNA
 <213> Escherichia coli

<400> 85
 gcgtatttca gcgtaattgg cagcagctgc ggatcgctcat caatcttctc tgacagcggc 60
 tgatgtactt caaccagacg cgcaccgttt ggttcggcag agacttttat cggagtgttg 120
 atgatattca ctttggtgcc tggggtgacc tggctaaaga g 161

<210> 86
 <211> 188
 <212> DNA
 <213> Escherichia coli

<400> 86
 caagggtgag catttgcagc gaatcagaaa gggcgcagaa cagtgaagac aacagaaaaa 60
 cgaccagacc gcatttataa atacgtcgat agccaaacat atcgcccaga aacgaaaacg 120
 agagcagggg gatgacaatg gcgatttgat aggcgttcac taccagatg gaactggctg 180
 gcgtggca 188

<210> 87
 <211> 175
 <212> DNA
 <213> Escherichia coli

<400> 87
 tgagcatttg cagcgaatca gaaagggcgc agaacagtga agacaacaga aaaacgacca 60
 gaccgcattt ataaatacgt cgatagccaa acatatcgcc cagaaacgaa aacgagagca 120
 gggagatgac aatggcgatt tgataggcgt tcactacca gatggaactg gctgg 175

<210> 88
 <211> 194
 <212> DNA

<213> Escherichia coli

<400> 88

cgcaagggtg agcattttgca gcgaatcaga aagggcgag aacagtgaag acaacagaaa 60
aacgaccaga ccgcatttat aaatacgtcg atagccaaac atatcgcca gaaacgaaaa 120
cgagagcagg gagatgacaa tggcgatttg ataggcggtc actaccaga tggaaactggc 180
tggcgtggca tgaa 194

<210> 89

<211> 272

<212> DNA

<213> Escherichia coli

<400> 89

ccttgtataa ggaaagggtt atgatgaagc tcgtcatcat actggttggtg ttgttactgt 60
taagtttccc gacttactaa caactcatca gaggggggag aaatcctccc ttacccttgt 120
tcctttactc taggttgaaa aaacaacagc gtcaataggc ctgccatgta cgaagcgaga 180
tctgtgaacc gctttccggt tagccttttt tatcctgttg gatcttcttg atgatgttg 240
tcgtcgagca accgtcttca aagttgagca cc 272

<210> 90

<211> 245

<212> DNA

<213> Escherichia coli

<400> 90

ccttgtataa ggaaagggtt atgatgaagc tcgtcatcat actggttggtg ttgttactgt 60
taagtttccc gacttactaa caactcatca gaggggggag aaatcctccc ttacccttgt 120
tcctttactc taggttgaaa aaacaacagc gtcaataggc ctgccatgta cgaagcgaga 180
tctgtgaacc gctttccggt tagccttttt tatcctgttg gatcttcttg atgatgttg 240
tcgtc 245

<210> 91

<211> 203

<212> DNA

<213> Escherichia coli

<400> 91

taccaaaaaa agccacgtta tcttggtgat gcaaaagagt gaacgtggcg ttaaagttaa 60
ccagttatat cagtagaaaa cctggttggt gttaacagtc taaccggtca attttttatg 120
atttttttga taaaaattaa attttatttg ctttaatcac caccagatga cgttcgccat 180
ccagggtgga aacctgaagt tta 203

<210> 92

<211> 189

<212> DNA

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)...(189)

<223> n = A,T,C or G

<400> 92

ctaataactt attttctgct taccaaaaaa agccacgtta tcttggtgat gcnaaagagt 60
gaacgtggcg ttaaagttaa cagttatatc agtagaaaac ctggttgntg ntaacagtct 120
aacgggcaat tttttatgat ttttttgata aaaattaaat tttatttgct ttaatcacca 180

ccagatgac

189

<210> 93

<211> 221

<212> DNA

<213> Escherichia coli

<400> 93

agcgcaacag cggaaccag ggtagccagt ttttcatgt tcatattcaa gatgtcctgt 60
agtcgttatt actgcttttt gttgtctacc agcaccgcca gcaaaatcac caccgctttg 120
acgatcatct ggtaatagga ggaaacacct aacaaattca atccattatt aaggaagcca 180
agaattaatg cgccgatcaa cgtcccaaca atgcgacctt t 221

<210> 94

<211> 117

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(117)

<400> 94

atg aaa gtt cgt gct tcc gtc aag aaa tta tgc cgt aac tgc aaa atc 48
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
1 5 10 15

gtt aag cgt gat ggt gtc atc cgt gtg att tgc agt gcc gag ccg aag 96
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
20 25 30

cat aaa cag cgc caa ggc tga 117
His Lys Gln Arg Gln Gly *
35

<210> 95

<211> 1332

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1332)

<400> 95

atg gct aaa caa ccg gga tta gat ttt caa agt gcc aaa ggt ggc tta 48
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
1 5 10 15

ggc gag ctg aaa cgc aga ctg ctg ttt gtt atc ggt gcg ctg att gtg 96
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
20 25 30

ttc cgt att ggc tct ttt att ccg atc cct ggt att gat gcc gct gta 144
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
35 40 45

ctt gcc aaa ctg ctt gag caa cag cga ggc acc atc att gag atg ttt	192
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe	
50 55 60	
aac atg ttc tct ggt ggt gct ctc agc cgt gct tct atc ttt gct ctg	240
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu	
65 70 75 80	
ggg atc atg ccg tat att tcg gcg tcg atc att atc cag ctg ctg acg	288
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr	
85 90 95	
gtg gtt cac cca acg ttg gca gaa att aag aaa gaa ggg gag tct ggt	336
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly	
100 105 110	
cgt cgt aag atc agc cag tac acc cgc tac ggt act ctg gtg ctg gca	384
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala	
115 120 125	
ata ttc cag tcg atc ggt att gct acc ggt ctg ccg aat atg cct ggt	432
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly	
130 135 140	
atg caa ggc ctg gtg att aac ccg ggc ttt gca ttc tac ttc acc gct	480
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala	
145 150 155 160	
gtt gta agt ctg gtc aca gga acc atg ttc ctg atg tgg ttg ggc gaa	528
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu	
165 170 175	
cag att act gaa cga ggt atc ggc aac ggt att tca atc att atc ttc	576
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe	
180 185 190	
gcc ggt att gtc gcg gga ctc ccg cca gcc att gcc cat act atc gag	624
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu	
195 200 205	
caa gcg cgt caa ggc gac ctg cac ttc ctc gtg ttg ctg ttg gtt gca	672
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala	
210 215 220	
gta tta gta ttt gca gtg acg ttc ttt gtt gta ttt gtt gag cgt ggt	720
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly	
225 230 235 240	
caa cgc cgc att gtg gta aac tac gcg aaa cgt cag caa ggt cgt cgt	768
Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg	
245 250 255	
gtc tat gct gca cag agc aca cat tta ccg ctg aaa gtg aat atg gcg	816
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala	
260 265 270	

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ggg gta atc ccg gca atc ttc gct tcc agt att att ctg ttc ccg gcg 864
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala
      275                      280                      285

acc atc gcg tca tgg ttc ggg ggc ggt act ggt tgg aac tgg ctg aca 912
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr
      290                      295                      300

aca att tcg ctg tat ttg cag cct ggg caa ccg ctt tat gtg tta ctc 960
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu
      305                      310                      315

tat gcg tct gca atc atc ttc ttc tgt ttc ttc tac acg gcg ttg gtt 1008
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val
      325                      330                      335

ttc aac ccg cgt gaa aca gca gat aac ctg aag aag tcc ggt gca ttt 1056
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe
      340                      345                      350

gta cca gga att cgt ccg gga gag caa acg gcg aag tat atc gat aaa 1104
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys
      355                      360                      365

gta atg acc cgc ctg acc ctg gtt ggt gcg ctg tat att acc ttt atc 1152
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile
      370                      375                      380

tgc ctg atc ccg gag ttc atg cgt gat gca atg aaa gta ccg ttc tac 1200
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr
      385                      390                      395                      400

ttc ggt ggg acc tca ctg ctt atc gtt gtt gtc gtg att atg gac ttt 1248
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe
      405                      410                      415

atg gct caa gtg caa act ctg atg atg tcc agt cag tat gag tct gca 1296
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala
      420                      425                      430

ttg aag aag gcg aac ctg aaa ggc tac ggc cga taa 1332
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg *
      435                      440

```

<210> 96
 <211> 435
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(435)

<400> 96
 atg cgt tta aat act ctg tct ccg gcc gaa ggc tcc aaa aag gcg ggt 48
 Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly

1	5	10	15	
aaa cgc ctg ggt cgt ggt atc ggt tct ggc ctc ggt aaa acc ggt ggt				96
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly	20	25	30	
cgt ggt cac aaa ggt cag aag tct cgt tct ggc ggt ggc gta cgt cgc				144
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Gly Val Arg Arg	35	40	45	
ggt ttc gag ggt ggt cag atg cct ctg tac cgt cgt ctg ccg aaa ttc				192
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe	50	55	60	
ggc ttc act tct cgt aaa gca gcg att aca gcc gaa att cgt ctg tct				240
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser	65	70	75	80
gac ctg gct aaa gta gaa ggc ggt gta gta gac ctg aac acg ctg aaa				288
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys	85	90	95	
gcg gct aac att atc ggt atc cag atc gag ttc gcg aaa gtg atc ctg				336
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu	100	105	110	
gct ggc gaa gta acg act ccg gta act gtt cgt ggc ctg cgt gtt act				384
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr	115	120	125	
aaa ggc gct cgt gct gct atc gaa gct gct ggc ggt aaa atc gag gaa				432
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu	130	135	140	
taa				435

*

<210> 97
 <211> 180
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(180)

<400> 97															
atg gca aag act att aaa att act caa acc cgc agt gca atc ggt cgt															48
Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg															
1			5				10						15		
ctg ccg aaa cac aag gca acg ctg ctt ggc ctg ggt ctg cgt cgt att															96
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile															
		20					25						30		

ggt cac acc gta gag cgc gag gat act cct gct att cgc ggt atg atc 144
 Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
 35 40 45

aac gcg gtt tcc ttc atg gtt aaa gtt gag gag taa 180
 Asn Ala Val Ser Phe Met Val Lys Val Glu Glu *
 50 55

<210> 98
 <211> 504
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(504)

<400> 98
 atg gct cac atc gaa aaa caa gct ggc gaa ctg cag gaa aag ctg atc 48
 Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
 1 5 10 15

gcg gta aac cgc gta tct aaa acc gtt aaa ggt ggt cgt att ttc tcc 96
 Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
 20 25 30

ttc aca gct ctg act gta gtt ggc gat ggt aac ggt cgc gtt ggt ttt 144
 Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
 35 40 45

ggt tac ggt aaa gcg cgt gaa gtt cca gca gcg atc cag aaa gcg atg 192
 Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
 50 55 60

gaa aaa gcc cgt cgc aat atg att aac gtc gcg ctg aat aac ggc act 240
 Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
 65 70 75 80

ctg caa cac cct gtt aaa ggt gtt cac acg ggt tct cgc gta ttc atg 288
 Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
 85 90 95

cag ccg gct tcc gaa ggt acc ggt atc atc gcc ggt ggt gca atg cgc 336
 Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
 100 105 110

gcc gtt ctg gaa gtc gct ggg gtt cat aac gtt ctg gct aaa gcc tat 384
 Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
 115 120 125

ggt tcc acc aac ccg atc aac gtg gtt cgt gca act att gat ggc ctg 432
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
 130 135 140

gaa aat atg aat tct cca gaa atg gtc gct gcc aag cgt ggt aaa tcc 480
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser

145 150 155 160

gtt gaa gaa att ctg ggg aaa taa 504
 Val Glu Glu Ile Leu Gly Lys *
 165

<210> 99
 <211> 354
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(354)

<400> 99

atg gat aag aaa tct gct cgt atc cgt cgt gcg acc cgc gca cgc cgc	48
Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg	
1 5 10 15	
aag ctc cag gag ctg ggc gca act cgc ctg gtg gta cat cgt acc ccg	96
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro	
20 25 30	
cgt cac att tac gca cag gta att gca ccg aac ggt tct gaa gtt ctg	144
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu	
35 40 45	
gta gct gct tct act gta gaa aaa gct atc gct gaa caa ctg aag tac	192
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr	
50 55 60	
acc ggt aac aaa gac gcg gct gca gct gtg ggt aaa gct gtc gct gaa	240
Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu	
65 70 75 80	
cgc gct ctg gaa aaa ggc atc aaa gat gta tcc ttt gac cgt tcc ggg	288
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly	
85 90 95	
ttc caa tat cat ggt cgt gtc cag gca ctg gca gat gct gcc cgt gaa	336
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu	
100 105 110	
gct ggc ctt cag ttc taa	354
Ala Gly Leu Gln Phe *	
115	

<210> 100
 <211> 534
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS

<222> (1)...(534)

<400> 100

atg tct cgt gtt gct aaa gca ccg gtc gtt gtt cct gcc ggc gtt gac 48
Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
1 5 10 15

gta aaa atc aac ggt cag gtt att acg atc aaa ggt aaa aac ggc gag 96
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
20 25 30

ctg act cgt act ctc aac gat gct gtt gaa gtt aaa cat gca gat aat 144
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
35 40 45

acc ctg acc ttc ggt ccg cgt gat ggt tac gca gac ggt tgg gca cag 192
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
50 55 60

gct ggt acc gcg cgt gcc ctg ctg aac tca atg gtt atc ggt gtt acc 240
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
65 70 75 80

gaa ggc ttc act aag aag ctg cag ctg gtt ggt gta ggt tac cgt gca 288
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
85 90 95

gcg gtt aaa ggc aat gtg att aac ctg tct ctg ggt ttc tct cat cct 336
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
100 105 110

gtt gac cat cag ctg cct gcg ggt atc act gct gaa tgt ccg act cag 384
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
115 120 125

act gaa atc gtg ctg aaa ggc gct gat aag cag gtg atc ggc cag gtt 432
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val
130 135 140

gca gcg gat ctg cgc gcc tac cgt cgt cct gag cct tat aaa ggc aag 480
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145 150 155 160

ggt gtt cgt tac gcc gac gaa gtc gtg cgt acc aaa gag gct aag aag 528
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165 170 175

aag taa 534
Lys *

<210> 101

<211> 393

<212> DNA

<213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(393)

<400> 101

atg agc atg caa gat ccg atc gcg gat atg ctg acc cgt atc cgt aac	48
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn	
1 5 10 15	
ggt cag gcc gcg aac aaa gct gcg gtc acc atg cct tcc tcc aag ctg	96
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu	
20 25 30	
aaa gtg gca atc gcc aac gtg ctg aag gaa gaa ggt ttt att gaa gat	144
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp	
35 40 45	
ttt aaa gtt gaa ggc gac acc aag cct gaa ctg gaa ctt act ctg aag	192
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys	
50 55 60	
tat ttc cag ggc aaa gct gtt gta gaa agc att cag cgt gtc agc cgc	240
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg	
65 70 75 80	
cca ggt ctg cgc atc tat aaa cgt aaa gat gag ctg ccg aaa gtt atg	288
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met	
85 90 95	
gcg ggt ctg ggt atc gca gtt gtt tct acc tct aaa ggt gtt atg act	336
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr	
100 105 110	
gat cgt gca gcg cgc cag gct ggt ctt ggt ggc gaa att atc tgc tac	384
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr	
115 120 125	
gta gcc taa	393
Val Ala *	
130	

<210> 102
 <211> 306
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(306)

<400> 102

atg gct aag caa tca atg aaa gca cgc gaa gta aaa cgc gta gct tta	48
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu	
1 5 10 15	
gct gat aaa tac ttc gcg aaa cgc gct gaa ctg aaa gcg atc atc tct	96

Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser	
20 25 30	
gat gtg aac gct tcc gac gaa gat cgt tgg aac gct gtt ctc aag ctg	144
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu	
35 40 45	
cag act ctg ccg cgt gat tcc agc ccg tct cgt cag cgt aac cgc tgc	192
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys	
50 55 60	
cgt caa aca ggt cgt ccg cat ggt ttc ctg cgg aag ttc ggg ttg agc	240
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser	
65 70 75 80	
cgt att aag gtc cgt gaa gcc gct atg cgc ggt gaa atc ccg ggt ctg	288
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu	
85 90 95	
aaa aag gct agc tgg taa	306
Lys Lys Ala Ser Trp *	
100	

<210> 103
 <211> 540
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(540)

<400> 103	
atg gcg aaa ctg cat gat tac tac aaa gac gaa gta gtt aaa aaa ctc	48
Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu	
1 5 10 15	
atg act gag ttt aac tac aat tct gtc atg caa gtc cct cgg gtc gag	96
Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu	
20 25 30	
aag atc acc ctg aac atg ggt gtt ggt gaa gcg atc gct gac aaa aaa	144
Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys	
35 40 45	
ctg ctg gat aac gca gca gca gac ctg gca gca atc tcc ggt caa aaa	192
Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys	
50 55 60	
ccg ctg atc acc aaa gca cgc aaa tct gtt gca ggc ttc aaa atc cgt	240
Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg	
65 70 75 80	
cag ggc tat ccg atc ggc tgt aaa gta act ctg cgt ggc gaa cgc atg	288
Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met	
85 90 95	

tgg	gag	ttc	ttt	gag	cgc	ctg	atc	act	att	gct	gta	cct	cgt	atc	cgt	336
Trp	Glu	Phe	Phe	Glu	Arg	Leu	Ile	Thr	Ile	Ala	Val	Pro	Arg	Ile	Arg	
			100					105					110			

gac	ttc	cgt	ggc	ctg	tcc	gct	aag	tct	ttc	gac	ggg	cgt	ggg	aac	tac	384
Asp	Phe	Arg	Gly	Leu	Ser	Ala	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr	
		115					120					125				

agc	atg	ggg	gtc	cgt	gag	cag	atc	atc	ttc	cca	gaa	atc	gac	tac	gat	432
Ser	Met	Gly	Val	Arg	Glu	Gln	Ile	Ile	Phe	Pro	Glu	Ile	Asp	Tyr	Asp	
	130					135					140					

aaa	gtc	gac	cgc	gtt	cgt	ggg	ttg	gat	att	acc	att	acc	act	act	gcg	480
Lys	Val	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ile	Thr	Ile	Thr	Thr	Thr	Ala	
145					150					155					160	

aaa	tct	gac	gaa	gaa	ggc	cgc	gct	ctg	ctg	gct	gcc	ttt	gac	ttc	ccg	528
Lys	Ser	Asp	Glu	Glu	Gly	Arg	Ala	Leu	Leu	Ala	Ala	Phe	Asp	Phe	Pro	
			165					170						175		

ttc	cgc	aag	taa													540
Phe	Arg	Lys	*													

<210> 104
 <211> 315
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(315)

<400>	104															
atg	gca	gcg	aaa	atc	cgt	cgt	gat	gac	gaa	gtt	atc	gtg	tta	acc	ggg	48
Met	Ala	Ala	Lys	Ile	Arg	Arg	Asp	Asp	Glu	Val	Ile	Val	Leu	Thr	Gly	
1				5					10				15			

aaa	gat	aaa	ggg	aaa	cgc	ggg	aaa	gtt	aag	aat	gtc	ctg	tct	tcc	ggc	96
Lys	Asp	Lys	Gly	Lys	Arg	Gly	Lys	Val	Lys	Asn	Val	Leu	Ser	Ser	Gly	
			20					25				30				

aag	gtc	att	gtt	gaa	ggg	atc	aac	ctg	gtt	aag	aaa	cat	cag	aag	ccg	144
Lys	Val	Ile	Val	Glu	Gly	Ile	Asn	Leu	Val	Lys	Lys	His	Gln	Lys	Pro	
		35					40					45				

gtt	ccg	gcc	ctg	aac	caa	ccg	ggg	ggc	atc	gtt	gaa	aaa	gaa	gcc	gct	192
Val	Pro	Ala	Leu	Asn	Gln	Pro	Gly	Gly	Ile	Val	Glu	Lys	Glu	Ala	Ala	
	50					55					60					

att	cag	gtt	tcc	aac	gta	gca	atc	ttc	aat	gcg	gca	acc	ggc	aag	gct	240
Ile	Gln	Val	Ser	Asn	Val	Ala	Ile	Phe	Asn	Ala	Ala	Thr	Gly	Lys	Ala	
	65				70				75						80	

gac	cgt	gta	ggc	ttt	aga	ttc	gaa	gac	ggg	aaa	aaa	gtc	cgt	ttc	ttc	288
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
85 90 95

aag tct aac agc gaa act atc aag taa 315
Lys Ser Asn Ser Glu Thr Ile Lys *
100

<210> 105
<211> 372
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(372)

<400> 105
atg atc caa gaa cag act atg ctg aac gtc gcc gac aac tcc ggt gca 48
Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
1 5 10 15

cgt cgc gta atg tgt atc aag gtt ctg ggt ggc tcg cac cgt cgc tac 96
Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
20 25 30

gca ggc gta ggc gac atc atc aag atc acc atc aaa gaa gca att ccg 144
Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
35 40 45

cgt ggt aag gtc aaa aaa ggt gat gtg ctg aag gcg gta gtg gtg cgc 192
Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
50 55 60

acc aag aag ggt gtt cgt cgc ccg gac ggt tct gtc att cgc ttc gat 240
Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
65 70 75 80

ggt aat gct tgt gtt ctt ctg aac aac aac agc gag cag cct atc ggt 288
Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
85 90 95

acg cgt att ttt ggg ccg gta act cgt gag ctt cgt agt gag aag ttc 336
Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
100 105 110

atg aaa att atc tct ctg gca cca gaa gta ctc taa 372
Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu *
115 120

<210> 106
<211> 1458
<212> DNA
<213> Escherichia coli

<220>

<221> CDS
 <222> (1)...(1458)

<400> 106

gtg gga att tat ttt act aat tca gat gat caa att tac ttt aaa agg	48
Met Gly Ile Tyr Phe Thr Asn Ser Asp Asp Gln Ile Tyr Phe Lys Arg	
1 5 10 15	
agt gaa ggg atg tct gat ata aac cat gca ggt tct gac ctt ata ttt	96
Ser Glu Gly Met Ser Asp Ile Asn His Ala Gly Ser Asp Leu Ile Phe	
20 25 30	
gaa ctg gag gat cgc cct ccc ttt cat cag gct ctc gtt ggt gcc att	144
Glu Leu Glu Asp Arg Pro Pro Phe His Gln Ala Leu Val Gly Ala Ile	
35 40 45	
acc cat ctg ttg gca att ttc gtt ccg atg gta acc ccc gcg tta atc	192
Thr His Leu Leu Ala Ile Phe Val Pro Met Val Thr Pro Ala Leu Ile	
50 55 60	
gtg ggt gcg gcc tta cag ctt tcc gct gaa aca act gcc tat ctt gtt	240
Val Gly Ala Ala Leu Gln Leu Ser Ala Glu Thr Thr Ala Tyr Leu Val	
65 70 75 80	
tct atg gcg atg atc gcc tct ggt att ggt acc tgg tta caa gta aac	288
Ser Met Ala Met Ile Ala Ser Gly Ile Gly Thr Trp Leu Gln Val Asn	
85 90 95	
cgc tac ggc atc gtc ggt tct ggc cta ctc tca att cag tca gtc aat	336
Arg Tyr Gly Ile Val Gly Ser Gly Leu Leu Ser Ile Gln Ser Val Asn	
100 105 110	
ttt tca ttt gtt acg gtc atg att gcg ctg ggc agc agc atg aaa agc	384
Phe Ser Phe Val Thr Val Met Ile Ala Leu Gly Ser Ser Met Lys Ser	
115 120 125	
gac ggt ttt cac gaa gag tta atc atg tcg tcg ctt ctc ggc gtc tcc	432
Asp Gly Phe His Glu Glu Leu Ile Met Ser Ser Leu Leu Gly Val Ser	
130 135 140	
ttc gtt ggc gca ttt ctg gtt gtc gga tct tca ttt atc ttg ccc tat	480
Phe Val Gly Ala Phe Leu Val Val Gly Ser Ser Phe Ile Leu Pro Tyr	
145 150 155 160	
tta cgt cgg gtt att acg cct acc gtc agc ggt att gtg gta ctg atg	528
Leu Arg Arg Val Ile Thr Pro Thr Val Ser Gly Ile Val Val Leu Met	
165 170 175	
atc ggc tta agc ctg att aaa gtc ggc att atc gat ttt ggt gga gga	576
Ile Gly Leu Ser Leu Ile Lys Val Gly Ile Ile Asp Phe Gly Gly Gly	
180 185 190	
ttt gca gcc aaa agc agc ggt acg ttc ggc aat tac gaa cat ctc ggc	624
Phe Ala Ala Lys Ser Ser Gly Thr Phe Gly Asn Tyr Glu His Leu Gly	
195 200 205	
gtt ggt tta ttg gtt tta att gtg gtg atc ggc ttt aac tgc tgt cgc	672

Arg	Leu	Ser	Ala	Tyr	Glu	Ala	Phe	Tyr	Leu	Ala	Thr	Leu	Gly	Gly	Ala	
	355						360					365				
aaa	tct	ctg	ggc	ctt	gac	gat	ttg	att	ggc	aac	ttt	tta	cct	ggc	aaa	1152
Lys	Ser	Leu	Gly	Leu	Asp	Asp	Leu	Ile	Gly	Asn	Phe	Leu	Pro	Gly	Lys	
	370					375				380						
gag	gct	gat	ttc	gtg	gtg	atg	gaa	ccc	acc	gcc	act	ccg	cta	cag	cag	1200
Glu	Ala	Asp	Phe	Val	Val	Met	Glu	Pro	Thr	Ala	Thr	Pro	Leu	Gln	Gln	
	385				390					395					400	
ctg	cgc	tat	gac	aac	tct	gtt	tct	tta	gtc	gac	aaa	ttg	ttc	gtg	atg	1248
Leu	Arg	Tyr	Asp	Asn	Ser	Val	Ser	Leu	Val	Asp	Lys	Leu	Phe	Val	Met	
				405					410					415		
atg	acg	ttg	ggc	gat	gac	cgt	tcg	atc	tac	cgc	acc	tac	gtt	gat	ggc	1296
Met	Thr	Leu	Gly	Asp	Asp	Arg	Ser	Ile	Tyr	Arg	Thr	Tyr	Val	Asp	Gly	
			420					425					430			
cgt	ctg	gtg	tac	gaa	cgc	aac	taa									1320
Arg	Leu	Val	Tyr	Glu	Arg	Asn	*									
			435													

<210> 108
 <211> 570
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(570)

<400>	108															
atg	tct	gga	gac	atc	cta	caa	aca	ccg	gac	gca	cca	aag	cca	cag	ggc	48
Met	Ser	Gly	Asp	Ile	Leu	Gln	Thr	Pro	Asp	Ala	Pro	Lys	Pro	Gln	Gly	
	1				5				10					15		
gcg	ctg	gat	aat	tat	ttt	aaa	att	acc	gct	cgt	ggc	agt	acc	gtt	cgt	96
Ala	Leu	Asp	Asn	Tyr	Phe	Lys	Ile	Thr	Ala	Arg	Gly	Ser	Thr	Val	Arg	
		20						25					30			
cag	gaa	gta	ctg	gct	ggc	tta	acg	acc	ttt	ctg	gcc	atg	gtt	tat	tcc	144
Gln	Glu	Val	Leu	Ala	Gly	Leu	Thr	Thr	Phe	Leu	Ala	Met	Val	Tyr	Ser	
		35					40					45				
gtt	atc	gtc	gtt	ccg	gga	atg	ctg	ggc	aaa	gca	ggc	ttt	cct	ccc	gca	192
Val	Ile	Val	Val	Pro	Gly	Met	Leu	Gly	Lys	Ala	Gly	Phe	Pro	Pro	Ala	
	50					55					60					
gct	gtg	ttt	gtt	gcc	acc	tgt	ctg	gtc	gcg	ggc	ttc	ggc	tcg	ttg	ctg	240
Ala	Val	Phe	Val	Ala	Thr	Cys	Leu	Val	Ala	Gly	Phe	Gly	Ser	Leu	Leu	
	65				70				75						80	
atg	gga	tta	tgg	gct	aat	ttg	cca	atg	gcg	att	ggc	tgc	gcg	att	tcc	288
Met	Gly	Leu	Trp	Ala	Asn	Leu	Pro	Met	Ala	Ile	Gly	Cys	Ala	Ile	Ser	
				85					90					95		

cag cca act gta ctt ccg agt gta ctg gca ttg gtg atg acc gca gtg	288
Gln Pro Thr Val Leu Pro Ser Val Leu Ala Leu Val Met Thr Ala Val	
85 90 95	
ttc gac gct act ggc acc atc cgt gcc gtc gcc ggt cag gcg aat ttg	336
Phe Asp Ala Thr Gly Thr Ile Arg Ala Val Ala Gly Gln Ala Asn Leu	
100 105 110	
ttg gat aaa gac aac cag atc atc aac ggc ggc aaa gcc ctg acc agt	384
Leu Asp Lys Asp Asn Gln Ile Ile Asn Gly Gly Lys Ala Leu Thr Ser	
115 120 125	
gac tca gta agt tca ata ttc tcc ggc ctg gtg ggc gca gcg ccc gca	432
Asp Ser Val Ser Ser Ile Phe Ser Gly Leu Val Gly Ala Ala Pro Ala	
130 135 140	
gcg gtt tat atc gaa tca gcg gca gga acc gcc gcc ggg ggt aaa aca	480
Ala Val Tyr Ile Glu Ser Ala Ala Gly Thr Ala Ala Gly Gly Lys Thr	
145 150 155 160	
ggg tta acc gca acc gta gtg ggg gcg tta ttc ctg tta att ctg ttt	528
Gly Leu Thr Ala Thr Val Val Gly Ala Leu Phe Leu Leu Ile Leu Phe	
165 170 175	
tta tca ccg ctg tca ttt ttg atc cct ggt tac gcc act gca ccc gct	576
Leu Ser Pro Leu Ser Phe Leu Ile Pro Gly Tyr Ala Thr Ala Pro Ala	
180 185 190	
ctg atg tac gta ggt ttg ctg atg tta agt aac gtc tcg aag ctg gat	624
Leu Met Tyr Val Gly Leu Leu Met Leu Ser Asn Val Ser Lys Leu Asp	
195 200 205	
ttc aat gat ttt att gac gct atg gct ggc ctg gtg tgt gcc gtg ttc	672
Phe Asn Asp Phe Ile Asp Ala Met Ala Gly Leu Val Cys Ala Val Phe	
210 215 220	
atc gtt ctg act tgt aat atc gtt acc ggt att atg ctg ggc ttt gtg	720
Ile Val Leu Thr Cys Asn Ile Val Thr Gly Ile Met Leu Gly Phe Val	
225 230 235 240	
aca ctg gtc gta ggc cgc gtc ttt gca cgc gaa tgg caa aag ctg aat	768
Thr Leu Val Val Gly Arg Val Phe Ala Arg Glu Trp Gln Lys Leu Asn	
245 250 255	
att ggt acg gtg atc att act gcc gca ctg gtc gca ttt tac gcg ggt	816
Ile Gly Thr Val Ile Ile Thr Ala Ala Leu Val Ala Phe Tyr Ala Gly	
260 265 270	
ggg tgg gca atc taa	831
Gly Trp Ala Ile *	
275	

<210> 110
 <211> 1401
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1401)

<400> 110

atg aat agc gaa ggg ggg aaa ccg ggg aat gta ctg acc gtt aac ggc	48
Met Asn Ser Glu Gly Gly Lys Pro Gly Asn Val Leu Thr Val Asn Gly	
1 5 10 15	
aac tat acc gga aac aat ggc ctg atg acg ttc aac gcg acg ctg ggc	96
Asn Tyr Thr Gly Asn Asn Gly Leu Met Thr Phe Asn Ala Thr Leu Gly	
20 25 30	
ggc gat aat tcg ccc acc gat aag atg aac gtg aaa ggc gat acc caa	144
Gly Asp Asn Ser Pro Thr Asp Lys Met Asn Val Lys Gly Asp Thr Gln	
35 40 45	
ggg aac act cgc gtt cgg gtt gat aac att ggc ggc gtc ggt gca caa	192
Gly Asn Thr Arg Val Arg Val Asp Asn Ile Gly Gly Val Gly Ala Gln	
50 55 60	
acg gtc aac ggt att gaa ctc att gag gtt ggc ggt aat tct gca ggt	240
Thr Val Asn Gly Ile Glu Leu Ile Glu Val Gly Gly Asn Ser Ala Gly	
65 70 75 80	
aac ttc gcg ctg acc acc gga act gtc gaa gct ggg gct tac gtc tac	288
Asn Phe Ala Leu Thr Thr Gly Thr Val Glu Ala Gly Ala Tyr Val Tyr	
85 90 95	
acg ctg gct aaa ggg aag ggg aat gac gag aaa aac tgg tat ctg acc	336
Thr Leu Ala Lys Gly Lys Gly Asn Asp Glu Lys Asn Trp Tyr Leu Thr	
100 105 110	
agt aaa tgg gac ggc gta acg cca gcg gat aca ccc gat ccc atc aat	384
Ser Lys Trp Asp Gly Val Thr Pro Ala Asp Thr Pro Asp Pro Ile Asn	
115 120 125	
aat ccc cct gtt gtg gat ccg gaa ggc cca tca gtt tat cgc ccg gag	432
Asn Pro Pro Val Val Asp Pro Glu Gly Pro Ser Val Tyr Arg Pro Glu	
130 135 140	
gcc gga agc tat atc agc aac att gcc gca gcc aac tcg ctg ttt agc	480
Ala Gly Ser Tyr Ile Ser Asn Ile Ala Ala Ala Asn Ser Leu Phe Ser	
145 150 155 160	
cat cgt tta cac gac cgt ctg ggt gag ccg cag tat aca gat tca ctg	528
His Arg Leu His Asp Arg Leu Gly Glu Pro Gln Tyr Thr Asp Ser Leu	
165 170 175	
cat tct cag ggg tcg gca agc agt atg tgg atg cgt cat gtc gga ggc	576
His Ser Gln Gly Ser Ala Ser Ser Met Trp Met Arg His Val Gly Gly	
180 185 190	
cac gaa cgt tca agg gcc ggt gac ggt cag cta aat act cag gct aac	624
His Glu Arg Ser Arg Ala Gly Asp Gly Gln Leu Asn Thr Gln Ala Asn	
195 200 205	

aaa gta aat aac aac ctt agc ctg tgg ggg aat gtc ggt gtg caa cta	1344
Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu	
435 440 445	

ggt gat aaa ggc tat agc gat act cag ggc atg ctg gga gtg aaa tat	1392
Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr	
450 455 460	

agc tgg taa	1401
Ser Trp *	
465	

<210> 111
 <211> 3978
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(3978)

<400> 111	
atg aat aga atc tat cgc gtg ata tgg aat tgc act cta cag gta ttt	48
Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe	
1 5 10 15	

cag gcc tgc tgc gaa tta act cgc agg gca ggt aaa aca tgc acg gtt	96
Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val	
20 25 30	

aat ttg cgt aaa tcc tct gga ctg aca acg aaa ttc agt aga ttg acg	144
Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr	
35 40 45	

ctg ggt gtt ttg ctg gca cta agc ggt tca gcg tct ggt gca agt ctg	192
Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu	
50 55 60	

gaa gtt gat aat gat cag att acc aat att gat act gat gtt gct tat	240
Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr	
65 70 75 80	

gat gcc tac ctg gtt ggc tgg tat ggc act gga gtg ctt aat att ttg	288
Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu	
85 90 95	

gct ggc ggt aat gcc tcc tta acc act att act acc agc gtc att ggc	336
Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly	
100 105 110	

gct aat gag gac tca gag ggc acc gtt aat gtt ttg ggt ggc acc tgg	384
Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp	
115 120 125	

cga ttg tat gat agc gga aat aat gca agg cct tta aat gtg ggt caa	432
Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln	

1045	1050	1055	
gat ggt gca ctt ggc aac acc cgg gaa ctg aac atc agc aac gcg gcc			3216
Asp Gly Ala Leu Gly Asn Thr Arg Glu Leu Asn Ile Ser Asn Ala Ala			
1060	1065	1070	
atc gtc gat ctt aat gga tgc acg cag acg gta gag aca ttc acc ggg			3264
Ile Val Asp Leu Asn Gly Ser Thr Gln Thr Val Glu Thr Phe Thr Gly			
1075	1080	1085	
cag atg ggt tgc act gtt ttg ttc aaa gag ggg gcg ctg acg gta aat			3312
Gln Met Gly Ser Thr Val Leu Phe Lys Glu Gly Ala Leu Thr Val Asn			
1090	1095	1100	
aaa ggt ggg atc agt cag ggt gaa ctg aca ggt ggc gga aac ctg aat			3360
Lys Gly Gly Ile Ser Gln Gly Glu Leu Thr Gly Gly Gly Asn Leu Asn			
1105	1110	1115	1120
gtt aca ggg gga acg ctg gct atc gag ggg ctt aat gca cgc tac aat			3408
Val Thr Gly Gly Thr Leu Ala Ile Glu Gly Leu Asn Ala Arg Tyr Asn			
1125	1130	1135	
gcg tta acc agc att agc cca aat gcg gaa gtc agc ctc gat aat act			3456
Ala Leu Thr Ser Ile Ser Pro Asn Ala Glu Val Ser Leu Asp Asn Thr			
1140	1145	1150	
cag ggg tta ggc aga gga aat att gcc aat gac ggt ctg tta acg cta			3504
Gln Gly Leu Gly Arg Gly Asn Ile Ala Asn Asp Gly Leu Leu Thr Leu			
1155	1160	1165	
aaa aac gtg act ggc gaa ctg cgt aat agc ata agc ggg aag ggt atc			3552
Lys Asn Val Thr Gly Glu Leu Arg Asn Ser Ile Ser Gly Lys Gly Ile			
1170	1175	1180	
gtg agc gca acc gcc agg aca gat gta gag ttg gat ggc gat aat agc			3600
Val Ser Ala Thr Ala Arg Thr Asp Val Glu Leu Asp Gly Asp Asn Ser			
1185	1190	1195	1200
cgc ttt gtg ggg caa ttc aac att gat aca ggc agc gcg ctc agc gtc			3648
Arg Phe Val Gly Gln Phe Asn Ile Asp Thr Gly Ser Ala Leu Ser Val			
1205	1210	1215	
aac gag cag aaa aac ctg ggt gat gct tcc gtt atc aat aat ggc ctg			3696
Asn Glu Gln Lys Asn Leu Gly Asp Ala Ser Val Ile Asn Asn Gly Leu			
1220	1225	1230	
ctc acc atc tcc act gag cgt agc tgg gcg atg acg cac agt atc agc			3744
Leu Thr Ile Ser Thr Glu Arg Ser Trp Ala Met Thr His Ser Ile Ser			
1235	1240	1245	
ggg agc ggt gat gtg aca aaa ctg ggt acc ggg atc ctg act ctt aac			3792
Gly Ser Gly Asp Val Thr Lys Leu Gly Thr Gly Ile Leu Thr Leu Asn			
1250	1255	1260	
aac gat tcc gcg gcg tat cag ggt acg acg gat atc gtg ggg ggg gaa			3840
Asn Asp Ser Ala Ala Tyr Gln Gly Thr Thr Asp Ile Val Gly Gly Glu			
1265	1270	1275	1280

att gct ttc ggt tcc gac tct gcc att aat atg gca agt caa cac att	3888
Ile Ala Phe Gly Ser Asp Ser Ala Ile Asn Met Ala Ser Gln His Ile	
1285 1290 1295	
aat atc cat aac agc ggt gtg atg tcg gga aat gtc acc act gca ggt	3936
Asn Ile His Asn Ser Gly Val Met Ser Gly Asn Val Thr Thr Ala Gly	
1300 1305 1310	
gat atg aac gtt atg cct ggg ggg ggc act gcg tgt cgc taa	3978
Asp Met Asn Val Met Pro Gly Gly Gly Thr Ala Cys Arg *	
1315 1320 1325	

<210> 112
 <211> 756
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(756)

<400> 112	
atg act gaa gca caa aga cat caa atc ctc ctg gaa atg ctc gca caa	48
Met Thr Glu Ala Gln Arg His Gln Ile Leu Leu Glu Met Leu Ala Gln	
1 5 10 15	
ttg ggc ttt gtg acc gtt gag aaa gtc gtt gag cgt ctg gga att tcg	96
Leu Gly Phe Val Thr Val Glu Lys Val Val Glu Arg Leu Gly Ile Ser	
20 25 30	
cct gcc act gcg cga cgc gat atc aat aaa ctt gac gaa agc ggc aaa	144
Pro Ala Thr Ala Arg Arg Asp Ile Asn Lys Leu Asp Glu Ser Gly Lys	
35 40 45	
ctg aaa aaa gtg cgc aat ggc gca gaa gct att acc caa cag cgc ccg	192
Leu Lys Lys Val Arg Asn Gly Ala Glu Ala Ile Thr Gln Gln Arg Pro	
50 55 60	
cgc tgg acg ccg atg aat ctg cat cag gcg cag aat cac gat gaa aaa	240
Arg Trp Thr Pro Met Asn Leu His Gln Ala Gln Asn His Asp Glu Lys	
65 70 75 80	
gta cgt atc gct aaa gcg gcc tcg cag ctg gtt aat ccg ggc gaa agc	288
Val Arg Ile Ala Lys Ala Ala Ser Gln Leu Val Asn Pro Gly Glu Ser	
85 90 95	
gta gtc atc aac tgc ggc tcc acc gcg ttt ctg ctt ggg cgg gaa atg	336
Val Val Ile Asn Cys Gly Ser Thr Ala Phe Leu Leu Gly Arg Glu Met	
100 105 110	
tgt ggc aag cca gtg caa atc atc act aat tat cta ccg ctg gca aat	384
Cys Gly Lys Pro Val Gln Ile Ile Thr Asn Tyr Leu Pro Leu Ala Asn	
115 120 125	

tac ctg atc gat caa gaa cat gac agc gtg atc att atg ggc gga cag 432
Tyr Leu Ile Asp Gln Glu His Asp Ser Val Ile Ile Met Gly Gly Gln
130 135 140

tac aac aaa agt cag tcc atc act tta agc ccg cag ggc agc gaa aac 480
Tyr Asn Lys Ser Gln Ser Ile Thr Leu Ser Pro Gln Gly Ser Glu Asn
145 150 155 160

agt ctc tat gcc ggg cac tgg atg ttt acc agc gga aaa ggg ctg acc 528
Ser Leu Tyr Ala Gly His Trp Met Phe Thr Ser Gly Lys Gly Leu Thr
165 170 175

gca gaa ggg ttg tat aaa acc gat atg ctg aca gca atg gca gag cag 576
Ala Glu Gly Leu Tyr Lys Thr Asp Met Leu Thr Ala Met Ala Glu Gln
180 185 190

aag atg ctg agc gtg gta ggg aaa ctg gtg gta ctg gtt gat agc agt 624
Lys Met Leu Ser Val Val Gly Lys Leu Val Val Leu Val Asp Ser Ser
195 200 205

aag att ggc gaa cgc gcg gga atg ctt ttt agc cgt gcc gat caa atc 672
Lys Ile Gly Glu Arg Ala Gly Met Leu Phe Ser Arg Ala Asp Gln Ile
210 215 220

gat atg ctt atc acc ggc aaa aat gct aac ccg gaa atc ctg caa caa 720
Asp Met Leu Ile Thr Gly Lys Asn Ala Asn Pro Glu Ile Leu Gln Gln
225 230 235 240

ctg gaa gcg caa ggg gtc agc att ctg cgt gtt taa 756
Leu Glu Ala Gln Gly Val Ser Ile Leu Arg Val *

<210> 113

<211> 825

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(825)

<400> 113

atg acc gaa ttt aca act ctt ctt cag caa gga aac gcc tgg ttc ttc 48
Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe
1 5 10 15

atc ccc agc gcc atc tta ctt ggt gcg ctt cat ggc ctg gaa cca ggg 96
Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
20 25 30

cac tca aaa acg atg atg gcg gcg ttt atc atc gcc atc aaa ggc acc 144
His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
35 40 45

att aaa caa gcg gtg atg ctc gga ctg gca gca act att tcg cat acc 192
Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr

<210> 114
 <211> 519
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(519)

<400> 114
 atg att ctt aaa tca gct att tcc gct gac tct ctg ctc gct aag gat 48
 Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1 5 10 15
 gct ttt agg gca tcc ttt cat tta cac ttt tta cga aat cat ggg atc 96
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 act aac aaa ata tcg ctt gtc agt tat att gta tgg cag gaa aga tat 144
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 gcg act gat att aca gat ccc caa agt gga gag ttt atg acc att aaa 192
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys
 50 55 60
 aat aag atg ttg ctg ggt gcg ctt ttg ctg gtt acc agt gcc gcc tgg 240
 Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp
 65 70 75 80
 gcc gca cca gcc acc gcg ggt tcg acc aat acc tcg gga att tct aag 288
 Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys
 85 90 95
 tat gag tta agt agt ttc att gct gac ttt aag cat ttc aaa cca ggg 336
 Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly
 100 105 110
 gac acc gta cca gaa atg tac cgt acc gat gag tac aac att aag cag 384
 Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln
 115 120 125
 tgg cag ttg cgt aac ctg ccc gcg cct gat gcc ggg acg cac tgg acc 432
 Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr
 130 135 140
 tat atg ggt ggc gcg tac gtg ttg atc agc gac acc gac ggt aaa atc 480
 Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile
 145 150 155 160
 att aaa gcc tac gac ggt gag att ttt tat cat cgc taa 519
 Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg *
 165 170

<210> 115
 <211> 1035
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1035)

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<400> 115
atg gaa att cgc ata atg cta ttt ata tta atg atg atg gtt atg cct 48
Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
  1             5             10             15

gtg agc tat gcg gca tgt tat agt gag tta tct gtt cag cac aac ttg 96
Val Ser Tyr Ala Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
      20             25             30

gtt gtt cag ggg gat ttt gca ctt act caa aca caa atg gcg aca tat 144
Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
      35             40             45

gag cat aat ttt aat gat tcg tca tgc gta agt aca aat act atc acc 192
Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
      50             55             60

cct atg agc ccg tcg gat att att gtt gga ctt tat aac gat acc ata 240
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
      65             70             75             80

aaa tta aat tta cat ttt gaa tgg acc aat aaa aac aac atc acg ttg 288
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
      85             90             95

tca aat aat cag acc agt ttc acc agt ggt tat tca gtt acg gtg aca 336
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
      100            105            110

cct gcg gcc agt aat gca aaa gtg aat gtt tct gcg ggg ggc ggc ggt 384
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
      115            120            125

tca gtg atg att aat ggt gtt gcg aca tta tcc agt gct tca tca tcg 432
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
      130            135            140

aca cgc ggg agt gcc gca gta caa ttt cta ctg tgt tta tta ggt ggc 480
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
      145            150            155            160

aag tca tgg gat gca tgt gta aat agc tac aga aat gca ttg gca caa 528
Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
      165            170            175

aat gca ggt gtc tat tcc ttt aat ctg aca ttg tca tac aac ccg ata 576
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
      180            185            190

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acc aca acc tgc aaa ccg gac gat tta tta att act tta gac agt att	624
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile	
195 200 205	
ccc gtt tca caa tta cca gcc aca ggt aac aaa gca aca ata aat agt	672
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser	
210 215 220	
aaa caa ggg gat att att ctg cgt tgt aaa aat tta tta ggt caa caa	720
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln	
225 230 235 240	
aat caa aca tca cgg aaa atg cag gtg tat tta tca agt tct gac ttg	768
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu	
245 250 255	
tta acc aac agc aac aca ata ctg aaa ggt gcg gaa gat aat ggc gta	816
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val	
260 265 270	
gga ttt att ctt gaa agt aat ggt tcg cca gtc aca ctt tta aat atc	864
Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile	
275 280 285	
act aac agc agt aaa gga tat aca aat tta aag gaa gtt gcg gcg aag	912
Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys	
290 295 300	
tca aaa ctt aca gat aca acg gtt tca att ccg ata aca gcc agt tac	960
Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr	
305 310 315 320	
tac gtc tac gat aca aac aaa gtt aaa tct ggc gca ctg gag gca acc	1008
Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr	
325 330 335	
gca tta atc aac gtg aaa tac gac taa	1035
Ala Leu Ile Asn Val Lys Tyr Asp *	
340	

<210> 116
 <211> 2481
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2481)

<400> 116	
atg ttg aga atg acc cca ctt gca tca gca atc gta gcg tta ttg ctc	48
Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu	
1 5 10 15	

ggc att gaa gct tat gca gct gaa gaa acc ttt gat acc cat ttt atg	96
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Gly	Ile	Glu	Ala	Tyr	Ala	Ala	Glu	Glu	Thr	Phe	Asp	Thr	His	Phe	Met	
			20					25					30			
ata	ggt	gga	atg	aaa	gac	cag	cag	ggt	gca	aat	att	cgt	ctt	gat	gat	144
Ile	Gly	Gly	Met	Lys	Asp	Gln	Gln	Val	Ala	Asn	Ile	Arg	Leu	Asp	Asp	
		35					40				45					
aat	caa	ccc	tta	ccg	ggg	cag	tat	gac	atc	gat	att	tat	gtc	aat	aag	192
Asn	Gln	Pro	Leu	Pro	Gly	Gln	Tyr	Asp	Ile	Asp	Ile	Tyr	Val	Asn	Lys	
		50				55					60					
caa	tgg	cgc	ggg	aaa	tat	gag	att	att	ggt	aaa	gac	aac	ccg	caa	gaa	240
Gln	Trp	Arg	Gly	Lys	Tyr	Glu	Ile	Ile	Val	Lys	Asp	Asn	Pro	Gln	Glu	
	65				70				75						80	
aca	tgt	tta	tca	aga	gaa	ggt	atc	aag	cgg	tta	ggc	att	aat	agc	gat	288
Thr	Cys	Leu	Ser	Arg	Glu	Val	Ile	Lys	Arg	Leu	Gly	Ile	Asn	Ser	Asp	
				85				90						95		
aac	ttc	gcc	agc	ggt	aag	caa	tgt	tta	aca	ttt	gag	caa	ctt	ggt	cag	336
Asn	Phe	Ala	Ser	Gly	Lys	Gln	Cys	Leu	Thr	Phe	Glu	Gln	Leu	Val	Gln	
			100					105					110			
ggt	ggg	agc	tat	acc	tgg	gat	atc	ggg	ggt	ttt	cgt	ctc	gat	ttc	agt	384
Gly	Gly	Ser	Tyr	Thr	Trp	Asp	Ile	Gly	Val	Phe	Arg	Leu	Asp	Phe	Ser	
		115					120					125				
gtc	ccg	cag	gcc	tgg	gtg	gaa	gaa	ctg	gaa	agt	ggc	tat	ggt	cca	ccg	432
Val	Pro	Gln	Ala	Trp	Val	Glu	Glu	Leu	Glu	Ser	Gly	Tyr	Val	Pro	Pro	
		130				135					140					
gaa	aac	tgg	gag	cgg	ggt	att	aat	gcg	ttt	tat	acc	tct	tat	tat	ctg	480
Glu	Asn	Trp	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Tyr	Thr	Ser	Tyr	Tyr	Leu	
	145				150				155						160	
agt	cag	tat	tac	agc	gac	tat	aaa	gcg	tcg	ggt	aat	aac	aag	agt	aca	528
Ser	Gln	Tyr	Tyr	Ser	Asp	Tyr	Lys	Ala	Ser	Gly	Asn	Asn	Lys	Ser	Thr	
				165				170						175		
tat	gta	cgt	ttt	aac	agc	ggg	tta	aat	tta	ctg	ggg	tgg	caa	ctg	cat	576
Tyr	Val	Arg	Phe	Asn	Ser	Gly	Leu	Asn	Leu	Leu	Gly	Trp	Gln	Leu	His	
			180					185					190			
tct	gat	gcc	agt	ttc	agt	aaa	aca	aat	aac	aat	cca	ggg	gtg	tgg	aaa	624
Ser	Asp	Ala	Ser	Phe	Ser	Lys	Thr	Asn	Asn	Asn	Pro	Gly	Val	Trp	Lys	
		195					200					205				
agc	aat	acc	ctg	tat	ctg	gaa	cgt	gga	ttt	gcc	caa	ctt	ctc	ggc	acg	672
Ser	Asn	Thr	Leu	Tyr	Leu	Glu	Arg	Gly	Phe	Ala	Gln	Leu	Leu	Gly	Thr	
		210				215					220					
ctt	cgc	gtg	ggt	gat	atg	tac	aca	tca	agc	gat	att	ttt	gat	tct	ggt	720
Leu	Arg	Val	Gly	Asp	Met	Tyr	Thr	Ser	Ser	Asp	Ile	Phe	Asp	Ser	Val	
	225				230					235					240	
cgc	ttc	aga	ggt	gtg	cgg	ttg	ttt	cgt	gat	atg	cag	atg	ttg	cct	aac	768
Arg	Phe	Arg	Gly	Val	Arg	Leu	Phe	Arg	Asp	Met	Gln	Met	Leu	Pro	Asn	

	245	250	255	
tcg aaa caa aat ttt acg cca cgg gtg cag ggg att gct cag agt aac				816
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn				
	260	265	270	
gcg ctg gta act att gaa cag aat ggt ttt gtg gtt tat cag aaa gag				864
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu				
	275	280	285	
gtt cct cct ggc ccg ttc gcg att aca gat ttg cag ttg gcc ggt ggt				912
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly				
	290	295	300	
gga gca gat ctt gat gtc agc gtg aaa gag gcg gac ggc tcg gta acc				960
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr				
	305	310	315	320
acc tat ctg gtg cct tat gca gcg gtg cca aat atg ctg caa ccc ggc				1008
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly				
	325	330	335	
gtg tcg aaa tat gat tta gcg gcg ggt cgt agc cat att gaa ggg gcg				1056
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala				
	340	345	350	
agc aaa caa agt gat ttt gtc cag gcg ggt tat cag tat ggt ttt aat				1104
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn				
	355	360	365	
aat tta ttg acg ctg tat ggt ggc tcg atg gtc gcg aat aat tat tac				1152
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr				
	370	375	380	
gcg ttt act ttg ggg gct ggc tgg aat aca cgc att ggt gcc att tcc				1200
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser				
	385	390	395	400
gtc gat gcc act aag tcg cat agt aaa caa gac aac ggc gat gtg ttt				1248
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe				
	405	410	415	
gac ggg caa agt tat caa att gcc tac aac aaa ttt gtg agc caa acg				1296
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr				
	420	425	430	
tcg acg cgt ttt ggt ctg gcg gcc tgg cgt tat tcg tcg cgt gat tac				1344
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr				
	435	440	445	
cgg aca ttt aac gat cac gtt tgg gca aac aat aaa gat aat tat cgc				1392
Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg				
	450	455	460	
cgt gat gaa aac gat gtc tat gac att gcc gat tat tac cag aac gat				1440
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp				
	465	470	475	480

[illegible]

```
<210> 119
<211> 288
<212> DNA
<213> Escherichia coli
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58

<222> (1)...(288)

<400> 119

atg	ctg	cac	aca	tta	cat	cgc	tca	ccc	tgg	ctg	acg	gat	ttt	gct	gcg	48
Met	Leu	His	Thr	Leu	His	Arg	Ser	Pro	Trp	Leu	Thr	Asp	Phe	Ala	Ala	
1				5				10						15		

ctg	ctg	cgt	ctg	ctc	agt	gaa	gga	gac	gaa	ctg	cta	tta	ttg	caa	gat	96
Leu	Leu	Arg	Leu	Leu	Ser	Glu	Gly	Asp	Glu	Leu	Leu	Leu	Leu	Gln	Asp	
			20					25					30			

ggc	gta	act	gcc	gca	gtt	gac	ggt	aac	cgc	tac	ctt	gaa	agt	ctg	cgt	144
Gly	Val	Thr	Ala	Ala	Val	Asp	Gly	Asn	Arg	Tyr	Leu	Glu	Ser	Leu	Arg	
		35					40					45				

aat	gcc	ccc	att	aag	gtc	tat	gcc	ctg	aac	gaa	gac	ctt	att	gcc	cgc	192
Asn	Ala	Pro	Ile	Lys	Val	Tyr	Ala	Leu	Asn	Glu	Asp	Leu	Ile	Ala	Arg	
	50					55					60					

ggt	ttg	act	ggt	caa	att	tcg	aac	gac	atc	att	ctc	att	gac	tat	act	240
Gly	Leu	Thr	Gly	Gln	Ile	Ser	Asn	Asp	Ile	Ile	Leu	Ile	Asp	Tyr	Thr	
65					70				75						80	

gat	ttc	gtc	aga	ctt	acg	gtt	aag	cac	ccc	agc	cag	atg	gcc	tgg	tga	288
Asp	Phe	Val	Arg	Leu	Thr	Val	Lys	His	Pro	Ser	Gln	Met	Ala	Trp	*	
				85					90					95		

<210> 120

<211> 360

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(360)

<400> 120

atg	aaa	cga	att	gcg	ttt	gtt	ttt	tct	act	gca	cct	cat	ggt	aca	gcc	48
Met	Lys	Arg	Ile	Ala	Phe	Val	Phe	Ser	Thr	Ala	Pro	His	Gly	Thr	Ala	
1				5				10					15			

gca	ggc	cgg	gaa	ggt	tta	gat	gct	tta	ctg	gca	act	tcc	gca	tta	act	96
Ala	Gly	Arg	Glu	Gly	Leu	Asp	Ala	Leu	Leu	Ala	Thr	Ser	Ala	Leu	Thr	
			20					25					30			

gac	gat	ctg	gct	gtc	ttc	ttt	ata	gct	gat	ggc	gtt	ttt	cag	ctg	ctg	144
Asp	Asp	Leu	Ala	Val	Phe	Phe	Ile	Ala	Asp	Gly	Val	Phe	Gln	Leu	Leu	
		35					40					45				

cca	gga	caa	aag	ccc	gat	gca	gtg	ctg	gcg	cgt	gat	tac	att	gcc	act	192
Pro	Gly	Gln	Lys	Pro	Asp	Ala	Val	Leu	Ala	Arg	Asp	Tyr	Ile	Ala	Thr	
	50					55					60					

ttt	aaa	ttg	ttg	ggt	ctg	tac	gac	att	gaa	cag	tgc	tgg	gtt	tgt	gcg	240
Phe	Lys	Leu	Leu	Gly	Leu	Tyr	Asp	Ile	Glu	Gln	Cys	Trp	Val	Cys	Ala	

65	70	75	80	
gct tca ctg cgc gaa cgc ggg tta gat ccg cag aca ccc ttt gtt gtc				288
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val				
	85	90	95	
gaa gcc acg ccg ctc gaa gca gat gcc tta cgc cgc gaa ctc gcc aac				336
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn				
	100	105	110	
tac gat gtt att ttg agg ttt tga				360
Tyr Asp Val Ile Leu Arg Phe *				
	115			
<210> 121				
<211> 387				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(387)				
<400> 121				
atg cgt ttt gcc atc gtg gtg acc ggg cca gca tac ggt acg caa cag				48
Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln				
1	5	10	15	
gcg agt agt gct ttt cag ttt gcg cag gcg ctg ata gca gat ggc cat				96
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His				
	20	25	30	
gag tta agc agc gtc ttt ttc tat cgg gaa ggg gtc tat aac gct aac				144
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn				
	35	40	45	
caa ttg acc tct ccg gca agt gac gaa ttt gac ctc gta cgg gcc tgg				192
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp				
	50	55	60	
caa caa ctg aat gcg caa cat ggt gtg gcg ctg aat atc tgc gta gcg				240
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala				
65	70	75	80	
gca gca tta cgc cgt ggc gtt gtt gat gaa acg gag gcc gga aga ctg				288
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu				
	85	90	95	
ggg ctg gct tcg tca aac ctt cag cag gga ttt acc tta agc gga ctt				336
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu				
	100	105	110	
ggg gcg ctg gcg gaa gcc tcg ctg acc tgt gac agg gtg gta cag ttc				384
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe				
	115	120	125	

tga
*

387

<210> 122
<211> 735
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(735)

<400> 122

gtg ttt ttt ttc atg tcc agg tcg ctt tta acc aac gaa acc agt gag	48
Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu	
1 5 10 15	
ttg gat tta ctg gat caa cgt cct ttc gac cag acc gat ttt gat att	96
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile	
20 25 30	
ctg aaa tcc tac gaa gcg gtg gtg gac ggg tta gcg atg ctt att ggc	144
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly	
35 40 45	
tcc cac tgt gaa atc gtt ttg cac tct ttg cag gat cta aaa tgt tca	192
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser	
50 55 60	
gcc att cgc att gct aac ggt gaa cat aca ggc cgg aag att ggt tcg	240
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser	
65 70 75 80	
cca att act gac ctg gcg cta cgt atg ctg cac gat atg acg gga gcg	288
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala	
85 90 95	
gat agc agc gtt tct aaa tgc tac ttt act cgc gcc aaa agc ggc gta	336
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val	
100 105 110	
tta atg aag tcc ctg act atc gcg att cgt aac cgc gaa cag cgt gta	384
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val	
115 120 125	
att ggt ctg ctg tgc atc aat atg aat ctt gat gtt ccc ttc tcg cag	432
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln	
130 135 140	
att atg agc acc ttt gtg ccg cca gaa acc ccg gat gtc ggt tca agc	480
Ile Met Ser Thr Phe Val Pro Pro Glu Thr Pro Asp Val Gly Ser Ser	
145 150 155 160	
gtc aac ttt gcc tct tct gtt gaa gat ctg gtt acc caa acg ctg gag	528
Val Asn Phe Ala Ser Ser Val Glu Asp Leu Val Thr Gln Thr Leu Glu	

165

170

175

ttc acc atc gaa gaa gtg aat gcc gat cgc aat gtt tct aat aac gcc	576
Phe Thr Ile Glu Glu Val Asn Ala Asp Arg Asn Val Ser Asn Asn Ala	
180 185 190	
aaa aat cgt cag atc gtg ctg aat ctc tac gag aaa ggg atc ttc gat	624
Lys Asn Arg Gln Ile Val Leu Asn Leu Tyr Glu Lys Gly Ile Phe Asp	
195 200 205	
att aaa gat gcg atc aac cag gtt gct gac cgc ctg aac atc tcc aaa	672
Ile Lys Asp Ala Ile Asn Gln Val Ala Asp Arg Leu Asn Ile Ser Lys	
210 215 220	
cac act gtc tat ctc tac atc cgc cag ttc aag agc ggt gat ttc cag	720
His Thr Val Tyr Leu Tyr Ile Arg Gln Phe Lys Ser Gly Asp Phe Gln	
225 230 235 240	
ggg caa gat aag taa	735
Gly Gln Asp Lys *	

<210> 123

<211> 255

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(255)

<400> 123

atg acc gat aaa atc cgt act ctg caa ggt cgc gtt gtt agc gac aaa	48
Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys	
1 5 10 15	

atg gag aaa tcc att gtt gtt gct atc gaa cgt ttt gtg aaa cac ccg	96
Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro	
20 25 30	

atc tac ggt aaa ttc atc aag cgt acg acc aaa ctg cac gta cat gac	144
Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp	
35 40 45	

gag aac aac gaa tgc ggt atc ggt gac gtg gtt gaa atc cgc gaa tgc	192
Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys	
50 55 60	

cgt ccg ctg tcc aag act aaa tcc tgg acg ctg gtt cgc gtt gta gag	240
Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu	
65 70 75 80	

aaa gcg gtt ctg taa	255
Lys Ala Val Leu *	

<210> 124
 <211> 192
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(192)

<400> 124
 atg aaa gca aaa gag ctg cgt gag aag agc gtt gaa gag ctg aac acc 48
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 gag ctg ctg aac ctg ctg cgt gag cag ttc aac ctg cgt atg cag gct 96
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 gca agt ggc cag ctg caa cag tct cac ctg ttg aag caa gtg cgt cgc 144
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 gat gtc gca cgc gtt aag act tta ctg aac gag aag gcg ggt gcg taa 192
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala *
 50 55 60

<210> 125
 <211> 411
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(411)

<400> 125
 atg tta caa cca aag cgt aca aaa ttc cgt aaa atg cac aaa ggc cgt 48
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 aac cgc ggt ctg gcg cag ggt acg gat gtt agc ttc ggc agc ttc ggt 96
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 ctg aaa gct gtt ggc cgt ggt cgt ctg act gcc cgt cag atc gaa gca 144
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 gca cgt cgt gct atg acc cgt gca gtt aag cgt caa ggt aag atc tgg 192
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 atc cgt gtg ttc ccg gac aaa ccg atc act gaa aag ccg ctg gca gtg 240
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val

gca aaa ctg gtt gct gac agc atc act tct cag ctg gaa cgt cgc gtt 384
Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
115 120 125

atg ttc cgt cgt gct atg aag cgt gct gta cag aac gca atg cgt ctg 432
Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
130 135 140

ggc gct aaa ggt att aaa gtt gaa gtt agc ggc cgt ctg ggc ggc gcg 480
Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
145 150 155 160

gaa atc gca cgt acc gaa tgg tac cgc gaa ggt cgc gta ccg ctg cac 528
Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
165 170 175

act ctg cgt gct gac atc gac tac aac acc tct gaa gcg cac acc act 576
Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
180 185 190

tac ggt gta atc ggc gtt aaa gtg tgg atc ttc aaa ggc gag atc ctg 624
Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
195 200 205

ggc ggt atg gct gct gtt gaa caa ccg gaa aaa ccg gct gct cag cct 672
Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
210 215 220

aaa aag cag cag cgt aaa ggc cgt aaa taa 702
Lys Lys Gln Gln Arg Lys Gly Arg Lys *
225 230

<210> 127
<211> 333
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(333)

<400> 127
atg gaa act atc gct aaa cat cgc cat gct cgt tct tct gct cag aag 48
Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
1 5 10 15

gtt cgc ctt gtt gct gac ctg att cgc ggt aag aaa gtg tcg cag gct 96
Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
20 25 30

ctg gat att ttg acc tac acc aac aag aaa gcg gct gta ctg gtc aag 144
Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
35 40 45

aaa gtt ctg gaa tct gcc att gct aac gct gaa cac aac gat ggc gct 192
Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala

50	55	60	
gac att gac gat ctg aaa gtt acg aaa att ttc gta gac gaa ggc ccg	240		
Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro			
65 70 75 80			
agc atg aag cgc att atg ccg cgt gca aaa ggt cgt gca gat cgc atc	288		
Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile			
85 90 95			
ctg aag cgc acc agc cac atc act gtg gtt gtg tcc gat cgc tga	333		
Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg *			
100 105 110			

<210> 128
 <211> 279
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(279)

<400> 128	
atg cca cgt tct ctc aag aaa ggt cct ttt att gac ctg cac ttg ctg	48
Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu	
1 5 10 15	
aag aag gta gag aaa gcg gtg gaa agc gga gac aag aag ccc ctg cgc	96
Lys Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg	
20 25 30	
act tgg tcc cgt cgt tca acg atc ttt cct aac atg atc ggt ttg acc	144
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr	
35 40 45	
atc gct gtc cat aat ggt cgt cag cac gtt ccg gta ttt gta acc gac	192
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp	
50 55 60	
gaa atg gtt ggt cac aaa ctg ggt gaa ttc gca ccg act cgt act tat	240
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr	
65 70 75 80	
cgc ggc cac gct gct gat aaa aaa gcg aag aag aaa taa	279
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys *	
85 90	

<210> 129
 <211> 822
 <212> DNA
 <213> Escherichia coli

<220>

<221> CDS
 <222> (1)...(822)

<400> 129

atg gca gtt gtt aaa tgt aaa ccg aca tct ccg ggt cgt cgc cac gta	48
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val	
1 5 10 15	
gtt aaa gtg gtt aac cct gag ctg cac aag ggc aaa cct ttt gct ccg	96
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro	
20 25 30	
ttg ctg gaa aaa aac agc aaa tcc ggt ggt cgt aac aac aat ggc cgt	144
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg	
35 40 45	
atc acc act cgt cat atc ggt ggt ggc cac aag cag gct tac cgt att	192
Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile	
50 55 60	
gtt gac ttc aaa cgc aac aaa gac ggt atc ccg gca gtt gtt gaa cgt	240
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg	
65 70 75 80	
ctt gag tac gat ccg aac cgt tcc gcg aac atc gcg ctg gtt ctg tac	288
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr	
85 90 95	
aaa gac ggt gaa cgc cgt tac atc ctg gcc cct aaa ggc ctg aaa gct	336
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala	
100 105 110	
ggc gac cag att cag tct ggc gtt gat gct gca atc aaa cca ggt aac	384
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn	
115 120 125	
acc ctg ccg atg cgc aac atc ccg gtt ggt tct act gtt cat aac gta	432
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val	
130 135 140	
gaa atg aaa cca ggt aaa ggc ggt cag ctg gca cgt tcc gct ggt act	480
Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr	
145 150 155 160	
tac gtt cag atc gtt gct cgt gat ggt gct tat gtc acc ctg cgt ctg	528
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu	
165 170 175	
cgt tct ggt gaa atg cgt aaa gta gaa gca gac tgc cgt gca act ctg	576
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu	
180 185 190	
ggc gaa gtt ggc aat gct gag cat atg ctg cgc gtt ctg ggt aaa gca	624
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala	
195 200 205	
ggg gct gca cgc tgg cgt ggt gtt cgt ccg acc gtt cgc ggt acc gcg	672

<210> 131
 <211> 606
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(606)

<400> 131

atg gaa tta gta ttg aaa gac gcg cag agc gcg ctg act gtt tcc gaa	48
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu	
1 5 10 15	
act acc ttc ggt cgt gat ttc aac gaa gcg ctg gtt cac cag gtt gtt	96
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val	
20 25 30	
gtt gct tat gca gct ggt gct cgt cag ggt act cgt gct cag aag act	144
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr	
35 40 45	
cgt gct gaa gta act ggt tcc ggt aaa aaa ccg tgg cgc cag aaa ggc	192
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly	
50 55 60	
acc ggc cgt gcg cgt tct ggt tct atc aag agc ccg atc tgg cgt tct	240
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser	
65 70 75 80	
ggt ggc gtg acc ttt gct gct cgt ccg cag gac cac agt caa aaa gtt	288
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val	
85 90 95	
aac aag aag atg tac cgc ggc gcg ctg aaa agc atc ctg tcc gaa ctg	336
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu	
100 105 110	
gta cgt cag gat cgt ctg atc gtt gtc gag aag ttc tct gta gaa gcg	384
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala	
115 120 125	
ccg aaa act aag ctg ctg gca cag aaa ctg aaa gac atg gct ctg gaa	432
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu	
130 135 140	
gat gtg ctg atc atc acc ggt gag ctg gac gaa aac ctg ttc ctg gct	480
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala	
145 150 155 160	
gcg cgc aac ctg cac aag gtt gac gta cgc gat gca act ggt atc gac	528
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp	
165 170 175	
ccg gtt agc ctg atc gcc ttc gac aaa gtc gta atg act gct gat gct	576

Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190

gtt aag caa gtt gag gag atg ctg gca tga 606
 Val Lys Gln Val Glu Glu Met Leu Ala *
 195 200

<210> 132
 <211> 630
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(630)

<400> 132
 atg att ggt tta gtc ggt aaa aaa gtg ggt atg acc cgt atc ttc aca 48
 Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1 5 10 15

gaa gac ggc gtt tct atc cca gta acc gta atc gaa gtt gaa gca aac 96
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
 20 25 30

cgc gtt act cag gtt aaa gac ctg gct aac gat ggc tac cgt gct att 144
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
 35 40 45

cag gtg acc acc ggt gct aaa aaa gct aac cgt gtg acc aag cct gaa 192
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
 50 55 60

gct ggc cac ttc gct aaa gct ggc gta gaa gct ggc cgt ggt ctg tgg 240
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
 65 70 75 80

gaa ttc cgc ctg gct gaa ggc gaa gag ttc act gta ggt cag agc att 288
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
 85 90 95

agc gtt gaa ctg ttt gct gac gtt aaa aaa gtt gac gta act ggc acc 336
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
 100 105 110

tct aaa ggt aaa ggt ttc gca ggt acc gtt aag cgc tgg aac ttc cgt 384
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
 115 120 125

acc cag gac gct act cac ggt aac tcc ttg tct cac cgc gtt ccg ggt 432
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
 130 135 140

tct atc ggt cag aac cag act ccg ggc aaa gtg ttc aaa ggc aag aaa 480
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
 145 150 155 160

atg gca ggt cag atg ggt aac gaa cgt gta acc gtt cag agc ctt gac	528
Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp	
165 170 175	
gta gta cgc gtt gac gct gag cgc aac ctg ctg ctg gtt aaa ggt gct	576
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala	
180 185 190	
gtc ccg ggt gca acc ggt agc gac ctg atc gtt aaa cca gct gtg aag	624
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys	
195 200 205	
gcg taa	630
Ala *	

<210> 133
 <211> 312
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(312)

<400> 133	
atg cag aac caa aga atc cgt atc cgc ctg aaa gcg ttt gat cat cgt	48
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg	
1 5 10 15	
ctg atc gat caa gca acc gcg gaa atc gtc gag act gcc aag cgc act	96
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr	
20 25 30	
ggt gcg cag gtc cgt ggt ccg atc ccg ctg ccg aca cgc aaa gag cgc	144
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg	
35 40 45	
ttc act gtt ctg atc tcc ccg cac gtc aac aaa gac gcg cgc gat cag	192
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln	
50 55 60	
tac gaa atc cgt act cac ttg cgt ctg gtt gac atc gtt gag cca acc	240
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr	
65 70 75 80	
gag aaa acc gtt gat gct ctg atg cgt ctg gat ctg gct gcc ggt gta	288
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val	
85 90 95	
gac gtg cag atc agc ctg ggt taa	312
Asp Val Gln Ile Ser Leu Gly *	
100	

<210> 134
 <211> 315
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(315)

<400> 134
 atg atc cgc aaa gcc ttt gtc atg cag gta aac ccc gac gcc cac gaa 48
 Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
 1 5 10 15
 gag tat cag cgt cgg cat aat ccc atc tgg cca gaa ctg gaa gca gtg 96
 Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
 20 25 30
 ctg aaa tct cac ggt gcg cat aac tac gcc atc tat ctc gac aaa gcg 144
 Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
 35 40 45
 cgt aat ctg ctg ttt gcc atg gta gag att gaa tct gaa gaa cgc tgg 192
 Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
 50 55 60
 aat gcg gtt gcc agc act gat gtt tgc caa cgt tgg tgg aaa tat atg 240
 Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
 65 70 75 80
 acc gat gtt atg ccc gct aac ccg gat aac agc ccg gtg agt agc gag 288
 Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
 85 90 95
 ctg caa gaa gtg ttt tac ctg ccg taa 315
 Leu Gln Glu Val Phe Tyr Leu Pro *

<210> 135
 <211> 864
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(864)

<400> 135
 atg atc cgc agt atg acc gcc tac gcc cgg cgt gaa atc aag ggt gaa 48
 Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
 1 5 10 15
 tgg ggg agc gca acc tgg gaa atg cgc tcg gta aac cag cgt tat ctg 96
 Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
 20 25 30

gaa act tac ttt cgt ctg ccg gag cag ttc cgt agc ctt gaa cct gtc	144
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val	
35 40 45	
gtt cgc gag cgt att cgt tct cgc ctg acg cgc ggt aaa gtg gaa tgt	192
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys	
50 55 60	
acc ctg cgc tat gag cca gat gtt agc gcg caa ggt gag ctg atc ctc	240
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu	
65 70 75 80	
aac gaa aaa ctg gct aaa cag ctg gta act gcc gcg aac tgg gta aaa	288
Asn Glu Lys Leu Ala Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys	
85 90 95	
atg cag agt gac gaa ggg gaa atc aac ccg gtt gat att cta cgc tgg	336
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp	
100 105 110	
ccg ggc gtg atg gca gcc cag gag cag gat ctt gac gcc att gcc gct	384
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala	
115 120 125	
gaa att ctc gcg gcg ctg gat ggt acg ctg gac gac ttt att gtc gcg	432
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala	
130 135 140	
cgc gaa acc gaa ggt cag gca ctg aaa gca ttg atc gag cag cgt ctg	480
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu	
145 150 155 160	
gaa ggc gtc acc gcc gaa gtg gtc aaa gtc cgc tcc cat atg ccg gaa	528
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu	
165 170 175	
atc ctg caa tgg cag cgt gag cgt ctg gtc gcg aag ctg gaa gat gct	576
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala	
180 185 190	
cag gtg caa ctg gaa aac aac cgt ctg gag cag gaa ctg gtt ctg ctg	624
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Leu Val Leu Leu	
195 200 205	
gca caa cga att gac gtt gcc gaa gaa ctg gat cgc ctc gaa gcg cat	672
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His	
210 215 220	
gtc aaa gag acc tac aac att ctg aag aaa aaa gaa gcg gtt ggt cgt	720
Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg	
225 230 235 240	
cgt ctg gat ttt atg atg cag gag ttc aac cgc gag tcg aac act ctt	768
Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu	
245 250 255	
gcg tcg aag tct atc aat gcc gaa gtg aca aac tcc gcc atc gag ctg	816

Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
 260 265 270

aaa gtg ttg att gag cag atg cgc gag cag att cag aac atc gaa taa 864
 Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu *
 275 280 285

<210> 136
 <211> 492
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(492)

<400> 136
 atg agc aca gaa aca att gaa ata ttc aat aat agt gat gaa tgg gca 48
 Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
 1 5 10 15
 aat caa cta aaa cac gca tta tcg aaa gga gaa aat ctg gca tta cta 96
 Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
 20 25 30
 cat ggt tta act cct gat atc ctt gat aga ata tat gca tat gca ttc 144
 His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
 35 40 45
 gac tac cat gaa aag ggt aat ata acg gac gca gaa att tat tat aaa 192
 Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
 50 55 60
 ttc ttg tgc att tat gcg ttc gaa aat cat gag tat cta aaa gat ttt 240
 Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
 65 70 75 80
 gca tca gta tgt cag ccc aaa aag aaa tat caa caa gca tat gac ctt 288
 Ala Ser Val Cys Gln Pro Lys Lys Lys Tyr Gln Gln Ala Tyr Asp Leu
 85 90 95
 tac aaa cta agt tac aat tac ttc ccg tat gat gac tat tca gtt att 336
 Tyr Lys Leu Ser Tyr Asn Tyr Phe Pro Tyr Asp Asp Tyr Ser Val Ile
 100 105 110
 tat cgt atg ggt caa tgt cag att ggg gct aaa aat atc gat aac gca 384
 Tyr Arg Met Gly Gln Cys Gln Ile Gly Ala Lys Asn Ile Asp Asn Ala
 115 120 125
 atg caa tgt ttc tat cac att att aac aat tgt gag gat gat agt gtt 432
 Met Gln Cys Phe Tyr His Ile Ile Asn Asn Cys Glu Asp Asp Ser Val
 130 135 140
 aag agt aaa gcg cag gca tat att gaa ctc tta aac gat aat tca gaa 480
 Lys Ser Lys Ala Gln Ala Tyr Ile Glu Leu Leu Asn Asp Asn Ser Glu

145 150 155 160

gat aat ggc taa 492
Asp Asn Gly *

<210> 137
<211> 1947
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1947)

<400> 137
atg aat att tta ggt ttt ttc cag cga ctc ggt agg gcg tta cag ctc 48
Met Asn Ile Leu Gly Phe Phe Gln Arg Leu Gly Arg Ala Leu Gln Leu
1 5 10 15
cct atc gcg gtg ctg ccg gtg gcg gca ctg ttg ctg cga ttc ggt cag 96
Pro Ile Ala Val Leu Pro Val Ala Ala Leu Leu Leu Arg Phe Gly Gln
20 25 30
cca gat tta ctt aac gtt gcg ttt att gcc cag gcg ggc ggt gcg att 144
Pro Asp Leu Leu Asn Val Ala Phe Ile Ala Gln Ala Gly Gly Ala Ile
35 40 45
ttt gat aac ctc gca tta atc ttc gcc atc ggt gtg gca tcc agc tgg 192
Phe Asp Asn Leu Ala Leu Ile Phe Ala Ile Gly Val Ala Ser Ser Trp
50 55 60
tcg aaa gac agc gct ggt gcg gcg gcg ctg gcg ggt gcg gta ggt tac 240
Ser Lys Asp Ser Ala Gly Ala Ala Ala Leu Ala Gly Ala Val Gly Tyr
65 70 75 80
ttt gtg tta acc aaa gcg atg gtg acc atc aac cca gaa att aac atg 288
Phe Val Leu Thr Lys Ala Met Val Thr Ile Asn Pro Glu Ile Asn Met
85 90 95
ggt gta ctg gcg ggt atc att acc ggt ctg gtt ggt ggc gca gcc tat 336
Gly Val Leu Ala Gly Ile Ile Thr Gly Leu Val Gly Gly Ala Ala Tyr
100 105 110
aac cgt tgg tcc gat att aaa ctg ccg gac ttc ctg agc ttc ttc ggc 384
Asn Arg Trp Ser Asp Ile Lys Leu Pro Asp Phe Leu Ser Phe Phe Gly
115 120 125
ggc aaa cgc ttt gtg ccg att gcc acc gga ttc ttc tgc ctg gtg ctg 432
Gly Lys Arg Phe Val Pro Ile Ala Thr Gly Phe Phe Cys Leu Val Leu
130 135 140
gcg gcc att ttt ggt tac gtc tgg ccg ccg gta cag cac gct atc cat 480
Ala Ala Ile Phe Gly Tyr Val Trp Pro Pro Val Gln His Ala Ile His
145 150 155 160

610

615

620

ttc agt ggc ttg atc att aaa gct cag ggc cat att gtg gcg ggt caa 1920
 Phe Ser Gly Leu Ile Ile Lys Ala Gln Gly His Ile Val Ala Gly Gln
 625 630 635 640

aca ccg ctg tat gaa atc aaa aag taa 1947
 Thr Pro Leu Tyr Glu Ile Lys Lys *
 645

<210> 138

<211> 1239

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1239)

<400> 138

atg aag act atc ttc agg tac att ctt ttt tta gca ctg tat tct tgt 48
 Met Lys Thr Ile Phe Arg Tyr Ile Leu Phe Leu Ala Leu Tyr Ser Cys
 1 5 10 15

tgt aat aca gtc agt gca tat aca agt ttt att gtg gga aat aat gca 96
 Cys Asn Thr Val Ser Ala Tyr Thr Ser Phe Ile Val Gly Asn Asn Ala
 20 25 30

gga gtt gat aac tat cga ggc ccc tcc act gcc gca cag atg acc ttt 144
 Gly Val Asp Asn Tyr Arg Gly Pro Ser Thr Ala Ala Gln Met Thr Phe
 35 40 45

aat tac aca tca aca gca agc aac ttg gtt ttt tat aaa ccc acg cag 192
 Asn Tyr Thr Ser Thr Ala Ser Asn Leu Val Phe Tyr Lys Pro Thr Gln
 50 55 60

ctc ggc ccg act ggg gta aaa atg tac tgg tca tac ctg gat aca ggt 240
 Leu Gly Pro Thr Gly Val Lys Met Tyr Trp Ser Tyr Leu Asp Thr Gly
 65 70 75 80

acc ggt ggt ggt att ctt tac tgc aat aca tct ggc aga gcg aat cct 288
 Thr Gly Gly Gly Ile Leu Tyr Cys Asn Thr Ser Gly Arg Ala Asn Pro
 85 90 95

ggt cca ata act att gaa aat gcc atg gtc tat tca ggt aaa gat tat 336
 Gly Pro Ile Thr Ile Glu Asn Ala Met Val Tyr Ser Gly Lys Asp Tyr
 100 105 110

ggc gga cat aaa cta ttt aat aca tct gtt cct ggt ctg tat tac acc 384
 Gly Gly His Lys Leu Phe Asn Thr Ser Val Pro Gly Leu Tyr Tyr Thr
 115 120 125

atg tta ata tca agg gtc tgg tct gca tac gat aca ata act gac att 432
 Met Leu Ile Ser Arg Val Trp Ser Ala Tyr Asp Thr Ile Thr Asp Ile
 130 135 140

caa tgc cca gga atc tat atc gga gat cct tcc aac caa gaa ttt ttc	480
Gln Ser Pro Gly Ile Tyr Ile Gly Asp Pro Ser Asn Gln Glu Phe Phe	
145 150 155 160	
ttt tcc gtc aca gac agc gat cta caa act aag ggt tgc aac aaa gca	528
Phe Ser Val Thr Asp Ser Asp Leu Gln Thr Lys Gly Cys Asn Lys Ala	
165 170 175	
gac gac tac gat aag ttt tgg gct att ggt ggt ata gta cac aac ata	576
Asp Asp Tyr Asp Lys Phe Trp Ala Ile Gly Gly Ile Val His Asn Ile	
180 185 190	
act gtt gaa ttt tat aca gat act aat ttc gat cct aca ctt aat cag	624
Thr Val Glu Phe Tyr Thr Asp Thr Asn Phe Asp Pro Thr Leu Asn Gln	
195 200 205	
caa gtc cag tta tcc agt tca tca aat tac ctt tat tgc ttt aag gcc	672
Gln Val Gln Leu Ser Ser Ser Ser Asn Tyr Leu Tyr Ser Phe Lys Ala	
210 215 220	
tac agt cct ggt aca aaa gtt gta gat cac agc aac cac att tat gtc	720
Tyr Ser Pro Gly Thr Lys Val Val Asp His Ser Asn His Ile Tyr Val	
225 230 235 240	
aat ttc aca ctg aat aat gtc aaa tta acc tta cca aca tgt ttt acc	768
Asn Phe Thr Leu Asn Asn Val Lys Leu Thr Leu Pro Thr Cys Phe Thr	
245 250 255	
tcc ata ctt acc ggg cca tca gtc aat ggt tca acg gtt aga atg gga	816
Ser Ile Leu Thr Gly Pro Ser Val Asn Gly Ser Thr Val Arg Met Gly	
260 265 270	
gaa tat agc tct ggg aca att aaa aat ggc gct tca cct gtt ccc ttt	864
Glu Tyr Ser Ser Gly Thr Ile Lys Asn Gly Ala Ser Pro Val Pro Phe	
275 280 285	
gat atc tgc ctt cag aat tgt att cgt gtg cgt aat att gaa aca aaa	912
Asp Ile Ser Leu Gln Asn Cys Ile Arg Val Arg Asn Ile Glu Thr Lys	
290 295 300	
ctc gtc act gga aaa gta ggt act caa aac aca caa ctg ctt ggt aat	960
Leu Val Thr Gly Lys Val Gly Thr Gln Asn Thr Gln Leu Leu Gly Asn	
305 310 315 320	
acg ctt act gga agc act gcc gcc aaa ggc gtt ggc gta ctc att gaa	1008
Thr Leu Thr Gly Ser Thr Ala Ala Lys Gly Val Gly Val Leu Ile Glu	
325 330 335	
ggt tta gca acc agt aaa aat ccg cta atg aca tta aaa cct aat gat	1056
Gly Leu Ala Thr Ser Lys Asn Pro Leu Met Thr Leu Lys Pro Asn Asp	
340 345 350	
acg aat tct gtt tat ata gat tat gaa acc gaa gat gac acc tcc gat	1104
Thr Asn Ser Val Tyr Ile Asp Tyr Glu Thr Glu Asp Asp Thr Ser Asp	
355 360 365	
ggg gtt tac cct aat caa ggt aac ggc aca tca cag cct ctt cat ttc	1152

Gly	Val	Tyr	Pro	Asn	Gln	Gly	Asn	Gly	Thr	Ser	Gln	Pro	Leu	His	Phe		
370						375					380						
cag	gca	aca	tta	aag	caa	gac	ggg	aat	att	gct	atc	gaa	ccc	ggc	gaa	1200	
Gln	Ala	Thr	Leu	Lys	Gln	Asp	Gly	Asn	Ile	Ala	Ile	Glu	Pro	Gly	Glu		
385					390					395					400		
ttt	aaa	gcc	acc	agt	act	ttc	cag	gta	acc	tat	ccc	tga				1239	
Phe	Lys	Ala	Thr	Ser	Thr	Phe	Gln	Val	Thr	Tyr	Pro	*					
				405					410								

<210> 139
 <211> 597
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(597)

<400>	139																
atg	cat	ccc	act	caa	cgt	aag	ctg	atg	aag	aga	ata	att	ctg	ttt	ctg	48	
Met	His	Pro	Thr	Gln	Arg	Lys	Leu	Met	Lys	Arg	Ile	Ile	Leu	Phe	Leu		
1				5				10					15				
tca	tta	ctg	ttt	tgc	atc	gcc	tgt	cca	gcc	att	gct	gga	cag	gat	att	96	
Ser	Leu	Leu	Phe	Cys	Ile	Ala	Cys	Pro	Ala	Ile	Ala	Gly	Gln	Asp	Ile		
			20					25					30				
gac	ctt	gtt	gcc	aat	gta	aaa	aac	agc	acc	tgc	aaa	agc	gga	atc	agt	144	
Asp	Leu	Val	Ala	Asn	Val	Lys	Asn	Ser	Thr	Cys	Lys	Ser	Gly	Ile	Ser		
		35				40						45					
aac	cag	ggt	aat	att	gat	ctt	ggc	gtc	gtt	ggg	gtg	gga	tat	ttt	tca	192	
Asn	Gln	Gly	Asn	Ile	Asp	Leu	Gly	Val	Val	Gly	Val	Gly	Tyr	Phe	Ser		
	50					55					60						
ggt	aat	gtt	act	cct	gaa	agt	tat	caa	cca	ggt	gga	aaa	gag	ttc	act	240	
Gly	Asn	Val	Thr	Pro	Glu	Ser	Tyr	Gln	Pro	Gly	Gly	Lys	Glu	Phe	Thr		
65					70				75					80			
atc	act	gta	tcc	gac	tgt	gca	tta	cag	gga	act	ggc	gat	gtg	cta	aat	288	
Ile	Thr	Val	Ser	Asp	Cys	Ala	Leu	Gln	Gly	Thr	Gly	Asp	Val	Leu	Asn		
				85					90					95			
cag	tta	cat	att	gat	ttt	aga	gcc	ctt	agc	ggt	gtc	atg	gct	gct	ggc	336	
Gln	Leu	His	Ile	Asp	Phe	Arg	Ala	Leu	Ser	Gly	Val	Met	Ala	Ala	Gly		
			100					105					110				
tct	agg	caa	ata	ttt	gct	aat	gaa	att	tcg	tca	gga	gca	agt	aat	gta	384	
Ser	Arg	Gln	Ile	Phe	Ala	Asn	Glu	Ile	Ser	Ser	Gly	Ala	Ser	Asn	Val		
		115					120					125					
gga	gta	gtt	ata	ttt	tct	act	cag	gat	tcg	gcg	aat	aca	ttc	aat	gtt	432	
Gly	Val	Val	Ile	Phe	Ser	Thr	Gln	Asp	Ser	Ala	Asn	Thr	Phe	Asn	Val		
	130					135					140						

Ala Gly Phe Ala Asn Gly Ser Thr Ala Ala Asp Lys Ala Ser Ala Val	
115 120 125	
gcc gtt gaa gtc tgg agc act gta act ccg gca aca ggg agt gca aca	432
Ala Val Glu Val Trp Ser Thr Val Thr Pro Ala Thr Gly Ser Ala Thr	
130 135 140	
caa ttt agc tgt gta aca cca gca tca caa gag gta aca atc tcc act	480
Gln Phe Ser Cys Val Thr Pro Ala Ser Gln Glu Val Thr Ile Ser Thr	
145 150 155 160	
gca gcc aat gcg gtc gtt tat tat ccg atg agt gca cgc ctg gtc gtg	528
Ala Ala Asn Ala Val Val Tyr Tyr Pro Met Ser Ala Arg Leu Val Val	
165 170 175	
gaa aaa aat aaa acc gta aac aat gtc act gcg ggt aag ttt tct gca	576
Glu Lys Asn Lys Thr Val Asn Asn Val Thr Ala Gly Lys Phe Ser Ala	
180 185 190	
cca gcc aca ttt aca gta acc tat aac taa	606
Pro Ala Thr Phe Thr Val Thr Tyr Asn *	
195 200	
<210> 141	
<211> 612	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(612)	
<400> 141	
atg gaa ttc ggt gtc aga ttc agt aac tac aag gga cgt caa atg ata	48
Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile	
1 5 10 15	
aaa aca acg cca cat aaa ata gtg ata ctg atg gga ata tta tta tca	96
Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser	
20 25 30	
ccc tca gta ttt gca acg gat att aat gta gag ttt aca gcc act gtc	144
Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val	
35 40 45	
aaa gcg aca acc tgt aac atc aca ctt act ggt aat aac gtc acg aat	192
Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn	
50 55 60	
gat ggc aat aat aac tac aca ttg aga atc cct aag atg ggt ctg gat	240
Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp	
65 70 75 80	
aag atc gcg aat aaa acg aca gaa tct cag gct gat ttt aaa ctg gtt	288
Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val	
85 90 95	

gcc agt ggg tgc agc agt ggc atc agt tgg att gat acc act ctg acc 336
Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
100 105 110

gga aat gca tca tca agc tca cct aag ctt att ata ccg cag tct ggt 384
Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
115 120 125

gat tca tct tcg acg aca agt aat atc ggt atg ggt ttc aaa aaa cgg 432
Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
130 135 140

act act gat gat gcc act ttc ctt aaa cct aac agt gcg gaa aag ata 480
Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
145 150 155 160

cgc tgg agc aca gac gag atg cag ccc gat aag ggt ctt gaa atg acc 528
Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
165 170 175

ggt gcg cta cgt gaa aca gat gca ggg caa ggc gta ccg ggg aat ttt 576
Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
180 185 190

cgt gca ctg gcg acg ttt aat ttc atc tat caa taa 612
 Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln *
 195 200

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<210> 142
<211> 420
<212> DNA
<213> Escherichia coli
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<220>  
<221> CDS  
<222> (1)...(420)
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Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
  1             5             10             15
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ttc	tct	ggt	ctg	gtc	gag	aaa	atc	cag	gta	acg	ggt	agc	gaa	ggt	gaa	96
Phe	Ser	Gly	Leu	Val	Glu	Lys	Ile	Gln	Val	Thr	Gly	Ser	Glu	Gly	Glu	
			20					25					30			

ctg ggg atc tac cct ggc cac gca ccg ctg ctc acc gcc att aag cct 144
Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
35 40 45

ggt atg att cgc atc gtg aaa cag cac ggt cac gaa gag ttt atc tat 192
Gly Met Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
50 55 60

ctg tct ggc ggc att ctt qaa gtg cag cct ggc aac gtg acc gtt ctg 240

gca gca cct tcc tac gaa gag ctg tca aac tct cag gaa ctg ctg gaa	384
Ala Ala Pro Ser Tyr Glu Glu Leu Ser Asn Ser Gln Glu Leu Leu Glu	
115 120 125	
acc ggt atc aaa gtt atc gac ctg atg tgt ccg ttc gct aag ggc ggt	432
Thr Gly Ile Lys Val Ile Asp Leu Met Cys Pro Phe Ala Lys Gly Gly	
130 135 140	
aaa gtt ggt ctg ttc ggt ggt gcg ggt gta ggt aaa acc gta aac atg	480
Lys Val Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Asn Met	
145 150 155 160	
atg gag ctc att cgt aac atc gcg atc gag cac tcc ggt tac tct gtg	528
Met Glu Leu Ile Arg Asn Ile Ala Ile Glu His Ser Gly Tyr Ser Val	
165 170 175	
ttt gcg ggc gta ggt gaa cgt act cgt gag ggt aac gac ttc tac cac	576
Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Phe Tyr His	
180 185 190	
gaa atg acc gac tcc aac gtt atc gac aaa gta tcc ctg gtg tat ggc	624
Glu Met Thr Asp Ser Asn Val Ile Asp Lys Val Ser Leu Val Tyr Gly	
195 200 205	
cag atg aac gag ccg ccg gga aac cgt ctg cgc gtt gct ctg acc ggt	672
Gln Met Asn Glu Pro Pro Gly Asn Arg Leu Arg Val Ala Leu Thr Gly	
210 215 220	
ctg acc atg gct gag aaa ttc cgt gac gaa ggt cgt gac gtt ctg ctg	720
Leu Thr Met Ala Glu Lys Phe Arg Asp Glu Gly Arg Asp Val Leu Leu	
225 230 235 240	
ttc gtt gac aac atc tat cgt tac acc ctg gcc ggt acg gaa gta tcc	768
Phe Val Asp Asn Ile Tyr Arg Tyr Thr Leu Ala Gly Thr Glu Val Ser	
245 250 255	
gca ctg ctg ggc cgt atg cct tca gcg gta ggt tat cag ccg acc ctg	816
Ala Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu	
260 265 270	
gcg gaa gag atg ggc gtt ctg cag gaa cgt atc acc tcc acc aaa act	864
Ala Glu Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Thr	
275 280 285	
ggt tct atc acc tcc gta cag gca gta tac gta cct gcg gat gac ttg	912
Gly Ser Ile Thr Ser Val Gln Ala Val Tyr Val Pro Ala Asp Asp Leu	
290 295 300	
act gac ccg tct ccg gca acc acc ttt gcg cac ctt gac gca acc gtg	960
Thr Asp Pro Ser Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Val	
305 310 315 320	
gta ctg agc cgt cag atc gcg tct ctg ggt atc tac ccg gcc gtt gac	1008
Val Leu Ser Arg Gln Ile Ala Ser Leu Gly Ile Tyr Pro Ala Val Asp	
325 330 335	

ccg ctg gac tcc acc agc cgt cag ctg gac ccg ctg gtg gtt ggt cag	1056
Pro Leu Asp Ser Thr Ser Arg Gln Leu Asp Pro Leu Val Val Gly Gln	
340 345 350	
gaa cac tac gac acc gcg cgt ggc gtt cag tcc atc ctg caa cgt tat	1104
Glu His Tyr Asp Thr Ala Arg Gly Val Gln Ser Ile Leu Gln Arg Tyr	
355 360 365	
cag gaa ctg aaa gac atc atc gcc atc ctg ggt atg gat gaa ctg tct	1152
Gln Glu Leu Lys Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser	
370 375 380	
gaa gaa gac aaa ctg gtg gta gcg cgt gct cgt aag atc cag cgc ttc	1200
Glu Glu Asp Lys Leu Val Val Ala Arg Ala Arg Lys Ile Gln Arg Phe	
385 390 395 400	
ctg tcc cag ccg ttc ttc gtg gca gaa gta ttc acc ggt tct ccg ggt	1248
Leu Ser Gln Pro Phe Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly	
405 410 415	
aaa tac gtc tcc ctg aaa gac acc atc cgt ggc ttt aaa ggc atc atg	1296
Lys Tyr Val Ser Leu Lys Asp Thr Ile Arg Gly Phe Lys Gly Ile Met	
420 425 430	
gaa ggc gaa tac gat cac ctg ccg gag cag gcg ttc tac atg gtc ggt	1344
Glu Gly Glu Tyr Asp His Leu Pro Glu Gln Ala Phe Tyr Met Val Gly	
435 440 445	
tcc atc gaa gaa gct gtg gaa aaa gcc aaa aaa ctt taa	1383
Ser Ile Glu Glu Ala Val Glu Lys Ala Lys Lys Leu *	
450 455 460	
<210> 144	
<211> 864	
<212> DNA	
<213> Escherichia coli	
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<221> CDS	
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Met Ala Gly Ala Lys Glu Ile Arg Ser Lys Ile Ala Ser Val Gln Asn	
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acg caa aag atc act aaa gcg atg gag atg gtc gcc gct tcc aaa atg	96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met	
20 25 30	
cgt aaa tcg cag gat cgc atg gcg gcc agc cgt cct tat gca gaa acc	144
Arg Lys Ser Gln Asp Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Thr	
35 40 45	
atg cgc aaa gtg att ggt cac ctt gca cac ggt aat ctg gaa tat aag	192
Met Arg Lys Val Ile Gly His Leu Ala His Gly Asn Leu Glu Tyr Lys	

<210> 145
 <211> 1542
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1542)

<400> 145
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 Met Gln Leu Asn Ser Thr Glu Ile Ser Glu Leu Ile Lys Gln Arg Ile
 1 5 10 15

gct cag ttc aat gtt gtg agt gaa gct cac aac gaa ggt act att gtt 96
 Ala Gln Phe Asn Val Val Ser Glu Ala His Asn Glu Gly Thr Ile Val
 20 25 30

tct gta agt gac ggt gtt atc cgc att cac ggc ctg gcc gat tgt atg 144
 Ser Val Ser Asp Gly Val Ile Arg Ile His Gly Leu Ala Asp Cys Met
 35 40 45

cag ggt gaa atg atc tcc ctg ccg ggt aac cgt tac gct atc gca ctg 192
 Gln Gly Glu Met Ile Ser Leu Pro Gly Asn Arg Tyr Ala Ile Ala Leu
 50 55 60

aac ctc gag cgc gac tct gta ggt gcg gtt gtt atg ggt ccg tac gct 240
 Asn Leu Glu Arg Asp Ser Val Gly Ala Val Val Met Gly Pro Tyr Ala
 65 70 75 80

gac ctt gcc gaa ggc atg aaa gtt aag tgt act ggc cgt atc ctg gaa 288
 Asp Leu Ala Glu Gly Met Lys Val Lys Cys Thr Gly Arg Ile Leu Glu
 85 90 95

gtt ccg gtt ggc cgt ggc ctg ctg ggc cgt gtg gtt aac act ctg ggt 336
 Val Pro Val Gly Arg Gly Leu Leu Gly Arg Val Val Asn Thr Leu Gly
 100 105 110

gca cca atc gac ggt aaa ggt ccg ctg gat cac gac ggc ttc tct gct 384
 Ala Pro Ile Asp Gly Lys Gly Pro Leu Asp His Asp Gly Phe Ser Ala
 115 120 125

gta gaa gca atc gct ccg ggc gtt atc gaa cgt cag tcc gta gat cag 432
 Val Glu Ala Ile Ala Pro Gly Val Ile Glu Arg Gln Ser Val Asp Gln
 130 135 140

ccg gta cag acc ggt tat aaa gcc gtt gac tcc atg atc cca atc ggt 480
 Pro Val Gln Thr Gly Tyr Lys Ala Val Asp Ser Met Ile Pro Ile Gly
 145 150 155 160

cgt ggt cag cgt gaa ttg atc atc ggt gac cgt cag aca ggt aaa acc 528
 Arg Gly Gln Arg Glu Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr
 165 170 175

gca ctg gct atc gat gcc atc atc aac cag cgc gat tcc ggt atc aaa	576
Ala Leu Ala Ile Asp Ala Ile Ile Asn Gln Arg Asp Ser Gly Ile Lys	
180 185 190	
tgt atc tat gtc gct atc ggc cag aaa gcg tcc acc att tct aac gtg	624
Cys Ile Tyr Val Ala Ile Gly Gln Lys Ala Ser Thr Ile Ser Asn Val	
195 200 205	
gta cgt aaa ctg gaa gag cac ggc gca ctg gct aac acc atc gtt gtg	672
Val Arg Lys Leu Glu Glu His Gly Ala Leu Ala Asn Thr Ile Val Val	
210 215 220	
gta gca acc gcg tct gaa tcc gct gca ctg caa tac ctg gca ccg tat	720
Val Ala Thr Ala Ser Glu Ser Ala Ala Leu Gln Tyr Leu Ala Pro Tyr	
225 230 235 240	
gcc ggt tgc gca atg ggc gaa tac ttc cgt gac cgc ggt gaa gat gcg	768
Ala Gly Cys Ala Met Gly Glu Tyr Phe Arg Asp Arg Gly Glu Asp Ala	
245 250 255	
ctg atc att tac gat gac ctg tct aaa cag gct gtt gct tac cgt cag	816
Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala Tyr Arg Gln	
260 265 270	
atc tcc ctg ctg ctc cgt cgt ccg cca gga cgt gaa gca ttc ccg ggc	864
Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala Phe Pro Gly	
275 280 285	
gac gtt ttc tac ctc cac tct cgt ctg ctg gag cgt gct gca cgt gtt	912
Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala Ala Arg Val	
290 295 300	
aac gcc gaa tac gtt gaa gcc ttc acc aaa ggt gaa gtg aaa ggg aaa	960
Asn Ala Glu Tyr Val Glu Ala Phe Thr Lys Gly Glu Val Lys Gly Lys	
305 310 315 320	
acc ggt tct ctg acc gca ctg ccg att atc gaa act cag gcg ggt gac	1008
Thr Gly Ser Leu Thr Ala Leu Pro Ile Ile Glu Thr Gln Ala Gly Asp	
325 330 335	
gtt tct gcg ttc gtt ccg acc aac gta atc tcc att acc gat ggt cag	1056
Val Ser Ala Phe Val Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln	
340 345 350	
atc ttc ctg gaa acc aac ctg ttc aac gcc ggt att cgt cct gcg gtt	1104
Ile Phe Leu Glu Thr Asn Leu Phe Asn Ala Gly Ile Arg Pro Ala Val	
355 360 365	
aac ccg ggt att tcc gta tcc cgt gtt ggt ggt gca gca cag acc aag	1152
Asn Pro Gly Ile Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys	
370 375 380	
atc atg aaa aaa ctg tcc ggt ggt atc cgt acc gct ctg gca cag tat	1200
Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr	
385 390 395 400	
cgt gaa ctg gca gcg ttc tct cag ttt gca tcc gac ctt gac gat gca	1248

tgt ggt gag caa ctg gac gaa aac ggt cag aac ctg att cgg gtt atg	240
Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met	
65 70 75 80	

gct gaa aat ggt cgt ctt aac gcg ctc ccg gat gtt ctg gag cag ttt	288
Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe	
85 90 95	

att cac ctg cgt gcc gtg agt gag gct acc gct gag gta gac gtc att	336
Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile	
100 105 110	

tcc gct gcc gca ctg agt gaa caa cag ctc gcg aaa att tct gct gcg	384
Ser Ala Ala Ala Leu Ser Glu Gln Gln Leu Ala Lys Ile Ser Ala Ala	
115 120 125	

atg gaa aaa cgt ctg tca cgc aaa gtt aag ctg aat tgc aaa atc gat	432
Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp	
130 135 140	

aag tct gta atg gca ggc gtt atc atc cga gcg ggt gat atg gtc att	480
Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile	
145 150 155 160	

gat ggc agc gta cgc ggt cgt ctt gag cgc ctt gca gac gtc ttg cag	528
Asp Gly Ser Val Arg Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln	
165 170 175	

tct taa	534
Ser *	

<210> 147
 <211> 471
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(471)

<400> 147	
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Met Asn Leu Asn Ala Thr Ile Leu Gly Gln Ala Ile Ala Phe Val Leu	
1 5 10 15	

ttc gtt ctg ttc tgc atg aag tac gta tgg ccg cca tta atg gca gcc	96
Phe Val Leu Phe Cys Met Lys Tyr Val Trp Pro Pro Leu Met Ala Ala	
20 25 30	

atc gaa aaa cgt caa aaa gaa att gct gac ggc ctt gct tcc gca gaa	144
Ile Glu Lys Arg Gln Lys Glu Ile Ala Asp Gly Leu Ala Ser Ala Glu	
35 40 45	

cga gca cat aag gac ctt gac ctt gca aag gcc agc gcg acc gac cag	192
---	-----

<210> 149
 <211> 816
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(816)

<400> 149
 atg gct tca gaa aat atg acg ccg cag gat tac ata gga cac cac ctg 48
 Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu
 1 5 10 15
 aat aac ctt cag ctg gac ctg cgt aca ttc tcg ctg gtg gat cca caa 96
 Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln
 20 25 30
 aac ccc cca gcc acc ttc tgg aca atc aat att gac tcc atg ttc ttc 144
 Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe
 35 40 45
 tcg gtg gtg ctg ggt ctg ttg ttc ctg gtt tta ttc cgt agc gta gcc 192
 Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala
 50 55 60
 aaa aag gcg acc agc ggt gtg cca ggt aag ttt cag acc gcg att gag 240
 Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu
 65 70 75 80
 ctg gtg atc ggc ttt gtt aat ggt agc gtg aaa gac atg tac cat ggc 288
 Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly
 85 90 95
 aaa agc aag ctg att gct ccg ctg gcc ctg acg atc ttc gtc tgg gta 336
 Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val
 100 105 110
 ttc ctg atg aac ctg atg gat tta ctg cct atc gac ctg ctg ccg tac 384
 Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr
 115 120 125
 att gct gaa cat gta ctg ggt ctg cct gca ctg cgt gtg gtt ccg tct 432
 Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser
 130 135 140
 gcg gac gtg aac gta acg ctg tct atg gca ctg ggc gta ttt atc ctg 480
 Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu
 145 150 155 160
 att ctg ttc tac agc atc aaa atg aaa ggc atc ggc ggc ttc acg aaa 528
 Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys
 165 170 175

gag ttg acg ctg cag ccg ttc aat cac tgg gcg ttc att cct gtc aac	576
Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn	
180 185 190	
tta atc ctt gaa ggg gta agc ctg ctg tcc aaa cca gtt tca ctc ggt	624
Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly	
195 200 205	
ttg cga ctg ttc ggt aac atg tat gcc ggt gag ctg att ttc att ctg	672
Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu	
210 215 220	
att gct ggt ctg ttg ccg tgg tgg tca cag tgg atc ctg aat gtg ccg	720
Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro	
225 230 235 240	
tgg gcc att ttc cac atc ctg atc att acg ctg caa gcc ttc atc ttc	768
Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe	
245 250 255	
atg gtt ctg acg atc gtc tat ctg tgc atg gcg tct gaa gaa cat taa	816
Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His *	
260 265 270	
<210> 150	
<211> 393	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> CDS	
<222> (1)...(393)	
<400> 150	
gtg aaa aac gtg atg tct gtg tgc ctc gtg agt cga aac gtt gct ccg	48
Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg	
1 5 10 15	
aag ctt ctg ctc gtt cag tta ctg gtg gtg ata gca agt gga ttg ctg	96
Lys Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu	
20 25 30	
ttc agc ctc aaa gac ccc ttc tgg ggc gtc tct gca ata agc ggg ggc	144
Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly	
35 40 45	
ctg gca gtc ttt ctg cct aac gtt ttg ttt atg ata ttt gcc tgg cgt	192
Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg	
50 55 60	
cac cag gcg cat aca cca gcg aaa ggc cgg gtg gcc tgg aca ttc gca	240
His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala	
65 70 75 80	
ttt ggc gaa gct ttc aaa gtt ctg gcg atg ttg gtg tta ctg gtg gtg	288

Phe Gly Glu Ala	Phe Lys Val Leu Ala Met Leu Val Leu Leu Val Val	
85	90	95
gcg ttg gcg gtt tta aag gcg gta ttc ttg ccg ctg atc gtt acg tgg	336	
Ala Leu Ala Val Leu Lys Ala Val Phe Leu Pro Leu Ile Val Thr Trp		
100	105	110
gtt ttg gtg ctg gtg gtt cag ata ctg gca ccg gct gta att aac aac	384	
Val Leu Val Leu Val Val Gln Ile Leu Ala Pro Ala Val Ile Asn Asn		
115	120	125
aaa ggg taa	393	
Lys Gly *		
130		

<210> 151
 <211> 1242
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1242)

<400> 151	
atg caa aaa cac ggc gac cgc tat gtg tgg atc aac ccg cct gct att	48
Met Gln Lys His Gly Asp Arg Tyr Val Trp Ile Asn Pro Pro Ala Ile	
1 5 10 15	
ccg ctt tct acc gaa gag atg gac agc gtt ttt gcg ctg cca tac aag	96
Pro Leu Ser Thr Glu Glu Met Asp Ser Val Phe Ala Leu Pro Tyr Lys	
20 25 30	
cgc gtg cca cat ccg gcc tat ggc aat gcc cgt att ccg gct tac gaa	144
Arg Val Pro His Pro Ala Tyr Gly Asn Ala Arg Ile Pro Ala Tyr Glu	
35 40 45	
atg atc cgt ttt tcg gtc aac att atg cgt ggc tgc ttt ggc ggc tgc	192
Met Ile Arg Phe Ser Val Asn Ile Met Arg Gly Cys Phe Gly Gly Cys	
50 55 60	
tct ttc tgt tct atc acc gag cac gaa ggg cgc att att cag agc cgt	240
Ser Phe Cys Ser Ile Thr Glu His Glu Gly Arg Ile Ile Gln Ser Arg	
65 70 75 80	
tcc gaa gat tcg atc att aat gag atc gaa gcg atc cgc gac acc gtt	288
Ser Glu Asp Ser Ile Ile Asn Glu Ile Glu Ala Ile Arg Asp Thr Val	
85 90 95	
cca ggt ttt acg ggc gtg att tcc gat ctt ggt ggg cca act gcc aac	336
Pro Gly Phe Thr Gly Val Ile Ser Asp Leu Gly Gly Pro Thr Ala Asn	
100 105 110	
atg tat atg ttg cgc tgc aaa tcg cca cgc gct gaa caa act tgt cgc	384
Met Tyr Met Leu Arg Cys Lys Ser Pro Arg Ala Glu Gln Thr Cys Arg	
115 120 125	

cca acc att gaa gag atg cgt gaa gct cgt cgc cag aac cgc aat acc	1104
Pro Thr Ile Glu Glu Met Arg Glu Ala Arg Arg Gln Asn Arg Asn Thr	
355 360 365	
cgt ccg gcg ttg acg aaa cat acg ccg atg gcg acc cag cgt cag acg	1152
Arg Pro Ala Leu Thr Lys His Thr Pro Met Ala Thr Gln Arg Gln Thr	
370 375 380	
cct gct acg gca aaa aaa gcg tcg tct acg caa tct cgt ccg gtg aat	1200
Pro Ala Thr Ala Lys Lys Ala Ser Ser Thr Gln Ser Arg Pro Val Asn	
385 390 395 400	
gct ggt gcg aag aaa cgg cct aaa gcg gcg gtt gga cgt taa	1242
Ala Gly Ala Lys Lys Arg Pro Lys Ala Ala Val Gly Arg *	
405 410	

<210> 152
 <211> 978
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(978)

<400> 152	
atg agc tct atc tcc ctg atc caa ccg gat cgc gac ctg ttc tcc tgg	48
Met Ser Ser Ile Ser Leu Ile Gln Pro Asp Arg Asp Leu Phe Ser Trp	
1 5 10 15	
ccg cag tac tgg gcc gcc tgt ttt gga ccg gca ccg ttt ttg ccg atg	96
Pro Gln Tyr Trp Ala Ala Cys Phe Gly Pro Ala Pro Phe Leu Pro Met	
20 25 30	
tct cgt gaa gag atg gat caa ctt ggc tgg gat agc tgc gac atc att	144
Ser Arg Glu Glu Met Asp Gln Leu Gly Trp Asp Ser Cys Asp Ile Ile	
35 40 45	
ttg gtt act ggc gac gcg tat gtc gat cac cca agc ttc ggg atg gcg	192
Leu Val Thr Gly Asp Ala Tyr Val Asp His Pro Ser Phe Gly Met Ala	
50 55 60	
att tgc ggt cgt atg ctg gaa gcg cag ggc ttt cgc gtc ggg atc atc	240
Ile Cys Gly Arg Met Leu Glu Ala Gln Gly Phe Arg Val Gly Ile Ile	
65 70 75 80	
gcc cag ccg gac tgg agc agc aaa gac gac ttt atg cgt ctg ggt aaa	288
Ala Gln Pro Asp Trp Ser Ser Lys Asp Asp Phe Met Arg Leu Gly Lys	
85 90 95	
ccg aat ctg ttt ttc ggt gtt act gct ggc aac atg gat tcg atg atc	336
Pro Asn Leu Phe Phe Gly Val Thr Ala Gly Asn Met Asp Ser Met Ile	
100 105 110	
aac cgt tat acc gcc gat cgc cgt tta cgt cat gac gat gcc tac acg	384

<211> 681
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(681)

<400> 153

atg att cag tat ctg aac gtc ttt ttt tac gat atc tac ccg tac att	48
Met Ile Gln Tyr Leu Asn Val Phe Phe Tyr Asp Ile Tyr Pro Tyr Ile	
1 5 10 15	
tgt gcg acg gtg ttt ttc ctc ggc agc tgg ctg cgc tac gac tac ggg	96
Cys Ala Thr Val Phe Phe Leu Gly Ser Trp Leu Arg Tyr Asp Tyr Gly	
20 25 30	
cag tac acc tgg cgc gcc tcc tca agt caa atg ctc gat aaa cgc ggg	144
Gln Tyr Thr Trp Arg Ala Ser Ser Ser Gln Met Leu Asp Lys Arg Gly	
35 40 45	
atg gtg ata tgg tcg aat ctg ttc cat atc ggc att ttg ggg att ttc	192
Met Val Ile Trp Ser Asn Leu Phe His Ile Gly Ile Leu Gly Ile Phe	
50 55 60	
ttc ggg cac ttg ttc ggc atg tta acg ccg cac tgg atg tac gcg tgg	240
Phe Gly His Leu Phe Gly Met Leu Thr Pro His Trp Met Tyr Ala Trp	
65 70 75 80	
ttt ttg cca gtg gca gcg aaa caa ctc atg gcg atg gtg ctc ggc ggt	288
Phe Leu Pro Val Ala Ala Lys Gln Leu Met Ala Met Val Leu Gly Gly	
85 90 95	
att tgc ggt gtg ttg acg ttg att ggc ggc gca gga ctg ctg tgg cgc	336
Ile Cys Gly Val Leu Thr Leu Ile Gly Gly Ala Gly Leu Leu Trp Arg	
100 105 110	
agg ctg aca aat cag cgc gtg cgt gcc act tcc act acg ccg gat atc	384
Arg Leu Thr Asn Gln Arg Val Arg Ala Thr Ser Thr Thr Pro Asp Ile	
115 120 125	
atc atc atg agc att ttg ctg atc cag tgt ctg ttg ggg cta agt acc	432
Ile Ile Met Ser Ile Leu Leu Ile Gln Cys Leu Leu Gly Leu Ser Thr	
130 135 140	
ata ccg ttt tca gca cag tat cct gat ggt agc gaa atg atg aag ctg	480
Ile Pro Phe Ser Ala Gln Tyr Pro Asp Gly Ser Glu Met Met Lys Leu	
145 150 155 160	
gtg ggt tgg gcg caa agc att gtc act ttc cgt ggt gga tcg tca gag	528
Val Gly Trp Ala Gln Ser Ile Val Thr Phe Arg Gly Gly Ser Ser Glu	
165 170 175	
atg ctc aac ggc gta gcg ttc gtc ttc cgc ctg cat ctg gtg ttg gga	576
Met Leu Asn Gly Val Ala Phe Val Phe Arg Leu His Leu Val Leu Gly	
180 185 190	

atg acc atc ttc ctg ctc ttc ccg ttc acc cga ctg gtg cat gtg tgg	624
Met Thr Ile Phe Leu Leu Phe Pro Phe Thr Arg Leu Val His Val Trp	
195 200 205	
agc gcg ccg ttt gag tac ttt act cgt cga tat caa att gtg cgt tcg	672
Ser Ala Pro Phe Glu Tyr Phe Thr Arg Arg Tyr Gln Ile Val Arg Ser	
210 215 220	
cgg cga taa	681
Arg Arg *	
225	

<210> 154
 <211> 696
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(696)

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Met Gln Ile Leu Lys Val Ile Gly Leu Leu Met Glu Tyr Pro Asp Glu	
1 5 10 15	
ctg ttg tgg gaa tgc aag gag gac gcg ctg gcg ttg atc cgc cgc gac	96
Leu Leu Trp Glu Cys Lys Glu Asp Ala Leu Ala Leu Ile Arg Arg Asp	
20 25 30	
gcg ccg atg ctt acg gat ttc acc cac aac ctg ctt aac gcg ccg ctg	144
Ala Pro Met Leu Thr Asp Phe Thr His Asn Leu Leu Asn Ala Pro Leu	
35 40 45	
ctg gat aaa cag gcc gaa tgg tgc gaa gtg ttt gac cgc ggg cgc acc	192
Leu Asp Lys Gln Ala Glu Trp Cys Glu Val Phe Asp Arg Gly Arg Thr	
50 55 60	
acg tcg ctg ctg ctg ttc gaa cat gtt cat gcc gag tcc cgc gat cgc	240
Thr Ser Leu Leu Leu Phe Glu His Val His Ala Glu Ser Arg Asp Arg	
65 70 75 80	
ggc cag gca atg gtg gac ctg ctg gcg gag tat gaa aag gtc ggc ctg	288
Gly Gln Ala Met Val Asp Leu Leu Ala Glu Tyr Glu Lys Val Gly Leu	
85 90 95	
cag ctg gat tgt ccg gaa ctg ccc gat tat cta ccg ctg tat ctg gag	336
Gln Leu Asp Cys Arg Glu Leu Pro Asp Tyr Leu Pro Leu Tyr Leu Glu	
100 105 110	
tat tta agc gta ctg cct gac gat cag gcg aaa gaa gga ttg ctc aat	384
Tyr Leu Ser Val Leu Pro Asp Asp Gln Ala Lys Glu Gly Leu Leu Asn	
115 120 125	
gtt gcg ccg atc ctc gcc ctg ctt ggc ggt cgc tta aaa caa cgc gag	432
Val Ala Pro Ile Leu Ala Leu Leu Gly Gly Arg Leu Lys Gln Arg Glu	

<211> 3741
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(3741)

<400> 156

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Met Ser Lys Leu Leu Asp Arg Phe Arg Tyr Phe Lys Gln Lys Gly Glu	
1 5 10 15	
acc ttt gcc gat ggt cac gga cag gtg atg cat agc aac cgc gac tgg	96
Thr Phe Ala Asp Gly His Gly Gln Val Met His Ser Asn Arg Asp Trp	
20 25 30	
gag gac agc tat cgc cag cgt tgg cag ttc gac aaa atc gtg cgt tcc	144
Glu Asp Ser Tyr Arg Gln Arg Trp Gln Phe Asp Lys Ile Val Arg Ser	
35 40 45	
acc cac ggt gtt aac tgt aca ggc tcc tgt agc tgg aaa atc tac gtt	192
Thr His Gly Val Asn Cys Thr Gly Ser Cys Ser Trp Lys Ile Tyr Val	
50 55 60	
aaa aat ggt ctg gtg acc tgg gaa atc caa cag acc gac tac ccg cgc	240
Lys Asn Gly Leu Val Thr Trp Glu Ile Gln Gln Thr Asp Tyr Pro Arg	
65 70 75 80	
act cgc cct gac ctg ccc aat cat gaa cct cgc ggc tgc ccg cgt ggc	288
Thr Arg Pro Asp Leu Pro Asn His Glu Pro Arg Gly Cys Pro Arg Gly	
85 90 95	
gca agt tac tcc tgg tat ctt tac agc gct aac cgc ctg aaa tac ccg	336
Ala Ser Tyr Ser Trp Tyr Leu Tyr Ser Ala Asn Arg Leu Lys Tyr Pro	
100 105 110	
ctc att cgt aaa cga ctg att gaa ctg tgg cgc gaa gcc ctc aag caa	384
Leu Ile Arg Lys Arg Leu Ile Glu Leu Trp Arg Glu Ala Leu Lys Gln	
115 120 125	
cac agc gat ccg gta ctg gcg tgg gca tcg att atg aac gat ccg caa	432
His Ser Asp Pro Val Leu Ala Trp Ala Ser Ile Met Asn Asp Pro Gln	
130 135 140	
aag tgc ctg agc tac aaa caa gtg cgt ggg cgc ggc ggc ttt atc cgc	480
Lys Cys Leu Ser Tyr Lys Gln Val Arg Gly Arg Gly Gly Phe Ile Arg	
145 150 155 160	
tcc aac tgg cag gaa cta aac cag ctg att gcc gcc gct aac gtc tgg	528
Ser Asn Trp Gln Glu Leu Asn Gln Leu Ile Ala Ala Ala Asn Val Trp	
165 170 175	
acc atc aaa acc tac ggc ccg gat cgc gtt gcc ggt ttc tcg ccg atc	576
Thr Ile Lys Thr Tyr Gly Pro Asp Arg Val Ala Gly Phe Ser Pro Ile	
180 185 190	

ccg gcg atg tcg atg gtt tct tac gcc gcc gga acg cgt tat ctg tcg	624
Pro Ala Met Ser Met Val Ser Tyr Ala Ala Gly Thr Arg Tyr Leu Ser	
195 200 205	
ctg ctt ggc ggc acc tgt tta agt ttc tac gac tgg tat tgc gac ctg	672
Leu Leu Gly Gly Thr Cys Leu Ser Phe Tyr Asp Trp Tyr Cys Asp Leu	
210 215 220	
ccg ccc gcc tcg ccg atg acc tgg ggc gag caa acc gac gta ccg gaa	720
Pro Pro Ala Ser Pro Met Thr Trp Gly Glu Gln Thr Asp Val Pro Glu	
225 230 235 240	
tct gcc gac tgg tat aac tcc agc tac atc atc gcc tgg ggg tct aac	768
Ser Ala Asp Trp Tyr Asn Ser Ser Tyr Ile Ile Ala Trp Gly Ser Asn	
245 250 255	
gta ccg cag aca cgt acg ccg gac gcc cac ttc ttt acc gaa gta cgc	816
Val Pro Gln Thr Arg Thr Pro Asp Ala His Phe Phe Thr Glu Val Arg	
260 265 270	
tac aaa ggc act aaa acc atc gcc att acc cct gac tac tct gaa gtg	864
Tyr Lys Gly Thr Lys Thr Ile Ala Ile Thr Pro Asp Tyr Ser Glu Val	
275 280 285	
gcc aaa ttg tgc gac cag tgg ctg gca ccg aaa caa ggc act gat agc	912
Ala Lys Leu Cys Asp Gln Trp Leu Ala Pro Lys Gln Gly Thr Asp Ser	
290 295 300	
gcc ctg gcg atg gca atg ggc cat gtg att tta aaa gag ttt cat ctc	960
Ala Leu Ala Met Ala Met Gly His Val Ile Leu Lys Glu Phe His Leu	
305 310 315 320	
gat aat ccc agc gac tac ttt atc aac tac tgc cgc cgc tac agc gac	1008
Asp Asn Pro Ser Asp Tyr Phe Ile Asn Tyr Cys Arg Arg Tyr Ser Asp	
325 330 335	
atg ccg atg ctg gta atg ctg gag cct cgc gac gat ggt agc tac gtt	1056
Met Pro Met Leu Val Met Leu Glu Pro Arg Asp Asp Gly Ser Tyr Val	
340 345 350	
ccc ggg cgc atg atc cgc gca tct gac ctg gtg gat gga ctg ggc gaa	1104
Pro Gly Arg Met Ile Arg Ala Ser Asp Leu Val Asp Gly Leu Gly Glu	
355 360 365	
agc aac aat ccg cag tgg aaa acc gta gca gtt aat acc gca ggt gaa	1152
Ser Asn Asn Pro Gln Trp Lys Thr Val Ala Val Asn Thr Ala Gly Glu	
370 375 380	
ttg gta gtg ccg aac ggt tcg att ggt ttc cgc tgg gga gaa aaa ggc	1200
Leu Val Val Pro Asn Gly Ser Ile Gly Phe Arg Trp Gly Glu Lys Gly	
385 390 395 400	
aaa tgg aat ctg gaa tcc att gcc gcc ggt acg gaa acc gaa ttg tcg	1248
Lys Trp Asn Leu Glu Ser Ile Ala Ala Gly Thr Glu Thr Glu Leu Ser	
405 410 415	
tta acc ctg ctc ggt caa cat gac gct gtt gca ggc gtg gcc ttc ccc	1296

225	230	235	240	
gaa ctg tac ctc aag cgt ctg gtg gtt ggt ggc ttc gag cgt gta ttc				768
Glu Leu Tyr Leu Lys Arg Leu Val Val Gly Gly Phe Glu Arg Val Phe	245	250	255	
gaa atc aac cgt aac ttc cgt aac gaa ggt att tcc gta cgt cat aac				816
Glu Ile Asn Arg Asn Phe Arg Asn Glu Gly Ile Ser Val Arg His Asn	260	265	270	
cca gag ttc acc atg atg gaa ctc tac atg gct tac gca gat tac aaa				864
Pro Glu Phe Thr Met Met Glu Leu Tyr Met Ala Tyr Ala Asp Tyr Lys	275	280	285	
gat ctg atc gag ctg acc gaa ttc ctg ttc cgt act ctg gca cag gat				912
Asp Leu Ile Glu Leu Thr Glu Ser Leu Phe Arg Thr Leu Ala Gln Asp	290	295	300	
att ctc ggt aag acg gaa gtg acc tac ggc gac gtg acg ctg gac ttc				960
Ile Leu Gly Lys Thr Glu Val Thr Tyr Gly Asp Val Thr Leu Asp Phe	305	310	315	320
ggt aaa ccg ttc gaa aaa ctg acc atg cgt gaa gcg atc aag aaa tat				1008
Gly Lys Pro Phe Glu Lys Leu Thr Met Arg Glu Ala Ile Lys Lys Tyr	325	330	335	
cgc ccg gaa acc gac atg gcg gat ctg gac aac ttc gac tct gcg aaa				1056
Arg Pro Glu Thr Asp Met Ala Asp Leu Asp Asn Phe Asp Ser Ala Lys	340	345	350	
gca att gct gaa tct atc ggc atc cac gtt gag aag agc tgg ggt ctg				1104
Ala Ile Ala Glu Ser Ile Gly Ile His Val Glu Lys Ser Trp Gly Leu	355	360	365	
ggc cgt atc gtt acc gag atc ttc gaa gaa gtg gca gaa gca cat ctg				1152
Gly Arg Ile Val Thr Glu Ile Phe Glu Glu Val Ala Glu Ala His Leu	370	375	380	
att cag ccg acc ttc att act gaa tat ccg gca gaa gtt tct ccg ctg				1200
Ile Gln Pro Thr Phe Ile Thr Glu Tyr Pro Ala Glu Val Ser Pro Leu	385	390	395	400
gcg cgt cgt aac gac gtt aac ccg gaa atc aca gac cgc ttt gag ttc				1248
Ala Arg Arg Asn Asp Val Asn Pro Glu Ile Thr Asp Arg Phe Glu Phe	405	410	415	
ttc att ggt ggt cgt gaa atc ggt aac ggc ttt agc gag ctg aat gac				1296
Phe Ile Gly Gly Arg Glu Ile Gly Asn Gly Phe Ser Glu Leu Asn Asp	420	425	430	
gcg gaa gat cag gcg caa cgc ttc ctg gat cag gtt gcc gcg aaa gac				1344
Ala Glu Asp Gln Ala Gln Arg Phe Leu Asp Gln Val Ala Ala Lys Asp	435	440	445	
gca ggt gac gac gaa gcg atg ttc tac gat gaa gat tac gtc acc gca				1392
Ala Gly Asp Asp Glu Ala Met Phe Tyr Asp Glu Asp Tyr Val Thr Ala	450	455	460	

ctg gaa cat ggc tta ccg ccg aca gca ggt ctg gga att ggt atc gac	1440
Leu Glu His Gly Leu Pro Pro Thr Ala Gly Leu Gly Ile Gly Ile Asp	
465 470 475 480	

cgt atg gta atg ctg ttc acc aac agc cat acc atc cgc gac gtt att	1488
Arg Met Val Met Leu Phe Thr Asn Ser His Thr Ile Arg Asp Val Ile	
485 490 495	

ctg ttc ccg gcg atg cgt ccg gta aaa taa	1518
Leu Phe Pro Ala Met Arg Pro Val Lys *	
500 505	

<210> 160
 <211> 1098
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
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<400> 160	
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Met Phe Glu Ile Asn Pro Val Asn Asn Arg Ile Gln Asp Leu Thr Glu	
1 5 10 15	

cgc tcc gac gtt ctt agg ggg tat ctt gac tac gac gcc aag aaa gag	96
Arg Ser Asp Val Leu Arg Gly Tyr Leu Asp Tyr Asp Ala Lys Lys Glu	
20 25 30	

cgt ctg gaa gaa gta aac gcc gag ctg gaa cag ccg gat gtc tgg aac	144
Arg Leu Glu Glu Val Asn Ala Glu Leu Glu Gln Pro Asp Val Trp Asn	
35 40 45	

gaa ccc gaa cgc gca cag gcg ctg ggt aaa gag cgt tcc tcc ctc gaa	192
Glu Pro Glu Arg Ala Gln Ala Leu Gly Lys Glu Arg Ser Ser Leu Glu	
50 55 60	

gcc gtt gtc gac acc ctc gac caa atg aaa cag ggg ctg gaa gat gtt	240
Ala Val Val Asp Thr Leu Asp Gln Met Lys Gln Gly Leu Glu Asp Val	
65 70 75 80	

tct ggt ctg ctg gaa ctg gct gta gaa gct gac gac gaa gaa acc ttt	288
Ser Gly Leu Leu Glu Leu Ala Val Glu Ala Asp Asp Glu Glu Thr Phe	
85 90 95	

aac gaa gcc gtt gct gaa ctc gac gcc ctg gaa gaa aaa ctg gcg cag	336
Asn Glu Ala Val Ala Glu Leu Asp Ala Leu Glu Glu Lys Leu Ala Gln	
100 105 110	

ctt gag ttc cgc cgt atg ttc tct ggc gaa tat gac agc gcc gac tgc	384
Leu Glu Phe Arg Arg Met Phe Ser Gly Glu Tyr Asp Ser Ala Asp Cys	
115 120 125	

tac ctc gat att cag gcg ggg tct ggc ggt acg gaa gca cag gac tgg	432
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Tyr	Leu	Asp	Ile	Gln	Ala	Gly	Ser	Gly	Gly	Thr	Glu	Ala	Gln	Asp	Trp	
130						135					140					
gcg	agc	atg	ctt	gag	cgt	atg	tat	ctg	cgc	tgg	gca	gaa	tcg	cgt	ggc	480
Ala	Ser	Met	Leu	Glu	Arg	Met	Tyr	Leu	Arg	Trp	Ala	Glu	Ser	Arg	Gly	
145					150					155					160	
ttc	aaa	act	gaa	atc	atc	gaa	gag	tcg	gaa	ggc	gaa	gtg	gcg	ggc	att	528
Phe	Lys	Thr	Glu	Ile	Ile	Glu	Glu	Ser	Glu	Gly	Glu	Val	Ala	Gly	Ile	
				165					170					175		
aaa	tcc	gtg	acg	atc	aaa	atc	tcc	ggc	gat	tac	gct	tac	ggc	tgg	ctg	576
Lys	Ser	Val	Thr	Ile	Lys	Ile	Ser	Gly	Asp	Tyr	Ala	Tyr	Gly	Trp	Leu	
			180					185					190			
cgt	aca	gaa	acc	ggc	gtt	cac	cgc	ctg	gtg	cgt	aaa	agc	ccg	ttt	gac	624
Arg	Thr	Glu	Thr	Gly	Val	His	Arg	Leu	Val	Arg	Lys	Ser	Pro	Phe	Asp	
		195					200					205				
tcc	ggc	ggc	cgt	cgc	cac	acg	tcg	ttc	agc	tcc	gcg	ttt	gtt	tat	ccg	672
Ser	Gly	Gly	Arg	Arg	His	Thr	Ser	Phe	Ser	Ser	Ala	Phe	Val	Tyr	Pro	
	210					215					220					
gaa	gtt	gat	gat	gat	att	gat	atc	gaa	atc	aac	ccg	gcg	gat	ctg	cgc	720
Glu	Val	Asp	Asp	Asp	Ile	Asp	Ile	Glu	Ile	Asn	Pro	Ala	Asp	Leu	Arg	
225					230					235				240		
att	gac	gtt	tat	cgc	acg	tcc	ggc	gcg	ggc	ggc	cag	cac	gtt	aac	cgt	768
Ile	Asp	Val	Tyr	Arg	Thr	Ser	Gly	Ala	Gly	Gly	Gln	His	Val	Asn	Arg	
				245					250					255		
acc	gaa	tct	gcg	gtg	cgt	att	acc	cac	atc	ccg	acc	ggg	atc	gtg	acc	816
Thr	Glu	Ser	Ala	Val	Arg	Ile	Thr	His	Ile	Pro	Thr	Gly	Ile	Val	Thr	
			260					265					270			
cag	tgc	cag	aac	gac	cgt	tcc	cag	cac	aag	aac	aaa	gat	cag	gcc	atg	864
Gln	Cys	Gln	Asn	Asp	Arg	Ser	Gln	His	Lys	Asn	Lys	Asp	Gln	Ala	Met	
		275					280					285				
aag	cag	atg	aaa	gcg	aag	ctt	tat	gaa	ctg	gag	atg	cag	aag	aaa	aat	912
Lys	Gln	Met	Lys	Ala	Lys	Leu	Tyr	Glu	Leu	Glu	Met	Gln	Lys	Lys	Asn	
	290					295					300					
gcc	gag	aaa	cag	gcg	atg	gaa	gat	aac	aaa	tcc	gac	atc	ggc	tgg	ggc	960
Ala	Glu	Lys	Gln	Ala	Met	Glu	Asp	Asn	Lys	Ser	Asp	Ile	Gly	Trp	Gly	
305				310						315					320	
agc	cag	att	cgt	tct	tat	gtc	ctt	gat	gac	tcc	cgc	att	aaa	gat	ctg	1008
Ser	Gln	Ile	Arg	Ser	Tyr	Val	Leu	Asp	Asp	Ser	Arg	Ile	Lys	Asp	Leu	
				325					330					335		
cgc	acc	ggg	gta	gaa	acc	cgc	aac	acg	cag	gcc	gtg	ctg	gac	ggc	agc	1056
Arg	Thr	Gly	Val	Glu	Thr	Arg	Asn	Thr	Gln	Ala	Val	Leu	Asp	Gly	Ser	
			340					345					350			
ctg	gat	caa	ttt	atc	gaa	gca	agt	ttg	aaa	gca	ggg	tta	tga			1098
Leu	Asp	Gln	Phe	Ile	Glu	Ala	Ser	Leu	Lys	Ala	Gly	Leu	*			

355

360

365

<210> 161
 <211> 1734
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1734)

<400> 161

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Met	Lys	Gln	Gln	Ile	Gln	Leu	Arg	Arg	Arg	Glu	Val	Asp	Glu	Thr	Ala	
1				5					10					15		
gac	ttg	ccc	gct	gaa	ttg	cct	ccc	ttg	ctg	cgc	cgt	tta	tac	gcc	agc	96
Asp	Leu	Pro	Ala	Glu	Leu	Pro	Pro	Leu	Leu	Arg	Arg	Leu	Tyr	Ala	Ser	
			20					25					30			
cgg	gga	gta	cgc	agt	gcg	caa	gaa	ctg	gaa	cgc	agt	gtt	aaa	ggg	atg	144
Arg	Gly	Val	Arg	Ser	Ala	Gln	Glu	Leu	Glu	Arg	Ser	Val	Lys	Gly	Met	
		35					40					45				
ctg	ccc	tgg	cag	caa	ctg	agc	ggc	gtc	gaa	aag	gcc	gtt	gag	atc	ctt	192
Leu	Pro	Trp	Gln	Gln	Leu	Ser	Gly	Val	Glu	Lys	Ala	Val	Glu	Ile	Leu	
	50					55					60					
tac	aac	gct	ttt	cgc	gaa	gga	acg	cgg	att	att	gtg	gtc	ggg	gat	ttc	240
Tyr	Asn	Ala	Phe	Arg	Glu	Gly	Thr	Arg	Ile	Ile	Val	Val	Gly	Asp	Phe	
65				70					75					80		
gac	gcc	gac	ggc	gcg	acc	agc	acg	gct	cta	agc	gtg	ctg	gcg	atg	cgc	288
Asp	Ala	Asp	Gly	Ala	Thr	Ser	Thr	Ala	Leu	Ser	Val	Leu	Ala	Met	Arg	
			85					90					95			
tcg	ctt	ggg	tgc	agc	aat	atc	gac	tac	ctg	gta	cca	aac	cgt	ttc	gaa	336
Ser	Leu	Gly	Cys	Ser	Asn	Ile	Asp	Tyr	Leu	Val	Pro	Asn	Arg	Phe	Glu	
		100					105					110				
gac	ggg	tac	ggc	tta	agc	ccg	gaa	gtg	gtc	gat	cag	gcc	cat	gcc	cgt	384
Asp	Gly	Tyr	Gly	Leu	Ser	Pro	Glu	Val	Val	Asp	Gln	Ala	His	Ala	Arg	
	115						120					125				
ggc	gcg	cag	tta	att	gtc	acg	gtg	gat	aac	ggg	att	tcc	tcc	cat	gcg	432
Gly	Ala	Gln	Leu	Ile	Val	Thr	Val	Asp	Asn	Gly	Ile	Ser	Ser	His	Ala	
	130					135				140						
ggg	gtt	gag	cac	gct	cgc	tcg	ttg	ggc	atc	ccg	gtt	att	gtt	acc	gat	480
Gly	Val	Glu	His	Ala	Arg	Ser	Leu	Gly	Ile	Pro	Val	Ile	Val	Thr	Asp	
145				150					155					160		
cac	cat	ttg	cca	ggc	gac	aca	tta	ccc	gca	gcg	gaa	gcg	atc	att	aac	528
His	His	Leu	Pro	Gly	Asp	Thr	Leu	Pro	Ala	Ala	Glu	Ala	Ile	Ile	Asn	
			165					170					175			

cgc tcc att cag ggg ctg cat atg cgt gat gcg ctg gag cga tta gac	1248
Arg Ser Ile Gln Gly Leu His Met Arg Asp Ala Leu Glu Arg Leu Asp	
405 410 415	
aca ctc tac cct ggc atg atg ctg aag ttt ggc ggt cat gcg atg gcg	1296
Thr Leu Tyr Pro Gly Met Met Leu Lys Phe Gly Gly His Ala Met Ala	
420 425 430	
gcg ggt ttg tgc ctg gaa gag gat aaa ttc aaa ctc ttt caa caa cgg	1344
Ala Gly Leu Ser Leu Glu Glu Asp Lys Phe Lys Leu Phe Gln Gln Arg	
435 440 445	
ttt ggc gaa ctg gtt act gag tgg ctg gac cct tgc cta ttg caa ggc	1392
Phe Gly Glu Leu Val Thr Glu Trp Leu Asp Pro Ser Leu Leu Gln Gly	
450 455 460	
gaa gtg gta tca gac ggt ccg tta agc ccg gcc gaa atg acc atg gaa	1440
Glu Val Val Ser Asp Gly Pro Leu Ser Pro Ala Glu Met Thr Met Glu	
465 470 475 480	
gtg gcg cag ctg ctg cgc gat gct ggc ccg tgg ggg cag atg ttc ccg	1488
Val Ala Gln Leu Leu Arg Asp Ala Gly Pro Trp Gly Gln Met Phe Pro	
485 490 495	
gag ccg ctg ttt gac ggt cat ttc cgt ctg ctg caa cag cgg ctg gtg	1536
Glu Pro Leu Phe Asp Gly His Phe Arg Leu Leu Gln Gln Arg Leu Val	
500 505 510	
ggc gaa cgt cat ttg aag gtg atg gtc gaa ccg gtc ggc ggc ggt cca	1584
Gly Glu Arg His Leu Lys Val Met Val Glu Pro Val Gly Gly Gly Pro	
515 520 525	
ctg ctg gat ggt att gct ttt aat gtc gat acc gcc ctc tgg ccg gat	1632
Leu Leu Asp Gly Ile Ala Phe Asn Val Asp Thr Ala Leu Trp Pro Asp	
530 535 540	
aac ggc gtg cgc gaa gtg caa ctg gct tat aag ctc gat atc aac gag	1680
Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu	
545 550 555 560	
ttt cgc ggc aac cgc agc ctg caa att atc atc gac aat atc tgg cca	1728
Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro	
565 570 575	
att tag	1734
Ile *	

<210> 162
 <211> 711
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(711)

ttc ctc gac gaa cac caa aaa atg acc agc ggt aaa taa 711
Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys *
225 230 235

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<210> 163
<211> 897
<212> DNA
<213> Escherichia coli
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<220>  
<221> CDS  
<222> (1) ... (897)
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<400> 163
gtg aaa cag gat ctg gca cgc atc gag cag ttt ctt gat gct ctg tgg 48
Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
1 5 10 15

ctg gaa aaa aat ctg gct gaa aat acg ttg aac gct tac cgt cgc gat 96
Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
20 25 30

ctg	tca	atg	atg	gtg	gag	tgg	ttg	cat	cac	cgc	ggg	ttg	acg	ctg	gcg	144
Leu	Ser	Met	Met	Val	Glu	Trp	Leu	His	His	Arg	Gly	Leu	Thr	Leu	Ala	
		35					40					45				

acg gcg caa agt gac gat ttg cag gca tta ctg gca gaa cgg ctg gag 192
Thr Ala Gln Ser Asp Asp Leu Gln Ala Leu Leu Ala Glu Arg Leu Glu
50 55 60

ggc ggg tat aaa gcc acc agc tca gcg cgt ttg ctg agt gca gtg cgc 240
Gly Gly Tyr Lys Ala Thr Ser Ser Ala Arg Leu Leu Ser Ala Val Arg
65 70 75 80

cga ttg ttc cag tat ctt tat cgc gaa aag ttt cgt gaa gac gat ccc 288
Arg Leu Phe Gln Tyr Leu Tyr Arg Glu Lys Phe Arg Glu Asp Asp Pro
85 90 95

agt gcg cat ctc gct tca ccg aaa ttg ccc cag cgt ttg cca aaa gat 336
Ser Ala His Leu Ala Ser Pro Lys Leu Pro Gln Arg Leu Pro Lys Asp
100 105 110

tta	agc	gaa	gcg	cag	gtc	gaa	cgt	tta	tta	cag	gca	cca	tta	atc	gat	384
Leu	Ser	Glu	Ala	Gln	Val	Glu	Arg	Leu	Leu	Gln	Ala	Pro	Leu	Ile	Asp	
		115					120					125				

cag cca ctg gag cta cgc gat aaa gcc atg ctt gaa gtg ttg tat gct 432
Gln Pro Leu Glu Leu Arg Asp Lys Ala Met Leu Glu Val Leu Tyr Ala
130 135 140

acc ggg ctg cgt gtc tct gaa ctg gtc gga ctg aca atg agt gat atc 480
Thr Gly Leu Arg Val Ser Glu Leu Val Gly Leu Thr Met Ser Asp Ile
145 150 155 160

agc ctg cgt cag ggc gtg gta cgg gtc att ggt aaa ggc aac aaa gag 528

	50				55				60							
act	ggt	gat	ttt	caa	aaa	gaa	tta	gcg	tac	tta	caa	aat	gta	att	ctt	240
Thr	Gly	Asp	Phe	Gln	Lys	Glu	Leu	Ala	Tyr	Leu	Gln	Asn	Val	Ile	Leu	
65					70					75					80	
tat	aat	gtc	tcg	tct	ctt	cgt	ctg	gat	ttt	tta	ggg	tat	aac	gcc	caa	288
Tyr	Asn	Val	Ser	Ser	Leu	Arg	Leu	Asp	Phe	Leu	Gly	Tyr	Asn	Ala	Gln	
				85					90					95		
att	att	caa	cga	tcg	gac	aat	act	tgt	gaa	ctt	acc	att	aat	gaa	ccg	336
Ile	Ile	Gln	Arg	Ser	Asp	Asn	Thr	Cys	Glu	Leu	Thr	Ile	Asn	Glu	Pro	
			100					105					110			
tta	aaa	aac	cag	gaa	ata	tcc	aca	ggg	aat	atc	aat	att	aat	tgc	cca	384
Leu	Lys	Asn	Gln	Glu	Ile	Ser	Thr	Gly	Asn	Ile	Asn	Ile	Asn	Cys	Pro	
		115					120					125				
tta	aaa	gat	att	tac	aat	gaa	atc	agg	agg	tta	aac	gta	att	ttt	agt	432
Leu	Lys	Asp	Ile	Tyr	Asn	Glu	Ile	Arg	Arg	Leu	Asn	Val	Ile	Phe	Ser	
		130				135					140					
tgt	ggg	act	gga	gat	atc	gtt	gat	cta	tcc	tct	ctg	gac	tta	cgt	aat	480
Cys	Gly	Thr	Gly	Asp	Ile	Val	Asp	Leu	Ser	Ser	Leu	Asp	Leu	Arg	Asn	
145					150					155					160	
gtc	gat	tta	gat	tat	tat	gat	ttc	aca	gat	aaa	cat	atg	gct	aat	act	528
Val	Asp	Leu	Asp	Tyr	Tyr	Asp	Phe	Thr	Asp	Lys	His	Met	Ala	Asn	Thr	
				165					170					175		
att	tta	aat	cct	ttt	aaa	ttg	aat	tca	aca	aat	ttt	act	aat	gcc	aac	576
Ile	Leu	Asn	Pro	Phe	Lys	Leu	Asn	Ser	Thr	Asn	Phe	Thr	Asn	Ala	Asn	
			180					185					190			
atg	ttt	cag	ggt	aat	ttt	ggt	agt	tca	aca	caa	aac	gcc	aca	atc	tcc	624
Met	Phe	Gln	Val	Asn	Phe	Val	Ser	Ser	Thr	Gln	Asn	Ala	Thr	Ile	Ser	
		195					200					205				
tgg	gat	tat	tta	cta	aaa	ata	acg	cct	ggt	tta	ata	agc	att	agc	gat	672
Trp	Asp	Tyr	Leu	Leu	Lys	Ile	Thr	Pro	Val	Leu	Ile	Ser	Ile	Ser	Asp	
	210					215					220					
atg	tat	tct	gaa	gaa	aaa	atc	aag	ttt	gtc	gaa	agt	tgt	tta	aat	gag	720
Met	Tyr	Ser	Glu	Glu	Lys	Ile	Lys	Phe	Val	Glu	Ser	Cys	Leu	Asn	Glu	
225					230					235					240	
cct	gga	gac	att	acc	gaa	gaa	caa	tta	aaa	att	atg	aga	ttt	gca	att	768
Pro	Gly	Asp	Ile	Thr	Glu	Glu	Gln	Leu	Lys	Ile	Met	Arg	Phe	Ala	Ile	
				245					250					255		
ata	aaa	tct	ata	cca	agg	gca	act	ctt	aca	gat	aaa	tta	gaa	aat	gaa	816
Ile	Lys	Ser	Ile	Pro	Arg	Ala	Thr	Leu	Thr	Asp	Lys	Leu	Glu	Asn	Glu	
			260					265					270			
tta	aca	aaa	gaa	ata	tat	aaa	agc									

aac aga att aaa tta aca gag atg aaa gaa ttc tca tca gaa aaa ata	912
Asn Arg Ile Lys Leu Thr Glu Met Lys Glu Phe Ser Ser Glu Lys Ile	
290 295 300	
tat gat tac atc gat ata atc att gaa gat tat gaa aat acc aaa gaa	960
Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu	
305 310 315 320	
aat gct tat ctg gtc gtc ccc caa att aat tat act atg gat tta aac	1008
Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn	
325 330 335	
ata gaa gac tct agc tca gaa gag tta ctt tca gat aat acc ctc gag	1056
Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu	
340 345 350	
aaa gac gaa aat tct ccg gac aat ggc ttt gag gtc ggg gaa tat aac	1104
Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn	
355 360 365	
aca tat gaa gca tat aac tca gag aag caa tat ttt acc aga gag gac	1152
Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp	
370 375 380	
tat acg tat gat tac gac ctt tta aat gca ata tag	1188
Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile *	
385 390 395	
<210> 168	
<211> 948	
<212> DNA	
<213> Escherichia coli	
<220>	
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<222> (1)...(948)	
<400> 168	
gtg tgt cat cgc gca ttt cga ctt cat ctt tgc aag gac tgg gtt ttc	48
Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe	
1 5 10 15	
atg ttt tct ggg ctg tta atc att ctg gtt ccc ctg att gtg ggt tac	96
Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr	
20 25 30	
ctc att ccg ctt cgc caa caa gct gcg tta aaa gtt att aat cag cta	144
Leu Ile Pro Leu Arg Gln Gln Ala Ala Leu Lys Val Ile Asn Gln Leu	
35 40 45	
tta agc tgg atg gtt tac ctt att ctc ttt ttt atg ggt atc agt ctg	192
Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu	
50 55 60	
gcg ttt ctc gat aac ctc gcc agt aac ctg ttg gcg att ctg cat tat	240

290	295	300	
tta gtg ccg atc ctc atc gcc ttt ttc tct gcg taa			948
Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala *			
305	310	315	

<210> 169
 <211> 291
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(291)

<400> 169	
atg caa aac aca act cat gac aac gta att ctg gag ctc acc gtt cgc	48
Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg	
1 5 10 15	
aac cat ccg ggc gta atg acc cac gtt tgt ggc ctt ttt gcc cgc cgc	96
Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg	
20 25 30	
gct ttt aac gtt gaa ggc att ctt tgt ctg ccg att cag gac agc gac	144
Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp	
35 40 45	
aaa agc cat atc tgg cta ctg gtc aat gac gac cag cgt ctg gag cag	192
Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln	
50 55 60	
atg ata agc caa atc gat aag ctg gaa gat gtc gtg aaa gtg cag cgt	240
Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg	
65 70 75 80	
aat cag tcc gat ccg acg atg ttt aac aag atc gcg gtg ttt ttt cag	288
Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln	
85 90 95	
taa	291
*	

<210> 170
 <211> 1689
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1689)

<400> 170	
atg gca agt tcg ggc aca aca tcg acg cgt aag cgc ttt acc ggc gca	48

<220>
 <221> CDS
 <222> (1)...(1017)

<400> 172

atg ttt gtc atc tgg agc cat aga aca ggg ttc atc atg agt cat caa	48
Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln	
1 5 10 15	
ctt acc ttc gcc gac agt gaa ttc agc agt aag cgc cgt cag acc aga	96
Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg	
20 25 30	
aaa gag att ttc ttg tcc cgc atg gag cag att ctg cca tgg caa aac	144
Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn	
35 40 45	
atg gtg gaa gtc atc gag ccg ttt tac ccc aag gct ggt aat ggc cgg	192
Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg	
50 55 60	
cga cct tat ccg ctg gaa acc atg cta cgc att cac tgc atg cag cat	240
Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His	
65 70 75 80	
tgg tac aac ctg agc gat ggc gcg atg gaa gat gct ctg tac gaa atc	288
Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile	
85 90 95	
gcc tcc atg cgt ctg ttt gcc cgg tta tcc ctg gat agc gcc ttg ccg	336
Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro	
100 105 110	
gac cgc acc acc atc atg aat ttc cgc cac ctg ctg gag cag cat caa	384
Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln	
115 120 125	
ctg gcc cgc caa ttg ttc aag acc atc aat cgc tgg ctg gcc gaa gca	432
Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala	
130 135 140	
ggc gtc atg atg act caa ggc acc ttg gtc gat gcc acc atc att gag	480
Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu	
145 150 155 160	
gca ccc agc tcg acc aag aac aaa gag cag caa cgc gat ccg gag atg	528
Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met	
165 170 175	
cat cag acc aag aaa ggc aat cag tgg cac ttt ggc atg aag gcc cac	576
His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His	
180 185 190	
att ggt gtc gat gcc aag agt ggc ctg acc cac agc ctg gtc acc acc	624
Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr	
195 200 205	

gcg gcc aac gag cat gac ctc aat cag ctg ggt aat ctg ctg cat gga	672
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly	
210 215 220	
gag gag caa ttt gtc tca gcc gat gcc ggc tac caa ggg gcg cca cag	720
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln	
225 230 235 240	
cgc gag gag ctg gcc gag gtg gat gtg gac tgg ctg atc gcc gag cgc	768
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg	
245 250 255	
ccc ggc aag gta aga acc ttg aaa cag cat cca cgc aag aac aaa acg	816
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr	
260 265 270	
gcc atc aac atc gaa tac atg aaa gcc agc atc cgg gcc agg gtg gag	864
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu	
275 280 285	
cac cca ttt cgc atc atc aag cga cag ttc ggc ttc gtg aaa gcc aga	912
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg	
290 295 300	
tac aag ggg ttg ctg aaa aac gat aac caa ctg gcg atg tta ttc acg	960
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr	
305 310 315 320	
ctg gcc aac ctg ttt cgg gcg gac caa atg ata cgt cag tgg gag aga	1008
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg	
325 330 335	
tct cac taa	1017
Ser His *	

<210> 173
 <211> 474
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(474)

<400> 173	
atg gta tat ata ata atc gtt tcc cac gga cat gaa gac tac atc aaa	48
Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys	
1 5 10 15	
aaa tta ctc gaa aat ctt aat gct gac gat gag cac tac aag att atc	96
Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile	
20 25 30	
gta cgc gac aac aaa gac tct cta tta ttg aaa caa ata tgc cag cat	144

Val	Arg	Asp	Asn	Lys	Asp	Ser	Leu	Leu	Leu	Lys	Gln	Ile	Cys	Gln	His	
		35					40					45				
tat	gca	ggc	ctg	gac	tat	att	agt	gga	ggg	gta	tac	ggc	ttt	ggg	cat	192
Tyr	Ala	Gly	Leu	Asp	Tyr	Ile	Ser	Gly	Gly	Val	Tyr	Gly	Phe	Gly	His	
	50					55				60						
aat	aat	aat	att	gcg	gtg	gcg	tat	gta	aag	gaa	aaa	tat	aga	ccc	gca	240
Asn	Asn	Asn	Ile	Ala	Val	Ala	Tyr	Val	Lys	Glu	Lys	Tyr	Arg	Pro	Ala	
	65				70				75						80	
gat	gat	gat	tac	att	ttg	ttt	ttg	aat	ccc	gat	atc	atc	atg	aag	cat	288
Asp	Asp	Asp	Tyr	Ile	Leu	Phe	Leu	Asn	Pro	Asp	Ile	Ile	Met	Lys	His	
				85				90						95		
gat	gat	ttg	ctg	aca	tat	att	aaa	tat	gtc	gaa	agt	aag	cgt	tat	gct	336
Asp	Asp	Leu	Leu	Thr	Tyr	Ile	Lys	Tyr	Val	Glu	Ser	Lys	Arg	Tyr	Ala	
		100					105						110			
ttt	agt	aca	tta	tgc	ctg	ttc	cga	gat	gaa	gcg	aaa	tct	tta	cat	gat	384
Phe	Ser	Thr	Leu	Cys	Leu	Phe	Arg	Asp	Glu	Ala	Lys	Ser	Leu	His	Asp	
		115					120					125				
tat	tcc	gta	aga	aaa	ttt	cct	gtg	ctt	tct	gat	ttt	att	gtg	tca	ttt	432
Tyr	Ser	Val	Arg	Lys	Phe	Pro	Val	Leu	Ser	Asp	Phe	Ile	Val	Ser	Phe	
	130					135				140						
atg	tta	ggg	att	aag	gaa	ggg	gcg	aac	aag	tcc	ctg	ata	tga			474
Met	Leu	Gly	Ile	Lys	Glu	Gly	Ala	Asn	Lys	Ser	Leu	Ile	*			
	145				150				155							
<210>	174															
<211>	1119															
<212>	DNA															
<213>	Escherichia coli															
<220>																
<221>	CDS															
<222>	(1)...(1119)															
<400>	174															
atg	gga	aaa	agc	ata	gtc	gtt	gtt	tct	gcg	gtc	aat	ttt	acc	act	ggc	48
Met	Gly	Lys	Ser	Ile	Val	Val	Val	Ser	Ala	Val	Asn	Phe	Thr	Thr	Gly	
	1				5				10					15		
ggg	cca	ttt	acc	att	ttg	aaa	aaa	ttt	ttg	gca	gca	act	aat	aat	aaa	96
Gly	Pro	Phe	Thr	Ile	Leu	Lys	Lys	Phe	Leu	Ala	Ala	Thr	Asn	Asn	Lys	
			20					25					30			
gaa	aat	gtc	agt	ttt	atc	gca	tta	gtc	cat	tct	gct	aaa	gag	tta	aaa	144
Glu	Asn	Val	Ser	Phe	Ile	Ala	Leu	Val	His	Ser	Ala	Lys	Glu	Leu	Lys	
		35				40						45				
gaa	agt	tat	cca	tgg	gtt	aaa	ttc	att	gag	ttt	cct	gag	gtt	aaa	ggg	192
Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly	

ccg	ttg	tct	gaa	gct	aaa	gag	cga	ggg	aag	tgg	gta	tta	gca	tca	gat	912
Pro	Leu	Ser	Glu	Ala	Lys	Glu	Arg	Gly	Lys	Trp	Val	Leu	Ala	Ser	Asp	
	290					295					300					

ttc	cca	ttt	act	aga	gaa	act	ctt	ggg	agt	tat	gaa	aag	aaa	gct	ttt	960
Phe	Pro	Phe	Thr	Arg	Glu	Thr	Leu	Gly	Ser	Tyr	Glu	Lys	Lys	Ala	Phe	
305					310					315					320	

ttt	gat	tct	aat	aac	gat	gac	atg	tta	gtt	aaa	ctt	att	att	gac	ttc	1008
Phe	Asp	Ser	Asn	Asn	Asp	Asp	Met	Leu	Val	Lys	Leu	Ile	Ile	Asp	Phe	
			325						330					335		

aaa	aaa	ggg	aac	ctc	aaa	aaa	gat	atc	tct	gat	gca	aat	ttc	att	tat	1056
Lys	Lys	Gly	Asn	Leu	Lys	Lys	Asp	Ile	Ser	Asp	Ala	Asn	Phe	Ile	Tyr	
			340					345					350			

cgt	aat	gaa	aat	gta	tta	gtt	ggg	ttt	gat	gaa	cta	gtt	aat	ttt	att	1104
Arg	Asn	Glu	Asn	Val	Leu	Val	Gly	Phe	Asp	Glu	Leu	Val	Asn	Phe	Ile	
		355					360					365				

act	gaa	gaa	cat	tga												1119
Thr	Glu	Glu	His	*												
			370													

<210> 175
 <211> 591
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(591)

<400>	175															
atg	atc	tta	aaa	ctc	gct	aaa	cga	tat	ggg	ctc	tgt	ggg	ttt	att	cgg	48
Met	Ile	Leu	Lys	Leu	Ala	Lys	Arg	Tyr	Gly	Leu	Cys	Gly	Phe	Ile	Arg	
1				5					10					15		

ctt	gtt	aga	gat	gtc	tta	ttg	act	cgt	gta	ttt	tac	cgg	aac	tgt	aga	96
Leu	Val	Arg	Asp	Val	Leu	Leu	Thr	Arg	Val	Phe	Tyr	Arg	Asn	Cys	Arg	
			20					25					30			

att	att	cga	ttt	ccc	tgc	tat	att	cgc	aat	gat	ggg	agc	att	aat	ttt	144
Ile	Ile	Arg	Phe	Pro	Cys	Tyr	Ile	Arg	Asn	Asp	Gly	Ser	Ile	Asn	Phe	
		35					40					45				

ggg	gaa	aat	ttc	aca	agt	gga	gtc	ggg	ctc	agg	ctg	gat	gca	ttt	gga	192
Gly	Glu	Asn	Phe	Thr	Ser	Gly	Val	Gly	Leu	Arg	Leu	Asp	Ala	Phe	Gly	
	50					55					60					

cgt	ggc	gtg	att	ttt	ttt	tcc	gat	aat	gtg	caa	gtt	aac	gac	tat	gtt	240
Arg	Gly	Val	Ile	Phe	Phe	Ser	Asp	Asn	Val	Gln	Val	Asn	Asp	Tyr	Val	
65					70					75					80	

cat	atc	gcc	tca	att	gag	agc	gtt	acg	ata	ggg	cgg	gat	acg	ctt	att	288
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gac	tcc	atg	aca	ata	gaa	act	tat	aag	caa	att	agt	gag	aat	aca	aaa	912
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys	
	290					295					300					

att	att	tct	cag	aaa	att	cga	aca	gga	agt	tac	ttc	agg	gat	gtt	ctt	960
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu	
	305				310					315					320	

gaa	gag	gtg	atc	gat	gat	ctt	aaa	act	cgc	taa						993
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg	*						
				325					330							

<210> 177
 <211> 1167
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1167)

<400> 177																
atg	atc	tat	ctt	gta	att	agt	gtc	ttt	ctc	att	aca	gca	ttt	atc	tgt	48
Met	Ile	Tyr	Leu	Val	Ile	Ser	Val	Phe	Leu	Ile	Thr	Ala	Phe	Ile	Cys	
	1			5					10					15		

tta	tat	ctt	aag	aag	gat	ata	ttt	tat	cca	gcc	gta	tgc	gtt	aat	atc	96
Leu	Tyr	Leu	Lys	Lys	Asp	Ile	Phe	Tyr	Pro	Ala	Val	Cys	Val	Asn	Ile	
			20					25					30			

atc	ttc	gca	ctg	gtc	tta	ttg	gga	tat	gaa	ata	acg	tca	gat	ata	tat	144
Ile	Phe	Ala	Leu	Val	Leu	Leu	Gly	Tyr	Glu	Ile	Thr	Ser	Asp	Ile	Tyr	
		35					40					45				

gct	ttt	cag	tta	aat	gac	gct	acg	ttg	att	ttt	cta	ctt	tgc	aat	gtt	192
Ala	Phe	Gln	Leu	Asn	Asp	Ala	Thr	Leu	Ile	Phe	Leu	Leu	Cys	Asn	Val	
	50				55						60					

ttg	aca	ttt	acc	ctg	tca	tgt	tta	ttg	acg	gaa	agt	gta	tta	gat	cta	240
Leu	Thr	Phe	Thr	Leu	Ser	Cys	Leu	Leu	Thr	Glu	Ser	Val	Leu	Asp	Leu	
	65				70				75					80		

aat	atc	aga	aaa	gtc	aat	aat	gct	att	tat	agc	ata	cca	tcg	aag	aaa	288
Asn	Ile	Arg	Lys	Val	Asn	Asn	Ala	Ile	Tyr	Ser	Ile	Pro	Ser	Lys	Lys	
				85				90						95		

gtg	cat	aat	gta	ggc	ttg	tta	gtt	att	tct	ttt	tcg	atg	ata	tat	ata	336
Val	His	Asn	Val	Gly	Leu	Leu	Val	Ile	Ser	Phe	Ser	Met	Ile	Tyr	Ile	
			100					105					110			

tgc	atg	agg	tta	agt	aac	tac	cag	ttc	ggg	act	agc	tta	ctt	agc	tat	384
Cys	Met	Arg	Leu	Ser	Asn	Tyr	Gln	Phe	Gly	Thr	Ser	Leu	Leu	Ser	Tyr	
		115					120					125				

atg	aat	ttg	ata	aga	gat	gct	gat	gtt	gaa	gac	aca	tca	aga	aat	ttc	432
Met	Asn	Leu	Ile	Arg	Asp	Ala	Asp	Val	Glu	Asp	Thr	Ser	Arg	Asn	Phe	

ata caa ata act ctt tgt atc ata gta ttc tct caa ttt ctt aag gcc 1152
 Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380

cag aaa ata aag tga 1167
 Gln Lys Ile Lys *
 385

<210> 178
 <211> 1104
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1104)

<400> 178
 atg tac gat tat atc att gtt ggt tct ggt ttg ttt ggt gcc gtt tgt 48
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15

gcg aat gag tta aaa aag cta aac aaa aaa gtt tta gtg att gag aaa 96
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
 20 25 30

aga aat cat atc ggt gga aat gcg tac aca gag gac tgt gag ggt atc 144
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
 35 40 45

cag att cat aaa tat ggt gca cat att ttt cat acc aat gat aaa tat 192
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
 50 55 60

ata tgg gat tac gtt aat gat tta gta gaa ttt aat cgt ttt act aat 240
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
 65 70 75 80

tct cca ctg gcg att tat aaa gac aaa tta ttc aac ctt cct ttt aat 288
 Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
 85 90 95

atg aat act ttc cac caa atg tgg gga gtt aaa gat cct caa gaa gct 336
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
 100 105 110

caa aat atc att aat gct cag aaa aaa aag tat ggt gac aag gta cct 384
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Lys Tyr Gly Asp Lys Val Pro
 115 120 125

gaa aat ttg gag gag cag gcg att tca tta gtt ggg gag gac tta tac 432
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
 130 135 140

caa gca ttg ata aag ggt tat acg gag aag cag tgg gga aga agt gca 480

<210> 179
 <211> 693
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(693)

<400> 179
 ttg aca tca tca ata acc aat gaa att atg caa tta tat acg gat agg 48
 Met Thr Ser Ser Ile Thr Asn Glu Ile Met Gln Leu Tyr Thr Asp Arg
 1 5 10 15
 gag gtt ctt aac atg ggg ctt tgt agt cgt tat aaa agt ctt aca tgc 96
 Glu Val Leu Asn Met Gly Leu Cys Ser Arg Tyr Lys Ser Leu Thr Cys
 20 25 30
 aat agt tgc tca atg cat tgc caa ata atg cca gaa gag tca ccg cgt 144
 Asn Ser Cys Ser Met His Cys Gln Ile Met Pro Glu Glu Ser Pro Arg
 35 40 45
 ttg cag tat tgc gca aac tcg tgt ttt tgt atg tgg ccc gaa gaa agt 192
 Leu Gln Tyr Cys Ala Asn Ser Cys Phe Cys Met Trp Pro Glu Glu Ser
 50 55 60
 tca tat ttt aat cgt ggt gtg gta gaa ggt atc tta aca aaa aac cac 240
 Ser Tyr Phe Asn Arg Gly Val Val Glu Gly Ile Leu Thr Lys Asn His
 65 70 75 80
 aat gcg aga tta agc gga tat att ttt gtc gat ttt tca gta agt ttt 288
 Asn Ala Arg Leu Ser Gly Tyr Ile Phe Val Asp Phe Ser Val Ser Phe
 85 90 95
 tta cgt cta ttc ctt gaa aaa gac tgg att gac tat ctt gca agt act 336
 Leu Arg Leu Phe Leu Glu Lys Asp Trp Ile Asp Tyr Leu Ala Ser Thr
 100 105 110
 gac atg ggg att gtt tta gtc agc gac cgc aat atg caa tcg tta gct 384
 Asp Met Gly Ile Val Leu Val Ser Asp Arg Asn Met Gln Ser Leu Ala
 115 120 125
 aat tac tgg cga aaa cac aac tca gca ata tct gct gtc ata tat aat 432
 Asn Tyr Trp Arg Lys His Asn Ser Ala Ile Ser Ala Val Ile Tyr Asn
 130 135 140
 gat gat ggt ctt gat gtt gcc aat gaa aag atc aga caa cta ttt att 480
 Asp Asp Gly Leu Asp Val Ala Asn Glu Lys Ile Arg Gln Leu Phe Ile
 145 150 155 160
 ggt cgt tat tta tca ttt acc gga ggt aac aca tta act cag atg gaa 528
 Gly Arg Tyr Leu Ser Phe Thr Gly Gly Asn Thr Leu Thr Gln Met Glu
 165 170 175
 ttc acc ata atg ggg tat atg gtt tct ggt tat aat cca tat cag att 576
 Phe Thr Ile Met Gly Tyr Met Val Ser Gly Tyr Asn Pro Tyr Gln Ile
 180 185 190

gct gaa gtt ctg gat atg gat atc cgt agc atc tac gcg tac aag caa 624
 Ala Glu Val Leu Asp Met Asp Ile Arg Ser Ile Tyr Ala Tyr Lys Gln
 195 200 205

cga atc gaa aag aga atg ggt ggt aaa ata aac gaa tta ttt att cgt 672
 Arg Ile Glu Lys Arg Met Gly Gly Lys Ile Asn Glu Leu Phe Ile Arg
 210 215 220

tca cat tcg gtc caa cat tga 693
 Ser His Ser Val Gln His *
 225 230

<210> 180
 <211> 1176
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1176)

<400> 180
 atg caa aaa ctc att aac tca gtg caa aac tat gcc tgg ggc agc aaa 48
 Met Gln Lys Leu Ile Asn Ser Val Gln Asn Tyr Ala Trp Gly Ser Lys
 1 5 10 15

acg gcg ttg act gaa ctt tat ggt atg gaa aat ccg tcc agc cag ccg 96
 Thr Ala Leu Thr Glu Leu Tyr Gly Met Glu Asn Pro Ser Ser Gln Pro
 20 25 30

atg gcc gag ctg tgg atg ggc gca cat ccg aaa agc agt tca cga gtg 144
 Met Ala Glu Leu Trp Met Gly Ala His Pro Lys Ser Ser Ser Arg Val
 35 40 45

cag aat gcc gcc gga gat atc gtt tca ctg cgt gat gtg att gag agt 192
 Gln Asn Ala Ala Gly Asp Ile Val Ser Leu Arg Asp Val Ile Glu Ser
 50 55 60

gat aaa tcg act ctg ctc gga gag gcc gtt gcc aaa cgc ttt ggc gaa 240
 Asp Lys Ser Thr Leu Leu Gly Glu Ala Val Ala Lys Arg Phe Gly Glu
 65 70 75 80

ctg cct ttc ctg ttc aaa gta tta tgc gca gca cag cca ctc tcc att 288
 Leu Pro Phe Leu Phe Lys Val Leu Cys Ala Ala Gln Pro Leu Ser Ile
 85 90 95

cag gtt cat cca aac aaa cac aat tct gaa atc ggt ttt gcc aaa gaa 336
 Gln Val His Pro Asn Lys His Asn Ser Glu Ile Gly Phe Ala Lys Glu
 100 105 110

aat gcc gca ggt atc ccg atg gat gcc gcc gag cgt aac tat aaa gat 384
 Asn Ala Ala Gly Ile Pro Met Asp Ala Ala Glu Arg Asn Tyr Lys Asp
 115 120 125

cct aac cac aag ccg gag ctg gtt ttt gcg ctg acg cct ttc ctt gcg 432

Pro Asn His Lys Pro Glu Leu Val Phe Ala Leu Thr Pro Phe Leu Ala
130 135 140

atg	aac	gcg	ttt	cgt	gaa	ttt	tcc	gag	att	gtc	tcc	cta	ctc	cag	ccg	480
Met	Asn	Ala	Phe	Arg	Glu	Phe	Ser	Glu	Ile	Val	Ser	Leu	Leu	Gln	Pro	
145					150					155					160	

gtc gca ggt gca cat ccg gcg att gct cac ttt tta caa cag cct gat 528
Val Ala Gly Ala His Pro Ala Ile Ala His Phe Leu Gln Gln Pro Asp
165 170 175

gcc gaa cgt tta agc gaa ctg ttc gcc agc ctg ttg aat atg cag ggt 576
Ala Glu Arg Leu Ser Glu Leu Phe Ala Ser Leu Leu Asn Met Gln Gly
180 185 190

gaa gaa aaa tcc cgc gcg ctg gcg att tta aaa tcg gcc ctc gat agc 624
Glu Glu Lys Ser Arg Ala Leu Ala Ile Leu Lys Ser Ala Leu Asp Ser
195 200 205

cag cag ggt gaa ccg tgg caa acg att cgt tta att tct gaa ttt tac 672
Gln Gln Gly Glu Pro Trp Gln Thr Ile Arg Leu Ile Ser Glu Phe Tyr
210 215 220

ccg gaa gac agc ggt ctg ttc tcc ccg cta ttg ctg aat gtg gtg aaa 720
Pro Glu Asp Ser Gly Leu Phe Ser Pro Leu Leu Leu Asn Val Val Lys
225 230 235 240

ttg	aac	cct	ggc	gaa	gcg	atg	ttc	ctg	ttc	gct	gaa	aca	ccg	cac	gct	768
Leu	Asn	Pro	Gly	Glu	Ala	Met	Phe	Leu	Phe	Ala	Glu	Thr	Pro	His	Ala	
				245					250					255		

tac	ctg	caa	ggc	gtg	gcg	ctg	gaa	gtg	atg	gca	aac	tcc	gat	aac	gtg	816
Tyr	Leu	Gln	Gly	Val	Ala	Leu	Glu	Val	Met	Ala	Asn	Ser	Asp	Asn	Val	
			260					265					270			

ctg	cgt	gcg	ggt	ctg	acg	cct	aaa	tac	att	gat	att	ccg	gaa	ctg	gtt	864
Leu	Arg	Ala	Gly	Leu	Thr	Pro	Lys	Tyr	Ile	Asp	Ile	Pro	Glu	Leu	Val	
		275					280					285				

gcc aat gtg aaa ttc gaa gcc aaa ccg gct aac cag ttg ttg acc cag 912
Ala Asn Val Lys Phe Glu Ala Lys Pro Ala Asn Gln Leu Leu Thr Gln
290 295 300

ccg gtg aaa caa ggt gca gaa ctg gac ttc ccg att cca gtg gat gat 960
Pro Val Lys Gln Gly Ala Glu Leu Asp Phe Pro Ile Pro Val Asp Asp
305 310 315 320

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ttt gcc ttc tcg ctg cat gac ctt agt gat aaa gaa acc acc att agc    1008
Phe Ala Phe Ser Leu His Asp Leu Ser Asp Lys Glu Thr Thr Ile Ser
                325                      330                      335

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cag cag agt gcc gcc att ttg ttc tgc gtc gaa ggc gat gca acg ttg 1056
Gln Gln Ser Ala Ala Ile Leu Phe Cys Val Glu Gly Asp Ala Thr Leu
340 345 350

tgg aaa ggt tct cag cag tta cag ctt aaa ccg ggt gaa tca gcg ttt 1104
 Trp Lys Gly Ser Gln Gln Leu Gln Leu Lys Pro Gly Glu Ser Ala Phe

50	55	60	
ttc ctc ggc gtc ttc ctc ggg gga cgt att ggt tat gtt ctg ttc tac	240		
Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr			
65 70 75 80			
aat ttc ccg cag ttt atg gcc gat ccg ctg tat ctg ttc cgt gtc tgg	288		
Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp			
85 90 95			
gac ggc ggc atg tct ttc cac ggc ggc ctg att ggc gtt atc gtg gtg	336		
Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val			
100 105 110			
atg att atc ttc gcc cgc cgt act aaa cgt tcc ttc ttc cag gtc tct	384		
Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser			
115 120 125			
gat ttt atc gca cca ctc att ccg ttt ggt ctt ggt gcc ggg cgt ctg	432		
Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu			
130 135 140			
ggc aac ttt att aac ggt gaa ttg tgg ggc cgc gtt gac ccg aac ttc	480		
Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe			
145 150 155 160			
ccg ttt gcc atg ctg ttc cct ggc tcc cgt aca gaa gat att ttg ctg	528		
Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu			
165 170 175			
ctg caa acc aac ccg cag tgg caa tcc att ttc gac act tac ggt gtg	576		
Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val			
180 185 190			
ctg ccg cgc cac cca tca cag ctt tac gag ctg ctg ctg gaa ggt gtg	624		
Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val			
195 200 205			
gtg ctg ttt att atc ctc aac ctg tat att cgt aaa cca cgc cca atg	672		
Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met			
210 215 220			
gga gct gtc tca ggt ttg ttc ctg att ggt tac ggc gcg ttt cgc atc	720		
Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile			
225 230 235 240			
att gtt gag ttt ttc cgc cag ccc gac gcg cag ttt acc ggt gcc tgg	768		
Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp			
245 250 255			
gtg cag tac atc agc atg ggg caa att ctt tcc atc ccg atg att gtc	816		
Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val			
260 265 270			
gcg ggt gtg atc atg atg gtc tgg gca tat cgt cgc agc cca cag caa	864		
Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln			
275 280 285			

cac gtt tcc tga
His Val Ser *
290

876

<210> 183
<211> 726
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(726)

<400> 183
atg gac agt ctc aat ctt aat aaa cat att tcc ggc cag ttc aac gcc 48
Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
1 5 10 15
gaa ctg gaa agt atc cgc acg cag gtg atg acc atg ggc ggc atg gtg 96
Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
20 25 30
gag cag cag ctt tct gat gca atc acc gcg atg cat aac cag gac agc 144
Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
35 40 45
gat ctg gcg aag cgc gtc atc gaa ggc gac aag aac gtc aac atg atg 192
Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
50 55 60
gaa gtg gcg atc gat gaa gcc tgc gtg cgc att atc gcc aaa cgt cag 240
Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
65 70 75 80
ccg acg gcg agc gac ctg cga ctg gtt atg gtg atc agt aaa acc att 288
Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
85 90 95
gcc gag ctg gag cgt att ggc gac gtg gcg gac aaa atc tgc cgt act 336
Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
100 105 110
gcg ctg gag aaa ttc tcc cag cag cat cag ccg ttg ctg gta agt ctg 384
Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
115 120 125
gag tcg ctg ggc cgt cat acc atc cag atg ctg cac gac gtg ctg gac 432
Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
130 135 140
gcg ttc gcg cgg atg gac att gac gaa gcg gta cgt att tat cgt gaa 480
Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
145 150 155 160
gat aaa aaa gtc gat cag gaa tac gaa ggt att gtt cgt caa ctg atg 528

Asp	Lys	Lys	Val	Asp	Gln	Glu	Tyr	Glu	Gly	Ile	Val	Arg	Gln	Leu	Met	
				165					170					175		
acc	tac	atg	atg	gaa	gat	tcg	cgt	acc	att	ccg	agc	gta	ctt	act	gcg	576
Thr	Tyr	Met	Met	Glu	Asp	Ser	Arg	Thr	Ile	Pro	Ser	Val	Leu	Thr	Ala	
			180					185					190			
ctg	ttc	tgc	gcg	cgt	tct	atc	gaa	cgt	att	ggc	gac	cgc	tgc	cag	aat	624
Leu	Phe	Cys	Ala	Arg	Ser	Ile	Glu	Arg	Ile	Gly	Asp	Arg	Cys	Gln	Asn	
		195					200				205					
att	tgt	gag	ttt	atc	ttc	tac	tac	gtg	aag	ggg	cag	gat	ttc	cgt	cac	672
Ile	Cys	Glu	Phe	Ile	Phe	Tyr	Tyr	Val	Lys	Gly	Gln	Asp	Phe	Arg	His	
	210					215					220					
gtc	ggg	ggc	gat	gag	ctg	gat	aaa	ctg	ctg	gcg	ggg	aaa	gat	agc	gac	720
Val	Gly	Gly	Asp	Glu	Leu	Asp	Lys	Leu	Leu	Ala	Gly	Lys	Asp	Ser	Asp	
225					230					235					240	
aaa	taa															726
Lys	*															

<210> 184
 <211> 774
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(774)

<400>	184															
atg	agt	atg	gtt	gaa	act	gcc	ccg	agt	aaa	att	cag	gtt	cgt	aat	ttg	48
Met	Ser	Met	Val	Glu	Thr	Ala	Pro	Ser	Lys	Ile	Gln	Val	Arg	Asn	Leu	
1				5					10					15		
aac	ttc	tac	tac	ggc	aaa	ttc	cat	gcc	ctg	aaa	aac	atc	aac	ctg	gat	96
Asn	Phe	Tyr	Tyr	Gly	Lys	Phe	His	Ala	Leu	Lys	Asn	Ile	Asn	Leu	Asp	
			20					25					30			
atc	gct	aaa	aac	cag	gta	acg	gcg	ttt	atc	ggg	ccg	tcc	ggc	tgc	ggg	144
Ile	Ala	Lys	Asn	Gln	Val	Thr	Ala	Phe	Ile	Gly	Pro	Ser	Gly	Cys	Gly	
		35					40					45				
aaa	tcg	acg	ctg	ctg	cgt	acc	ttc	aac	aaa	atg	ttt	gaa	ctg	tac	ccg	192
Lys	Ser	Thr	Leu	Leu	Arg	Thr	Phe	Asn	Lys	Met	Phe	Glu	Leu	Tyr	Pro	
	50					55				60						
gag	cag	cgt	gcg	gaa	ggg	gaa	att	ctg	ctt	gat	ggc	gac	aac	atc	ctg	240
Glu	Gln	Arg	Ala	Glu	Gly	Glu	Ile	Leu	Leu	Asp	Gly	Asp	Asn	Ile	Leu	
65					70					75					80	
acc	aac	tct	cag	gat	atc	gca	ctg	ctg	cgt	gcg	aaa	gtg	ggc	atg	gtg	288
Thr	Asn	Ser	Gln	Asp	Ile	Ala	Leu	Leu	Arg	Ala	Lys	Val	Gly	Met	Val	
				85					90					95		

ttc cag aaa ccg acg ccg ttt ccg atg tcc atc tac gac aac atc gct	336
Phe Gln Lys Pro Thr Pro Phe Pro Met Ser Ile Tyr Asp Asn Ile Ala	
100 105 110	
ttt ggc gtt cgt ctg ttt gag aag ctc tcc cgt gcc gac atg gac gag	384
Phe Gly Val Arg Leu Phe Glu Lys Leu Ser Arg Ala Asp Met Asp Glu	
115 120 125	
cgc gtg cag tgg gca ttg acc aaa gcc gca ttg tgg aac gaa acc aaa	432
Arg Val Gln Trp Ala Leu Thr Lys Ala Ala Leu Trp Asn Glu Thr Lys	
130 135 140	
gat aaa ttg cac cag agc ggt tac tct ctc tct ggt ggt cag caa cag	480
Asp Lys Leu His Gln Ser Gly Tyr Ser Leu Ser Gly Gly Gln Gln Gln	
145 150 155 160	
cgt ctg tgt att gcg cgt ggt atc gcc att cgc ccg gaa gtg ctg ctg	528
Arg Leu Cys Ile Ala Arg Gly Ile Ala Ile Arg Pro Glu Val Leu Leu	
165 170 175	
ctc gac gaa ccg tgt tcg gcg ctc gac cct atc tct acc ggg cgt att	576
Leu Asp Glu Pro Cys Ser Ala Leu Asp Pro Ile Ser Thr Gly Arg Ile	
180 185 190	
gaa gag ctg atc acc gaa ctg aag cag gat tac acc gtg gtg atc gtc	624
Glu Glu Leu Ile Thr Glu Leu Lys Gln Asp Tyr Thr Val Val Ile Val	
195 200 205	
acc cac aac atg cag cag gct gcg cgt tgt tcc gac cac acg gcg ttt	672
Thr His Asn Met Gln Gln Ala Ala Arg Cys Ser Asp His Thr Ala Phe	
210 215 220	
atg tac ctg ggc gaa ttg att gag ttc agc aac acg gac gat ctg ttc	720
Met Tyr Leu Gly Glu Leu Ile Glu Phe Ser Asn Thr Asp Asp Leu Phe	
225 230 235 240	
acc aag cca gcg aag aaa caa aca gaa gac tac atc acc ggt cgt tac	768
Thr Lys Pro Ala Lys Lys Gln Thr Glu Asp Tyr Ile Thr Gly Arg Tyr	
245 250 255	
ggt tga	774
Gly *	

<210> 185
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> .CDS
 <222> (1)...(891)

<400> 185
 atg gct atg gtt gaa atg caa acc act gcg gcg ctg gct gaa tct cgc 48

Met	Ala	Met	Val	Glu	Met	Gln	Thr	Thr	Ala	Ala	Leu	Ala	Glu	Ser	Arg	
1				5					10					15		
cgc	aaa	atg	cag	gcg	cgt	cgc	cgc	ctc	aaa	aac	cgt	att	gcg	ctg	acg	96
Arg	Lys	Met	Gln	Ala	Arg	Arg	Arg	Leu	Lys	Asn	Arg	Ile	Ala	Leu	Thr	
			20					25					30			
ctc	tcg	atg	gcg	acg	atg	gcc	ttc	ggc	ctg	ttc	tgg	ctg	atc	tgg	att	144
Leu	Ser	Met	Ala	Thr	Met	Ala	Phe	Gly	Leu	Phe	Trp	Leu	Ile	Trp	Ile	
			35				40					45				
tta	atg	tcc	acc	atc	act	cgc	ggc	atc	gac	ggc	atg	tcg	ctg	gcg	ctg	192
Leu	Met	Ser	Thr	Ile	Thr	Arg	Gly	Ile	Asp	Gly	Met	Ser	Leu	Ala	Leu	
	50					55					60					
ttc	act	gaa	atg	acg	ccg	ccg	ccc	aac	acg	gaa	ggc	ggc	ggc	ctg	gcg	240
Phe	Thr	Glu	Met	Thr	Pro	Pro	Pro	Asn	Thr	Glu	Gly	Gly	Gly	Leu	Ala	
	65				70					75					80	
aac	gct	ctg	gcg	ggc	agc	ggc	ctg	tta	att	ttg	tgg	gcc	acg	gta	ttc	288
Asn	Ala	Leu	Ala	Gly	Ser	Gly	Leu	Leu	Ile	Leu	Trp	Ala	Thr	Val	Phe	
				85					90					95		
ggc	acg	ccg	ctg	ggc	att	atg	gcg	ggc	att	tat	ctg	gcg	gaa	tat	ggc	336
Gly	Thr	Pro	Leu	Gly	Ile	Met	Ala	Gly	Ile	Tyr	Leu	Ala	Glu	Tyr	Gly	
			100					105					110			
cgt	aaa	tcc	tgg	ctg	gca	gaa	gtg	att	cgc	ttc	att	aac	gac	att	ctg	384
Arg	Lys	Ser	Trp	Leu	Ala	Glu	Val	Ile	Arg	Phe	Ile	Asn	Asp	Ile	Leu	
		115					120					125				
ctc	tct	gcg	ccg	tcg	att	gtg	gtt	ggc	ctg	ttt	gtt	tac	acc	att	gtg	432
Leu	Ser	Ala	Pro	Ser	Ile	Val	Val	Gly	Leu	Phe	Val	Tyr	Thr	Ile	Val	
			130				135					140				
gtg	gcg	cag	atg	gag	cac	ttc	tcc	ggc	tgg	gcg	ggc	gtg	att	gcc	ctg	480
Val	Ala	Gln	Met	Glu	His	Phe	Ser	Gly	Trp	Ala	Gly	Val	Ile	Ala	Leu	
	145				150					155					160	
gcg	ttg	ttg	cag	gtg	ccg	att	gtt	atc	cgc	acc	acc	gag	aac	atg	ctg	528
Ala	Leu	Leu	Gln	Val	Pro	Ile	Val	Ile	Arg	Thr	Thr	Glu	Asn	Met	Leu	
				165					170					175		
aaa	ctg	gtg	ccg	tac	agc	ctg	cgt	gaa	gcg	gct	tat	gcg	ctg	ggc	aca	576
Lys	Leu	Val	Pro	Tyr	Ser	Leu	Arg	Glu	Ala	Ala	Tyr	Ala	Leu	Gly	Thr	
			180					185					190			
ccg	aag	tgg	aag	atg	atc	tct	gcg	att	acg	ctg	aaa	gcg	tcg	gtg	tcc	624
Pro	Lys	Trp	Lys	Met	Ile	Ser	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Val	Ser	
			195				200					205				
ggg	att	atg	acc	ggc	atc	ctg	ctg	gcg	att	gcc	cgt	att	gct	ggc	gaa	672
Gly	Ile	Met	Thr	Gly	Ile	Leu	Leu	Ala	Ile	Ala	Arg	Ile	Ala	Gly	Glu	
	210					215					220					
acc	gcg	ccg	ctg	ctg	ttt	acc	gcg	ctc	tcc	aac	cag	ttc	tgg	agc	acg	720
Thr	Ala	Pro	Leu	Leu	Phe	Thr	Ala	Leu	Ser	Asn	Gln	Phe	Trp	Ser	Thr	

225	230	235	240	
gac atg atg cag ccg atc gcc aac ctg ccg gtg acg atc ttt aag ttt	768			
Asp Met Met Gln Pro Ile Ala Asn Leu Pro Val Thr Ile Phe Lys Phe				
245	250	255		
gcg atg agc ccg ttt gcg gaa tgg cag caa ttg gcc tgg gcc ggg gta	816			
Ala Met Ser Pro Phe Ala Glu Trp Gln Gln Leu Ala Trp Ala Gly Val				
260	265	270		
ttg atc att acc ctg tgc gta ctg ctg ctg aac att ctg gcg cgc gtt	864			
Leu Ile Ile Thr Leu Cys Val Leu Leu Leu Asn Ile Leu Ala Arg Val				
275	280	285		
gtt ttt gcg aag aat aaa cac ggt tga	891			
Val Phe Ala Lys Asn Lys His Gly *				
290	295			
<210> 186				
<211> 960				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(960)				
<400> 186				
atg gct gca acc aag cct gct ttt aac cca ccg ggt aaa aag ggc gac	48			
Met Ala Ala Thr Lys Pro Ala Phe Asn Pro Pro Gly Lys Lys Gly Asp				
1	5	10	15	
ata att ttc agc gtg ctg gta aaa ctg gcg gcg ctg att gtg cta ttg	96			
Ile Ile Phe Ser Val Leu Val Lys Leu Ala Ala Leu Ile Val Leu Leu				
20	25	30		
atg ttg ggt ggc att att gtc tct ctg atc atc tcc tcc tgg ccg agc	144			
Met Leu Gly Gly Ile Ile Val Ser Leu Ile Ile Ser Ser Trp Pro Ser				
35	40	45		
att cag aaa ttt ggt ctg gct ttc cta tgg acc aaa gag tgg gat gca	192			
Ile Gln Lys Phe Gly Leu Ala Phe Leu Trp Thr Lys Glu Trp Asp Ala				
50	55	60		
ccg aac gat atc tac ggg gcg ctg gtg ccg atc tac ggt acg ttg gtg	240			
Pro Asn Asp Ile Tyr Gly Ala Leu Val Pro Ile Tyr Gly Thr Leu Val				
65	70	75	80	
act tcg ttt atc gcg ctg ctg atc gcc gtc ccg gtg agt ttc ggt atc	288			
Thr Ser Phe Ile Ala Leu Leu Ile Ala Val Pro Val Ser Phe Gly Ile				
85	90	95		
gcc ctg ttc ctg act gag ctt gcg cct ggc tgg ctg aaa cgc ccg ctg	336			
Ala Leu Phe Leu Thr Glu Leu Ala Pro Gly Trp Leu Lys Arg Pro Leu				
100	105	110		

ggt Gly	atc Ile	gcc Ala 115	att Ile	gag Glu	ctg Leu	ctg Leu	gca Ala 120	gcc Ala	att Ile	cca Pro	agt Ser	atc Ile 125	gtt Val	tac Tyr	ggc Gly	384
atg Met	tgg Trp 130	ggc Gly	ctg Leu	ttt Phe	atc Ile	ttt Phe 135	gcg Ala	cgc Pro	ctg Leu	ttc Phe 140	gcc Ala 145	gtt Val	tac Tyr	ttt Phe	cag Gln	432
gag Glu 145	ccg Pro	gtc Val	ggc Gly	aat Asn	atc Ile 150	atg Met	tcg Ser	aat Asn	atc Ile	ccg Pro 155	att Ile	gtt Val	ggc Gly	gcg Ala	ctg Leu 160	480
ttc Phe	tct Ser	ggc Gly	ccc Pro	gca Ala 165	ttt Phe	ggt Gly	atc Ile	ggt Gly	atc Ile 170	ctc Leu	gcg Ala	gca Ala	ggc Gly	gtg Val 175	atc Ile	528
ctc Leu	gcc Ala	atc Ile 180	atg Met	att Ile	att Ile	ccg Pro	tac Tyr	att Ile 185	gcg Ala	gcg Ala	gta Val	atg Met	cgt Arg 190	gat Asp	gtg Val	576
ttc Phe	gaa Glu 195	caa Gln	acc Thr	ccg Pro	gtg Val	atg Met	atg Met 200	aaa Lys	gag Glu	tcg Ser	gcc Ala 205	tac Tyr	ggc Gly	att Ile	ggc Gly	624
tgc Cys	acc Thr 210	acc Thr	tgg Trp	gaa Glu	gtt Val	atc Ile 215	tgg Trp	cgt Arg	atc Ile	gtt Val 220	ctt Leu	ccg Pro	ttc Phe	acc Thr	aaa Lys	672
aat Asn 225	ggt Gly	gtt Val	atc Ile	ggc Gly	ggc Gly 230	atc Ile	atg Met	ctg Leu	ggg Gly 235	ctg Leu 240	ggc Gly	cgc Arg	gcg Ala	ctc Leu	ggt Gly 240	720
gaa Glu	acc Thr	atg Met	gcg Ala	gtg Val 245	acc Thr	ttt Phe	atc Ile	atc Ile	ggt Gly 250	aac Asn	acc Thr	tac Tyr	cag Gln	ctc Leu 255	gac Asp	768
agc Ser	gcc Ala	tcg Ser	ctg Leu 260	tat Tyr	atg Met	ccg Pro	ggc Gly	aac Asn 265	agt Ser	atc Ile	acc Thr	tct Ser	gcg Ala	ctg Leu	gcg Ala	816
aac Asn	gaa Glu	ttt Phe 275	gcg Ala	gaa Glu	gcg Ala	gaa Glu	tcc Ser 280	ggt Gly	ctg Leu	cac His	gtt Val	gcc Ala 285	gca Ala	ctg Leu	atg Met	864
gaa Glu 290	ctg Leu	ggc Gly	ctg Leu	atc Ile	ctg Leu	ttt Phe 295	gtg Val	att Ile	acc Thr	ttc Phe 300	atc Ile	gtc Val	ctc Leu	gcc Ala	gca Ala	912
tcg Ser 305	aag Lys	ttt Phe	atg Met	att Ile	atg Met 310	cgc Arg	ctg Leu	gct Ala	aag Lys	aat Asn 315	gag Glu	ggg Gly	gca Ala	cgc Arg	taa *	960

<210> 187
<211> 1041
<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1041)

<400> 187

atg	aaa	ggt	atg	cgt	acc	acc	gtc	gca	act	ggt	gtc	gcc	gcg	acc	tta	48
Met	Lys	Val	Met	Arg	Thr	Thr	Val	Ala	Thr	Val	Val	Ala	Ala	Thr	Leu	
1				5					10					15		

tgc	atg	agt	gct	ttc	tct	gtg	ttt	gca	gaa	gca	agc	ctg	aca	ggt	gca	96
Ser	Met	Ser	Ala	Phe	Ser	Val	Phe	Ala	Glu	Ala	Ser	Leu	Thr	Gly	Ala	
			20					25					30			

ggt	gca	acc	ttc	cct	gcg	ccg	gtg	tat	gcc	aaa	tgg	gct	gac	act	tac	144
Gly	Ala	Thr	Phe	Pro	Ala	Pro	Val	Tyr	Ala	Lys	Trp	Ala	Asp	Thr	Tyr	
		35					40					45				

cag	aaa	gaa	acc	ggt	aat	aaa	ggt	aac	tac	cag	ggt	atc	ggt	tct	tcc	192
Gln	Lys	Glu	Thr	Gly	Asn	Lys	Val	Asn	Tyr	Gln	Gly	Ile	Gly	Ser	Ser	
	50					55					60					

ggt	ggc	gta	aaa	cag	att	atc	gct	aat	acc	ggt	gat	ttt	ggt	gcc	tct	240
Gly	Gly	Val	Lys	Gln	Ile	Ile	Ala	Asn	Thr	Val	Asp	Phe	Gly	Ala	Ser	
65					70					75					80	

gac	gcg	ccg	ctg	tct	gac	gaa	aaa	ctg	gct	cag	gaa	ggt	ctg	ttc	cag	288
Asp	Ala	Pro	Leu	Ser	Asp	Glu	Lys	Leu	Ala	Gln	Glu	Gly	Leu	Phe	Gln	
				85				90						95		

ttc	ccg	acc	gtg	att	ggc	ggc	gtg	gtg	ctg	gcg	ggt	aac	att	cca	ggg	336
Phe	Pro	Thr	Val	Ile	Gly	Gly	Val	Val	Leu	Ala	Val	Asn	Ile	Pro	Gly	
			100					105					110			

ctg	aag	tct	ggc	gaa	ctg	gtg	ctg	gat	ggt	aaa	acc	ctc	ggc	gac	atc	384
Leu	Lys	Ser	Gly	Glu	Leu	Val	Leu	Asp	Gly	Lys	Thr	Leu	Gly	Asp	Ile	
		115					120					125				

tac	ctg	ggc	aaa	atc	aag	aag	tgg	gat	gat	gaa	gcc	atc	gcc	aaa	ctg	432
Tyr	Leu	Gly	Lys	Ile	Lys	Lys	Trp	Asp	Asp	Glu	Ala	Ile	Ala	Lys	Leu	
	130					135					140					

aat	ccg	ggt	ctg	aaa	ctg	cct	tca	caa	aac	att	gct	gta	gta	cgc	cgc	480
Asn	Pro	Gly	Leu	Lys	Leu	Pro	Ser	Gln	Asn	Ile	Ala	Val	Val	Arg	Arg	
145					150					155					160	

gca	gat	ggc	tcc	ggg	act	tcc	ttc	gtc	ttc	acc	agc	tac	ctg	gcg	aaa	528
Ala	Asp	Gly	Ser	Gly	Thr	Ser	Phe	Val	Phe	Thr	Ser	Tyr	Leu	Ala	Lys	
				165					170					175		

gtg	aac	gaa	gag	tgg	aaa	aac	aac	ggt	ggt	act	ggc	tct	acc	gta	aaa	576
Val	Asn	Glu	Glu	Trp	Lys	Asn	Asn	Val	Gly	Thr	Gly	Ser	Thr	Val	Lys	
			180					185					190			

tgg	ccg	atc	ggt	ctg	ggc	ggt	aaa	ggt	aac	gac	ggt	atc	gcc	gcg	ttc	624
Trp	Pro	Ile	Gly	Leu	Gly	Gly	Lys	Gly	Asn	Asp	Gly	Ile	Ala	Ala	Phe	

<220>
 <221> CDS
 <222> (1)...(546)

<400> 189

gtg	cag	gcc	aaa	att	gcg	gca	tca	aat	acg	ggg	gaa	ctg	gat	gcc	ctg	48
Met	Gln	Ala	Lys	Ile	Ala	Ala	Ser	Asn	Thr	Gly	Glu	Leu	Asp	Ala	Leu	
1				5					10					15		
caa	cag	ctg	gga	ttc	tcc	ctg	gta	gaa	ggg	gaa	gtt	gat	ttg	gcg	cta	96
Gln	Gln	Leu	Gly	Phe	Ser	Leu	Val	Glu	Gly	Glu	Val	Asp	Leu	Ala	Leu	
		20						25					30			
ccc	gtg	aac	aat	gcc	agt	gat	agc	ggg	gct	gta	gtg	gca	caa	gag	acc	144
Pro	Val	Asn	Asn	Ala	Ser	Asp	Ser	Gly	Ala	Val	Val	Ala	Gln	Glu	Thr	
		35					40					45				
gat	att	ccc	gca	tta	cgt	cag	tta	gcc	agc	gcc	gca	ttt	gcg	caa	agc	192
Asp	Ile	Pro	Ala	Leu	Arg	Gln	Leu	Ala	Ser	Ala	Ala	Phe	Ala	Gln	Ser	
	50					55					60					
cgt	ttt	cgt	gcg	ccg	tgg	tat	gcg	cct	gac	gcc	agc	agt	cgc	ttt	tat	240
Arg	Phe	Arg	Ala	Pro	Trp	Tyr	Ala	Pro	Asp	Ala	Ser	Ser	Arg	Phe	Tyr	
65					70				75					80		
gca	cag	tgg	att	gaa	aat	gcc	gtg	cgc	ggc	acc	ttt	gat	cat	caa	tgt	288
Ala	Gln	Trp	Ile	Glu	Asn	Ala	Val	Arg	Gly	Thr	Phe	Asp	His	Gln	Cys	
			85					90						95		
ctg	att	tta	cgt	gcg	gcg	tcc	ggc	gat	att	cgc	ggc	tat	gtc	tct	tta	336
Leu	Ile	Leu	Arg	Ala	Ala	Ser	Gly	Asp	Ile	Arg	Gly	Tyr	Val	Ser	Leu	
			100					105					110			
cgg	gaa	ctc	aat	gcg	aca	gat	gcg	cga	att	ggc	ctg	ctg	gct	gga	cgc	384
Arg	Glu	Leu	Asn	Ala	Thr	Asp	Ala	Arg	Ile	Gly	Leu	Leu	Ala	Gly	Arg	
		115					120					125				
ggg	gca	ggg	gct	gag	ctg	atg	caa	acg	gcg	cta	aac	tgg	gcg	tat	cgt	432
Gly	Ala	Gly	Ala	Glu	Leu	Met	Gln	Thr	Ala	Leu	Asn	Trp	Ala	Tyr	Arg	
	130					135					140					
cgc	ggg	aaa	aca	act	ttg	cgg	gtg	gcg	acc	caa	atg	ggc	aac	acc	gcc	480
Arg	Gly	Lys	Thr	Thr	Leu	Arg	Val	Ala	Thr	Gln	Met	Gly	Asn	Thr	Ala	
145					150					155					160	
gcg	ctt	aaa	cga	tac	ata	caa	agt	ggg	gcg	aat	gta	gaa	agc	acc	gcg	528
Ala	Leu	Lys	Arg	Tyr	Ile	Gln	Ser	Gly	Ala	Asn	Val	Glu	Ser	Thr	Ala	
				165					170					175		
tac	tgg	tta	tac	agg	tga											546
Tyr	Trp	Leu	Tyr	Arg	*											
			180													

<210> 190
 <211> 1131

<212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1131)

<400> 190

atg att cca ttt aac gca ccg ccg gtg gtg gga acc gaa ctc gac tat	48
Met Ile Pro Phe Asn Ala Pro Pro Val Val Gly Thr Glu Leu Asp Tyr	
1 5 10 15	
atg cag tcg gca atg ggt agc ggc aaa ctg tgt ggc gat ggc ggt ttt	96
Met Gln Ser Ala Met Gly Ser Gly Lys Leu Cys Gly Asp Gly Gly Phe	
20 25 30	
acc cgt cgc tgc cag cag tgg ctg gag caa cgt ttt ggc agc gcc aaa	144
Thr Arg Arg Cys Gln Gln Trp Leu Glu Gln Arg Phe Gly Ser Ala Lys	
35 40 45	
gtg tta ctg acg ccg tcc tgc acc gct tcg ctg gag atg gcg gcg ctg	192
Val Leu Leu Thr Pro Ser Cys Thr Ala Ser Leu Glu Met Ala Ala Leu	
50 55 60	
ctg ctc gat atc cag cct ggc gat gaa gtg atc atg ccg agc tac acc	240
Leu Leu Asp Ile Gln Pro Gly Asp Glu Val Ile Met Pro Ser Tyr Thr	
65 70 75 80	
ttt gtc tcc acc gcc aat gcc ttt gtg ctg cgt ggc gca aaa atc gtt	288
Phe Val Ser Thr Ala Asn Ala Phe Val Leu Arg Gly Ala Lys Ile Val	
85 90 95	
ttt gtg gat gtt cgc ccg gac acc atg aac atc gac gaa acg ctg att	336
Phe Val Asp Val Arg Pro Asp Thr Met Asn Ile Asp Glu Thr Leu Ile	
100 105 110	
gaa gcg gcg atc acc gac aaa acg cgc gtt atc gtg ccg gtc cat tac	384
Glu Ala Ala Ile Thr Asp Lys Thr Arg Val Ile Val Pro Val His Tyr	
115 120 125	
gcg ggt gtg gcc tgc gaa atg gac acc att atg gcg ttg gcg aaa aag	432
Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys	
130 135 140	
cat aat ttg ttt gtg gta gaa gat gcc gct cag ggc gtg atg tcc act	480
His Asn Leu Phe Val Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr	
145 150 155 160	
tac aaa ggg cgt gca ctg gga acc att ggt cat att ggc tgc ttt agc	528
Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser	
165 170 175	
ttc cat gaa acc aaa aac tac acg gcg ggc ggt gaa ggc ggc gcg acg	576
Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr	
180 185 190	
ctg att aac gat aaa gcg tta atc gaa cga gcc gag atc atc cgt gaa	624

<220>
 <221> CDS
 <222> (1)...(1353)

<400> 192

atg agt ctg ctg caa ttc agt ggc ctg ttt gtt gtc tgg ctg ctc tgc	48
Met Ser Leu Leu Gln Phe Ser Gly Leu Phe Val Val Trp Leu Leu Cys	
1 5 10 15	
acg ctg ttt att gcc acg ctg acc tgg ttt gag ttt cgc cgt gtg cgc	96
Thr Leu Phe Ile Ala Thr Leu Thr Trp Phe Glu Phe Arg Arg Val Arg	
20 25 30	
ttt aac ttc aat gtc ttc ttt tca ttg ctg ttt ttg ctc acc ttt ttc	144
Phe Asn Phe Asn Val Phe Phe Ser Leu Leu Phe Leu Leu Thr Phe Phe	
35 40 45	
ttc ggc ttc ccg ctg acc agc gtg ctg gta ttt cgc ttt gat gtt ggt	192
Phe Gly Phe Pro Leu Thr Ser Val Leu Val Phe Arg Phe Asp Val Gly	
50 55 60	
gtc gcg ccg cca gaa atc ttg ttg cag gcg ttg ctt tct gcg ggc tgc	240
Val Ala Pro Pro Glu Ile Leu Leu Gln Ala Leu Leu Ser Ala Gly Cys	
65 70 75 80	
ttc tac gcg gtt tac tat gtc acc tac aaa acc cgc cta cgc aaa cgc	288
Phe Tyr Ala Val Tyr Tyr Val Thr Tyr Lys Thr Arg Leu Arg Lys Arg	
85 90 95	
gtt gct gat gta ccg cgc cgt ccg ctg ttt acc atg aac cgc gtg gag	336
Val Ala Asp Val Pro Arg Arg Pro Leu Phe Thr Met Asn Arg Val Glu	
100 105 110	
acc aat ctt acg tgg gtg atc ctg atg ggt atc gcg ctg gta agc gtc	384
Thr Asn Leu Thr Trp Val Ile Leu Met Gly Ile Ala Leu Val Ser Val	
115 120 125	
ggc atc ttc ttc atg cac aac ggc ttt ttg ctg ttc cgg ctt aac tcc	432
Gly Ile Phe Phe Met His Asn Gly Phe Leu Leu Phe Arg Leu Asn Ser	
130 135 140	
tac agt cag atc ttt tcc agt gaa gtc tcc ggc gtg gcg tta aaa cgc	480
Tyr Ser Gln Ile Phe Ser Ser Glu Val Ser Gly Val Ala Leu Lys Arg	
145 150 155 160	
ttc ttt tac ttt ttc atc ccg gcg atg ctg gtg gtc tac ttt ctg cgc	528
Phe Phe Tyr Phe Phe Ile Pro Ala Met Leu Val Val Tyr Phe Leu Arg	
165 170 175	
cag gac agc aaa gcg tgg ctg ttt ttc ctc gtc agc acg gtc gcc ttt	576
Gln Asp Ser Lys Ala Trp Leu Phe Phe Leu Val Ser Thr Val Ala Phe	
180 185 190	
ggc ttg ctg act tat atg att gtc ggc ggc act cgc gcc aat atc atc	624
Gly Leu Leu Thr Tyr Met Ile Val Gly Gly Thr Arg Ala Asn Ile Ile	
195 200 205	

atc gca ttc gct atc ttc ctg ttt att ggc att att cgc ggc tgg att	672
Ile Ala Phe Ala Ile Phe Leu Phe Ile Gly Ile Ile Arg Gly Trp Ile	
210 215 220	
tcg ttg tgg atg ctg gcg gcg gcg ggc gtg ctg ggg att gtt ggc atg	720
Ser Leu Trp Met Leu Ala Ala Ala Gly Val Leu Gly Ile Val Gly Met	
225 230 235 240	
ttc tgg ctg gca cta aaa cgc tat gga atg aat gtg agc ggc gat gaa	768
Phe Trp Leu Ala Leu Lys Arg Tyr Gly Met Asn Val Ser Gly Asp Glu	
245 250 255	
gcg ttc tat acg ttt ctc tat ctc act cgc gac acc ttc tcg ccg tgg	816
Ala Phe Tyr Thr Phe Leu Tyr Leu Thr Arg Asp Thr Phe Ser Pro Trp	
260 265 270	
gag aat ctg gcg ttg ctg ttg cag aac tac gac aac atc gac ttc cag	864
Glu Asn Leu Ala Leu Leu Leu Gln Asn Tyr Asp Asn Ile Asp Phe Gln	
275 280 285	
ggc ctg gct cca att gtc cgc gat ttc tat gtc ttt atc cct tcc tgg	912
Gly Leu Ala Pro Ile Val Arg Asp Phe Tyr Val Phe Ile Pro Ser Trp	
290 295 300	
ctg tgg ccg ggt cgc ccg agt atg gtg ctg aac tca gcc aac tac ttt	960
Leu Trp Pro Gly Arg Pro Ser Met Val Leu Asn Ser Ala Asn Tyr Phe	
305 310 315 320	
acc tgg gaa gtg ctg aat aac cac tcc gga ctg gcg atc tcg cct acg	1008
Thr Trp Glu Val Leu Asn Asn His Ser Gly Leu Ala Ile Ser Pro Thr	
325 330 335	
ctt ata ggc tca ctg gtg gtg atg ggc ggc gcg ttg ttc atc ccg ctc	1056
Leu Ile Gly Ser Leu Val Val Met Gly Gly Ala Leu Phe Ile Pro Leu	
340 345 350	
ggg gcg atc gtg gtt ggt ctg atc atc aaa tgg ttc gac tgg ctg tat	1104
Gly Ala Ile Val Val Gly Leu Ile Ile Lys Trp Phe Asp Trp Leu Tyr	
355 360 365	
gag ctg ggc aac cgc gag cct aat cgc tat aaa gct gcg ata ttg cac	1152
Glu Leu Gly Asn Arg Glu Pro Asn Arg Tyr Lys Ala Ala Ile Leu His	
370 375 380	
agt ttc tgc ttt ggg gcg atc ttc aat atg atc gtg ctg gcg cgt gaa	1200
Ser Phe Cys Phe Gly Ala Ile Phe Asn Met Ile Val Leu Ala Arg Glu	
385 390 395 400	
ggg ctg gat tcg ttt gtc tca cgc gtg gtc ttt ttt atc gtg gtc ttc	1248
Gly Leu Asp Ser Phe Val Ser Arg Val Val Phe Phe Ile Val Val Phe	
405 410 415	
ggc gca tgt ctg atg atc gca aaa ctg ttg tac tgg ctt ttt gaa agc	1296
Gly Ala Cys Leu Met Ile Ala Lys Leu Leu Tyr Trp Leu Phe Glu Ser	
420 425 430	

gcc gga ctc att cat aaa cgt aca aaa tca tcg ctc cgg acg cag gtt 1344
 Ala Gly Leu Ile His Lys Arg Thr Lys Ser Ser Leu Arg Thr Gln Val
 435 440 445

gaa gga taa 1353
 Glu Gly *
 450

<210> 193
 <211> 741
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(741)

<400> 193
 atg aat aac aac acc acg gca cca acc tat acg ctg cgt ggc tta cag 48
 Met Asn Asn Asn Thr Thr Ala Pro Thr Tyr Thr Leu Arg Gly Leu Gln
 1 5 10 15

ttg att ggt tgg cgt gat atg cag cac gcc ctc gat tat ctg ttt gct 96
 Leu Ile Gly Trp Arg Asp Met Gln His Ala Leu Asp Tyr Leu Phe Ala
 20 25 30

gac ggg cag ctt aag cag gga acg ctg gtt gcc att aat gct gaa aaa 144
 Asp Gly Gln Leu Lys Gln Gly Thr Leu Val Ala Ile Asn Ala Glu Lys
 35 40 45

atg ctg act att gaa gat aac gcc gag gtc agg gag tta att aac gct 192
 Met Leu Thr Ile Glu Asp Asn Ala Glu Val Arg Glu Leu Ile Asn Ala
 50 55 60

gcc gaa ttt aaa tat gcg gat ggc atc agc gtt gta cgt tca gta cgt 240
 Ala Glu Phe Lys Tyr Ala Asp Gly Ile Ser Val Val Arg Ser Val Arg
 65 70 75 80

aaa aag tac ccg cag gcg cag gtt tcc cgc gtt gcc ggt gcc gat ctc 288
 Lys Lys Tyr Pro Gln Ala Gln Val Ser Arg Val Ala Gly Ala Asp Leu
 85 90 95

tgg gaa gag ctg atg gcg cgc gca ggc aaa gaa ggg acg ccg gta ttt 336
 Trp Glu Glu Leu Met Ala Arg Ala Gly Lys Glu Gly Thr Pro Val Phe
 100 105 110

ctt gtg ggc ggt aaa cct gaa gtg ctg gcg caa act gaa gct aaa ctg 384
 Leu Val Gly Gly Lys Pro Glu Val Leu Ala Gln Thr Glu Ala Lys Leu
 115 120 125

cgc aac cag tgg aat gtg aat atc gtt ggc agt cag gat ggt tat ttt 432
 Arg Asn Gln Trp Asn Val Asn Ile Val Gly Ser Gln Asp Gly Tyr Phe
 130 135 140

aaa ccc gag cag cgt cag gcg ctg ttt gaa cgc att cat gcc agc ggt 480
 Lys Pro Glu Gln Arg Gln Ala Leu Phe Glu Arg Ile His Ala Ser Gly

<210> 195
 <211> 615
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(615)

<400> 195
 gtg cgg ggc gaa ctg ctg ttc ttc ccg acg cgg atg gac cct tcg ctc 48
 Met Arg Gly Glu Leu Leu Phe Phe Pro Thr Arg Met Asp Pro Ser Leu
 1 5 10 15
 aat acg atg gcg aac gat cgg caa cgt gaa ggg aaa atg acc att ctg 96
 Asn Thr Met Ala Asn Asp Arg Gln Arg Glu Gly Lys Met Thr Ile Leu
 20 25 30
 gtg ggg aac tcc ggc gac cgc agc aat gag cat att gct gcc ttg cgc 144
 Val Gly Asn Ser Gly Asp Arg Ser Asn Glu His Ile Ala Ala Leu Arg
 35 40 45
 gcc gtt cat cag caa ttt ggc gat acg gta aaa gtg gtg gtg ccg atg 192
 Ala Val His Gln Gln Phe Gly Asp Thr Val Lys Val Val Val Pro Met
 50 55 60
 gga tat ccg cct aat aac gaa gcg tac att gag gaa gtt cgt cag gcg 240
 Gly Tyr Pro Pro Asn Asn Glu Ala Tyr Ile Glu Glu Val Arg Gln Ala
 65 70 75 80
 ggg ctg gag tta ttc agc gaa gaa aat cta caa att ctg agc gaa aaa 288
 Gly Leu Glu Leu Phe Ser Glu Glu Asn Leu Gln Ile Leu Ser Glu Lys
 85 90 95
 ctg gaa ttt gac gcc tat ctg gcg cta ctt cgt cag tgc gat ctt ggt 336
 Leu Glu Phe Asp Ala Tyr Leu Ala Leu Leu Arg Gln Cys Asp Leu Gly
 100 105 110
 tac ttt att ttt gcc cgc cag cag ggc att ggt acg ctg tgc tta ctg 384
 Tyr Phe Ile Phe Ala Arg Gln Gln Gly Ile Gly Thr Leu Cys Leu Leu
 115 120 125
 att cag gcg ggc att cct tgt gtg ctt aac cgg gaa aat ccg ttc tgg 432
 Ile Gln Ala Gly Ile Pro Cys Val Leu Asn Arg Glu Asn Pro Phe Trp
 130 135 140
 cag gat atg acg gaa caa cat ttg ccg gtg ctg ttt act acc gac gat 480
 Gln Asp Met Thr Glu Gln His Leu Pro Val Leu Phe Thr Thr Asp Asp
 145 150 155 160
 ctc aac gag gat att gtg cgt gaa gcg cag cgc cag ttg gcg tcg gtg 528
 Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
 165 170 175
 gat aaa aac acc att gcc ttc ttt agc cct aac tat cta caa ggc tgg 576
 Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp

180

185

190

cag cgg gcg ttg gcg att gcc gcc agg gag gtc gca tga 615
 Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala *
 195 200

<210> 196

<211> 549

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(549)

<400> 196

atg att cgg caa cgt cgt cgt gcg tta acg ccg gaa caa cag cag gaa 48
 Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Gln Glu
 1 5 10 15

atg ggt caa caa gcc gct acc cgg atg atg act tat ccc ccg gtg gtg 96
 Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
 20 25 30

atg gca cat acg gtc gct gta ttc ctc tct ttt gat ggc gaa ctc gac 144
 Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
 35 40 45

acc cag cca ctc ata gaa caa ctc tgg cgc gcc ggt aag cgc gta tat 192
 Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
 50 55 60

ctt cca gtt ttg cat ccc ttt agt gcc ggt aat ttg ctg ttc ctg aat 240
 Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
 65 70 75 80

tac cat ccg caa agc gaa ctg gtg atg aac agg ttg aag atc cat gag 288
 Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
 85 90 95

cca aaa ttg gat gtg cgt gac gtg cta ccc ctt tcc cga tta gac gtg 336
 Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
 100 105 110

ctg atc aca ccg ctg gtc gcc ttt gat gag tac ggt cag cgc ctg gga 384
 Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
 115 120 125

atg ggc ggt ggt ttt tat gat cgg acc tta caa aac tgg cag cac tat 432
 Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
 130 135 140

aaa acg caa ccg gtg ggt tat gcg cat gat tgt cag ttg gtg gaa aaa 480
 Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
 145 150 155 160

ctc ccc gtt gaa gag tgg gat atc cct ctt cct gcg gtg gtt aca ccg 528
 Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
 165 170 175

tcg aaa gtc tgg gag tgg taa 549
 Ser Lys Val Trp Glu Trp *
 180

<210> 197
 <211> 276
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(276)

<400> 197
 atg gca cgc gta act gtt cag gac gct gta gag aaa att ggt aac cgt 48
 Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
 1 5 10 15
 ttt gac ctg gta ctg gtc gcc gcg cgt cgc gct cgt cag atg cag gta 96
 Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
 20 25 30
 ggc gga aag gat ccg ctg gta ccg gaa gaa aac gat aaa acc act gta 144
 Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
 35 40 45
 atc gcg ctg cgc gaa atc gaa gaa ggt ctg atc aac aac cag atc ctc 192
 Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
 50 55 60
 gac gtt cgc gaa cgc cag gaa cag caa gag cag gaa gcc gct gaa tta 240
 Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Gln Glu Ala Ala Glu Leu
 65 70 75 80
 caa gcc gtt acc gct att gct gaa ggt cgt cgt taa 276
 Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg *
 85 90

<210> 198
 <211> 2109
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2109)

<400> 198
 ttg tat ctg ttt gaa agc ctg aat caa ctg att caa acc tac ctg ccg 48
 Met Tyr Leu Phe Glu Ser Leu Asn Gln Leu Ile Gln Thr Tyr Leu Pro
 1 5 10 15

gaa gac caa atc aag cgt ctg cgg cag gcg tat ctc gtt gca cgt gat	96
Glu Asp Gln Ile Lys Arg Leu Arg Gln Ala Tyr Leu Val Ala Arg Asp	
20 25 30	
gct cac gag ggg caa aca cgt tca agc ggt gaa ccc tat atc acg cac	144
Ala His Glu Gly Gln Thr Arg Ser Ser Gly Glu Pro Tyr Ile Thr His	
35 40 45	
ccg gta gcg gtt gcc tgc att ctg gcc gag atg aaa ctc gac tat gaa	192
Pro Val Ala Val Ala Cys Ile Leu Ala Glu Met Lys Leu Asp Tyr Glu	
50 55 60	
acg ctg atg gcg gcg ctg ctg cat gac gtg att gaa gat act ccc gcc	240
Thr Leu Met Ala Ala Leu Leu His Asp Val Ile Glu Asp Thr Pro Ala	
65 70 75 80	
acc tac cag gat atg gaa cag ctt ttt ggt aaa agc gtc gcc gag ctg	288
Thr Tyr Gln Asp Met Glu Gln Leu Phe Gly Lys Ser Val Ala Glu Leu	
85 90 95	
gta gag ggg gtg tgc aaa ctt gat aaa ctc aag ttc cgc gat aag aaa	336
Val Glu Gly Val Ser Lys Leu Asp Lys Leu Lys Phe Arg Asp Lys Lys	
100 105 110	
gag gcg cag gcc gaa aac ttt cgc aag atg att atg gcg atg gtg cag	384
Glu Ala Gln Ala Glu Asn Phe Arg Lys Met Ile Met Ala Met Val Gln	
115 120 125	
gat atc cgc gtc atc ctc atc aaa ctt gcc gac cgt acc cac aac atg	432
Asp Ile Arg Val Ile Leu Ile Lys Leu Ala Asp Arg Thr His Asn Met	
130 135 140	
cgc acg ctg ggc tca ctt cgc ccg gac aaa cgt cgc cgc atc gcc cgt	480
Arg Thr Leu Gly Ser Leu Arg Pro Asp Lys Arg Arg Arg Ile Ala Arg	
145 150 155 160	
gaa act ctc gaa att tat agc ccg ctg gcg cac cgt tta ggt atc cac	528
Glu Thr Leu Glu Ile Tyr Ser Pro Leu Ala His Arg Leu Gly Ile His	
165 170 175	
cac att aaa acc gaa ctc gaa gag ctg ggt ttt gag gcg ctg tat ccc	576
His Ile Lys Thr Glu Leu Glu Glu Leu Gly Phe Glu Ala Leu Tyr Pro	
180 185 190	
aac cgt tat cgc gta atc aaa gaa gtg gtg aaa gcc gcg cgc ggc aac	624
Asn Arg Tyr Arg Val Ile Lys Glu Val Val Lys Ala Ala Arg Gly Asn	
195 200 205	
cgt aaa gag atg atc cag aag att ctt tct gaa atc gaa ggg cgt ttg	672
Arg Lys Glu Met Ile Gln Lys Ile Leu Ser Glu Ile Glu Gly Arg Leu	
210 215 220	
cag gaa gcg gga ata ccg tgc cgc gtc agt ggt cgc gag aag cat ctt	720
Gln Glu Ala Gly Ile Pro Cys Arg Val Ser Gly Arg Glu Lys His Leu	
225 230 235 240	

Lys Ala Arg Ala Lys Ile Arg Gln Leu Leu Lys Asn Leu Lys Arg Asp
465 470 475 480

690

695

700

<210> 199
 <211> 690
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(690)

<400> 199
 atg aac cca aca cgt tat gca cgc atc tgc gaa atg ctc gcc agg cgg 48
 Met Asn Pro Thr Arg Tyr Ala Arg Ile Cys Glu Met Leu Ala Arg Arg
 1 5 10 15
 cag cct gat ctg acc gtc tgc atg gag cag gtc cac aaa cct cat aac 96
 Gln Pro Asp Leu Thr Val Cys Met Glu Gln Val His Lys Pro His Asn
 20 25 30
 gtt tct gcg att att cgt acc gca gat gcc gtt ggc gta cat gaa gtt 144
 Val Ser Ala Ile Ile Arg Thr Ala Asp Ala Val Gly Val His Glu Val
 35 40 45
 cac gcc gtc tgg cct ggt agc cgc atg cgc acc atg gct tcg gca gcg 192
 His Ala Val Trp Pro Gly Ser Arg Met Arg Thr Met Ala Ser Ala Ala
 50 55 60
 gcg ggt agt aac agc tgg gta cag gtg aaa aca cac cgc acc att ggc 240
 Ala Gly Ser Asn Ser Trp Val Gln Val Lys Thr His Arg Thr Ile Gly
 65 70 75 80
 gat gcc gtc gct cat ctc aaa ggc cag ggc atg cag att ctg gca acc 288
 Asp Ala Val Ala His Leu Lys Gly Gln Gly Met Gln Ile Leu Ala Thr
 85 90 95
 cat ctt tct gat aac gct gtc gat ttc cgc gaa att gat tac act cgc 336
 His Leu Ser Asp Asn Ala Val Asp Phe Arg Glu Ile Asp Tyr Thr Arg
 100 105 110
 ccg acc tgc att ttg atg gga cag gag aaa acg ggc atc acg cag gaa 384
 Pro Thr Cys Ile Leu Met Gly Gln Glu Lys Thr Gly Ile Thr Gln Glu
 115 120 125
 gca ttg gcc ctg gcg gat cag gac atc atc att ccg atg atc ggc atg 432
 Ala Leu Ala Leu Ala Asp Gln Asp Ile Ile Ile Pro Met Ile Gly Met
 130 135 140
 gtg cag tcg ctg aat gtt tcc gtt gcc tca gcc ctc att ctt tac gaa 480
 Val Gln Ser Leu Asn Val Ser Val Ala Ser Ala Leu Ile Leu Tyr Glu
 145 150 155 160
 gcc cag cgt cag cgg caa aat gca ggc atg tac ctg cgt gaa aac agc 528
 Ala Gln Arg Gln Arg Gln Asn Ala Gly Met Tyr Leu Arg Glu Asn Ser
 165 170 175

atg ttg ccg gaa gca gag caa caa cgc ctg ttg ttt gaa ggc ggc tat	576
Met Leu Pro Glu Ala Glu Gln Gln Arg Leu Leu Phe Glu Gly Gly Tyr	
180 185 190	
ccg gtg ctg gcg aaa gtc gca aaa cgc aaa ggc ctg cct tat ccc cac	624
Pro Val Leu Ala Lys Val Ala Lys Arg Lys Gly Leu Pro Tyr Pro His	
195 200 205	
gtc aat cag caa ggc gag atc gaa gct gat gcc gac tgg tgg gct act	672
Val Asn Gln Gln Gly Glu Ile Glu Ala Asp Ala Asp Trp Trp Ala Thr	
210 215 220	
atg cag gct gca ggg taa	690
Met Gln Ala Ala Gly *	
225	

<210> 200
 <211> 2082
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2082)

<400> 200	
atg aaa ggt cgc ctg tta gat gct gtc cca ctc agt tcc cta acg ggc	48
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly	
1 5 10 15	
gtt ggc gca gca ctt agt aac aaa ctg gcg aaa atc aac ctg cat acc	96
Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr	
20 25 30	
gtg cag gat cta ctc tta cac ctt ccc ctg cgc tac gaa gat cgc acc	144
Val Gln Asp Leu Leu Leu His Leu Pro Leu Arg Tyr Glu Asp Arg Thr	
35 40 45	
cat ctc tac ccc atc gga gaa cta ctg ccg ggc gtt tat gcc acg gtg	192
His Leu Tyr Pro Ile Gly Glu Leu Leu Pro Gly Val Tyr Ala Thr Val	
50 55 60	
gaa ggc gaa gtg ctg aac tgc aat atc tcc ttc ggc ggt cgg cgg atg	240
Glu Gly Glu Val Leu Asn Cys Asn Ile Ser Phe Gly Gly Arg Arg Met	
65 70 75 80	
atg acc tgc cag atc agc gac ggt tcc ggc atc ctc acc atg cgc ttt	288
Met Thr Cys Gln Ile Ser Asp Gly Ser Gly Ile Leu Thr Met Arg Phe	
85 90 95	
ttc aat ttc agc gcg gca atg aaa aat agc ctg gcg gcg ggc cgc cgt	336
Phe Asn Phe Ser Ala Ala Met Lys Asn Ser Leu Ala Ala Gly Arg Arg	
100 105 110	
gta ctg gct tat ggc gaa gca aag cgc ggt aaa tat ggt gcg gag atg	384

340				345				350								
ggt	aag	cag	aaa	ggt	aaa	gca	cgg	ctg	gca	cag	cag	gaa	gcc	atc	gcc	1104
Gly	Lys	Gln	Lys	Gly	Lys	Ala	Arg	Leu	Ala	Gln	Gln	Glu	Ala	Ile	Ala	
355				360				365								
agc	ggt	cag	gtg	cag	atg	att	gtc	ggt	aca	cac	gcc	atc	ttc	cag	gaa	1152
Ser	Gly	Gln	Val	Gln	Met	Ile	Val	Gly	Thr	His	Ala	Ile	Phe	Gln	Glu	
370				375				380								
cag	gtg	cag	ttt	aac	ggc	ctg	gcg	ctg	gtg	att	atc	gac	gaa	cag	cat	1200
Gln	Val	Gln	Phe	Asn	Gly	Leu	Ala	Leu	Val	Ile	Ile	Asp	Glu	Gln	His	
385				390				395				400				
cgt	ttt	ggc	gtg	cat	cag	cgt	ctg	gca	ttg	tgg	gag	aaa	ggc	cag	cag	1248
Arg	Phe	Gly	Val	His	Gln	Arg	Leu	Ala	Leu	Trp	Glu	Lys	Gly	Gln	Gln	
405				410				415								
cag	ggc	ttc	cat	ccg	cat	cag	ttg	atc	atg	acc	gcc	acg	ccg	atc	ccc	1296
Gln	Gly	Phe	His	Pro	His	Gln	Leu	Ile	Met	Thr	Ala	Thr	Pro	Ile	Pro	
420				425				430								
cgc	acg	ctg	gca	atg	act	gcg	tat	gcc	gat	ctc	gat	acc	tcg	gtg	ata	1344
Arg	Thr	Leu	Ala	Met	Thr	Ala	Tyr	Ala	Asp	Leu	Asp	Thr	Ser	Val	Ile	
435				440				445								
gat	gag	ctg	ccg	cca	ggc	cgc	acg	cca	gtg	act	acg	gtc	gct	att	cct	1392
Asp	Glu	Leu	Pro	Pro	Gly	Arg	Thr	Pro	Val	Thr	Thr	Val	Ala	Ile	Pro	
450				455				460								
gat	acc	cgc	cgt	acc	gac	atc	att	gac	cgc	gtg	cac	cac	gcc	tgc	ata	1440
Asp	Thr	Arg	Arg	Thr	Asp	Ile	Ile	Asp	Arg	Val	His	His	Ala	Cys	Ile	
465				470				475				480				
act	gaa	ggt	cgt	cag	gca	tac	tgg	gtt	tgt	acg	ttg	att	gaa	gag	tcg	1488
Thr	Glu	Gly	Arg	Gln	Ala	Tyr	Trp	Val	Cys	Thr	Leu	Ile	Glu	Glu	Ser	
485				490				495								
gaa	ttg	ctg	gaa	gcg	cag	gcg	gcg	gaa	gct	acc	tgg	gaa	gag	ttg	aaa	1536
Glu	Leu	Leu	Glu	Ala	Gln	Ala	Ala	Glu	Ala	Thr	Trp	Glu	Glu	Leu	Lys	
500				505				510								
ctg	gcg	cta	cca	gag	ttg	aac	gtt	ggc	ctg	gta	cac	ggg	cgg	atg	aaa	1584
Leu	Ala	Leu	Pro	Glu	Leu	Asn	Val	Gly	Leu	Val	His	Gly	Arg	Met	Lys	
515				520				525								
cct	gcc	gag	aaa	cag	gcg	gtg	atg	gcg	tcg	ttt	aaa	caa	ggt	gag	cta	1632
Pro	Ala	Glu	Lys	Gln	Ala	Val	Met	Ala	Ser	Phe	Lys	Gln	Gly	Glu	Leu	
530				535				540								
cac	ctg	ctg	gtt	gcc	aca	acc	gtt	att	gaa	gtc	ggc	gtt	gat	gtg	cct	1680
His	Leu	Leu	Val	Ala	Thr	Thr	Val	Ile	Glu	Val	Gly	Val	Asp	Val	Pro	
545				550				555				560				
aac	gcc	agt	ctg	atg	att	atc	gaa	aac	ccg	gag	cgt	ctg	ggg	ctg	gcg	1728
Asn	Ala	Ser	Leu	Met	Ile	Ile	Glu	Asn	Pro	Glu	Arg	Leu	Gly	Leu	Ala	
565				570				575								

cag tta cac cag ctg cgc ggg cgc gta ggt cgt ggc gcg gtg gct tct 1776
Gln Leu His Gln Leu Arg Gly Arg Val Gly Arg Gly Ala Val Ala Ser
580 585 590

cac tgc gtg ctg ctc tac aaa acg ccg ctt tct aaa acg gcg caa att 1824
His Cys Val Leu Leu Tyr Lys Thr Pro Leu Ser Lys Thr Ala Gln Ile
595 600 605

cgc ctg caa gtg ctg cgc gac agt aac gac ggt ttt gtg att gcg caa 1872
Arg Leu Gln Val Leu Arg Asp Ser Asn Asp Gly Phe Val Ile Ala Gln
610 615 620

aaa gat ctg gag att cgc ggc cct ggc gaa ttg tta ggc acg cgt cag 1920
Lys Asp Leu Glu Ile Arg Gly Pro Gly Glu Leu Leu Gly Thr Arg Gln
625 630 635 640

acg ggt aat gct gaa ttt aaa gtg gcg gat tta ctg cgc gat cag gcg 1968
Thr Gly Asn Ala Glu Phe Lys Val Ala Asp Leu Leu Arg Asp Gln Ala
645 650 655

atg atc ccg gaa gtt cag cgc ctg gca cgc cat att cac gaa cgt tac 2016
Met Ile Pro Glu Val Gln Arg Leu Ala Arg His Ile His Glu Arg Tyr
660 665 670

cca caa cag gca aaa gcc ctg ata gaa cgc tgg atg ccg gag acg gaa 2064
Pro Gln Gln Ala Lys Ala Leu Ile Glu Arg Trp Met Pro Glu Thr Glu
675 680 685

cgt tac tcg aat gcg taa 2082
Arg Tyr Ser Asn Ala *
690

<210> 201
<211> 1287
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1287)

<400> 201
atg aaa acc tct ctg ttt aaa agc ctt tac ttt cag gtc ctg aca gcg 48
Met Lys Thr Ser Leu Phe Lys Ser Leu Tyr Phe Gln Val Leu Thr Ala
1 5 10 15

ata gcc att ggt att ctc ctt ggc cat ttc tat cct gaa ata ggc gag 96
Ile Ala Ile Gly Ile Leu Leu Gly His Phe Tyr Pro Glu Ile Gly Glu
20 25 30

caa atg aaa ccg ctt ggc gac ggc ttc gtt aag ctc att aag atg atc 144
Gln Met Lys Pro Leu Gly Asp Gly Phe Val Lys Leu Ile Lys Met Ile
35 40 45

atc gct cct gtc atc ttt tgt acc gtc gta acg ggc att gcg ggc atg 192

275	280	285	
gtg gtg ggg ctg gtc atc ccg aca ggc tac tcg ttt aac ctt gat ggc			912
Val Val Gly Leu Val Ile Pro Thr Gly Tyr Ser Phe Asn Leu Asp Gly			
290	295	300	
aca tcg ata tac ctg aca atg gcg gcg gtg ttt atc gcc cag gcc act			960
Thr Ser Ile Tyr Leu Thr Met Ala Ala Val Phe Ile Ala Gln Ala Thr			
305	310	315	320
aac agt cag atg gat atc gtc cac caa atc acg ctg tta atc gtg ttg			1008
Asn Ser Gln Met Asp Ile Val His Gln Ile Thr Leu Leu Ile Val Leu			
	325	330	335
ctg ctt tct tct aaa ggg gcg gca ggg gta acg ggt agt ggc ttt atc			1056
Leu Leu Ser Ser Lys Gly Ala Ala Gly Val Thr Gly Ser Gly Phe Ile			
	340	345	350
gtg ctg gcg gcg acg ctc tct gcg gtg ggc cat ttg ccg gta gcg ggt			1104
Val Leu Ala Ala Thr Leu Ser Ala Val Gly His Leu Pro Val Ala Gly			
	355	360	365
ctg gcg ctg atc ctc ggt atc gac cgc ttt atg tca gaa gct cgt gcg			1152
Leu Ala Leu Ile Leu Gly Ile Asp Arg Phe Met Ser Glu Ala Arg Ala			
	370	375	380
ctg act aac ctg gtc ggt aac ggc gta gcg acc att gtc gtt gct aag			1200
Leu Thr Asn Leu Val Gly Asn Gly Val Ala Thr Ile Val Val Ala Lys			
385	390	395	400
tgg gtg aaa gaa ctg gac cac aaa aaa ctg gac gat gtg ctg aat aat			1248
Trp Val Lys Glu Leu Asp His Lys Lys Leu Asp Asp Val Leu Asn Asn			
	405	410	415
cgt gcg ccg gat ggc aaa acg cac gaa tta tcc tct taa			1287
Arg Ala Pro Asp Gly Lys Thr His Glu Leu Ser Ser *			
	420	425	

<210> 202
 <211> 1191
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1191)

<400> 202	
gtg acc acc cga cag cat tcg tcg ttt gct att gtt ttt atc ctt ggc	48
Met Thr Thr Arg Gln His Ser Ser Phe Ala Ile Val Phe Ile Leu Gly	
1	5 10 15
ctg ctg gcc atg ttg atg ccg ctg tcg att gat atg tat ctg ccc gcg	96
Leu Leu Ala Met Leu Met Pro Leu Ser Ile Asp Met Tyr Leu Pro Ala	
	20 25 30

Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
 260 265 270

gtc cgc cgc att ggc ggc tta aat atg ttc cgc tcg ggg ttg tgg ata 864
 Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
 275 280 285

caa ttt att atg gca ggc tgg atg gtc atc agt gcg ctg ctg ggg ctg 912
 Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
 290 295 300

gga ttt tgg tcg ctg gtg gtt ggc gtt gcg gcg ttt gtg ggc tgc gtg 960
 Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
 305 310 315 320

tcg atg gtg tca tcc aat gcg atg gcg gtc att ctt gat gag ttt ccc 1008
 Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro
 325 330 335

cat atg gcg gga acg gca tct tcg ctg gca gga acc ttc cgt ttt ggc 1056
 His Met Ala Gly Thr Ala Ser Ser Leu Ala Gly Thr Phe Arg Phe Gly
 340 345 350

ata ggg gca att gtt ggc gca ttg ctt tct ctt gcg acc ttt aac tct 1104
 Ile Gly Ala Ile Val Gly Ala Leu Leu Ser Leu Ala Thr Phe Asn Ser
 355 360 365

gca tgg ccg atg att tgg tca att gca ttc tgc gca acc agc tcc att 1152
 Ala Trp Pro Met Ile Trp Ser Ile Ala Phe Cys Ala Thr Ser Ser Ile
 370 375 380

ctc ttc tgt ctg tac gcc agt cgg ccg aaa aaa cgg tga 1191
 Leu Phe Cys Leu Tyr Ala Ser Arg Pro Lys Lys Arg *
 385 390 395

<210> 203

<211> 696

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(696)

<400> 203

atg cga ctt gat aaa ttt atc gca cag caa ctc ggc gtt agc cgt gct 48
 Met Arg Leu Asp Lys Phe Ile Ala Gln Gln Leu Gly Val Ser Arg Ala
 1 5 10 15

att gcc ggg cgt gaa atc cgc ggc aat cgt gtc acc gtc gat ggc gaa 96
 Ile Ala Gly Arg Glu Ile Arg Gly Asn Arg Val Thr Val Asp Gly Glu
 20 25 30

atc gtc cgt aat gca ggc ttc aaa ctg ctt cct gaa cat gat gtc gct 144
 Ile Val Arg Asn Ala Ala Phe Lys Leu Leu Pro Glu His Asp Val Ala
 35 40 45

tac gat ggc aac ccg ctg gcg cag caa cac ggt cca cgt tac ttc atg	192
Tyr Asp Gly Asn Pro Leu Ala Gln Gln His Gly Pro Arg Tyr Phe Met	
50 55 60	
ctc aat aag cct cag ggc tat gtt tgc tcc acg gac gac cct gat cac	240
Leu Asn Lys Pro Gln Gly Tyr Val Cys Ser Thr Asp Asp Pro Asp His	
65 70 75 80	
cca acg gtg ctc tat ttt ctt gat gaa ccg gta gcg tgg aaa ctg cat	288
Pro Thr Val Leu Tyr Phe Leu Asp Glu Pro Val Ala Trp Lys Leu His	
85 90 95	
gcg gcg ggg cgg ttg gat att gat acc acc ggt ctg gtg ctg atg act	336
Ala Ala Gly Arg Leu Asp Ile Asp Thr Thr Gly Leu Val Leu Met Thr	
100 105 110	
gat gat ggt cag tgg tgc cac cgc att act tct ccg cgc cat cat tgc	384
Asp Asp Gly Gln Trp Ser His Arg Ile Thr Ser Pro Arg His His Cys	
115 120 125	
gag aag acc tat ctg gtg aca ctg gaa tca cct gta gct gac gat acg	432
Glu Lys Thr Tyr Leu Val Thr Leu Glu Ser Pro Val Ala Asp Asp Thr	
130 135 140	
gca gag caa ttt gct aaa ggc gtg cag ctg cat aac gaa aaa gat ctc	480
Ala Glu Gln Phe Ala Lys Gly Val Gln Leu His Asn Glu Lys Asp Leu	
145 150 155 160	
act aag cct gcg gtg ctg gaa gtg att acc cca acg cag gtt cgt ctg	528
Thr Lys Pro Ala Val Leu Glu Val Ile Thr Pro Thr Gln Val Arg Leu	
165 170 175	
acc atc agc gaa ggg cgt tat cat cag gtg aaa cgc atg ttc gcc gcc	576
Thr Ile Ser Glu Gly Arg Tyr His Gln Val Lys Arg Met Phe Ala Ala	
180 185 190	
gtg ggt aac cac gtg gtt gag ctg cat cgt gaa cgt att ggc ggt att	624
Val Gly Asn His Val Val Glu Leu His Arg Glu Arg Ile Gly Gly Ile	
195 200 205	
acg ctg gat gct gat tta gcc ccc ggt gaa tat cgt ccg tta act gaa	672
Thr Leu Asp Ala Asp Leu Ala Pro Gly Glu Tyr Arg Pro Leu Thr Glu	
210 215 220	
gaa gaa att gcc agc gtc gtc taa	696
Glu Glu Ile Ala Ser Val Val *	
225 230	

<210> 204

<211> 1329

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1329)

<400> 204

atg	aaa	aaa	att	gaa	tgc	gct	tgc	aat	ttt	ctg	atg	gat	aaa	gat	gcg	48
Met	Lys	Lys	Ile	Glu	Cys	Ala	Cys	Asn	Phe	Leu	Met	Asp	Lys	Asp	Ala	
1				5					10						15	
cag	ggg	tat	atc	gac	ctg	tct	gat	ttg	gat	tta	aca	agt	tgt	cat	ttt	96
Gln	Gly	Tyr	Ile	Asp	Leu	Ser	Asp	Leu	Asp	Leu	Thr	Ser	Cys	His	Phe	
			20					25						30		
aaa	ggg	gac	gtt	ata	tcg	aag	gtg	tct	ttt	tta	tca	tca	aat	cta	caa	144
Lys	Gly	Asp	Val	Ile	Ser	Lys	Val	Ser	Phe	Leu	Ser	Ser	Asn	Leu	Gln	
		35					40						45			
cat	gta	aca	ttc	gaa	tgt	aaa	gaa	att	ggg	gat	tgc	aat	ttt	act	act	192
His	Val	Thr	Phe	Glu	Cys	Lys	Glu	Ile	Gly	Asp	Cys	Asn	Phe	Thr	Thr	
	50					55						60				
gca	ata	gtt	gat	aat	gtc	ata	ttt	aga	tgt	cga	cgt	tta	cac	aat	gtg	240
Ala	Ile	Val	Asp	Asn	Val	Ile	Phe	Arg	Cys	Arg	Arg	Leu	His	Asn	Val	
65					70					75					80	
att	ttt	atc	aaa	gcg	agt	ggg	gaa	tgt	gtc	gat	ttc	agc	aaa	aat	att	288
Ile	Phe	Ile	Lys	Ala	Ser	Gly	Glu	Cys	Val	Asp	Phe	Ser	Lys	Asn	Ile	
			85						90					95		
ctt	gat	aca	gtt	gac	ttc	tcg	cag	agt	caa	ctt	ggg	cat	agt	aat	ttt	336
Leu	Asp	Thr	Val	Asp	Phe	Ser	Gln	Ser	Gln	Leu	Gly	His	Ser	Asn	Phe	
			100					105					110			
cgc	gaa	tgt	cag	att	aga	aat	tca	aac	ttc	gat	aat	tgt	tat	ctt	tac	384
Arg	Glu	Cys	Gln	Ile	Arg	Asn	Ser	Asn	Phe	Asp	Asn	Cys	Tyr	Leu	Tyr	
		115					120					125				
gct	tcg	cac	ttc	acc	aga	gca	gag	ttt	ctg	tct	gcc	aaa	gaa	ata	tca	432
Ala	Ser	His	Phe	Thr	Arg	Ala	Glu	Phe	Leu	Ser	Ala	Lys	Glu	Ile	Ser	
	130					135					140					
ttt	att	aaa	tcg	aat	ttg	aca	gct	gtt	atg	ttt	gat	tat	gtg	cga	atg	480
Phe	Ile	Lys	Ser	Asn	Leu	Thr	Ala	Val	Met	Phe	Asp	Tyr	Val	Arg	Met	
145					150					155					160	
tcg	aca	ggg	aat	ttt	aaa	gat	tgc	att	aca	gaa	caa	ttg	gaa	tta	act	528
Ser	Thr	Gly	Asn	Phe	Lys	Asp	Cys	Ile	Thr	Glu	Gln	Leu	Glu	Leu	Thr	
			165						170					175		
att	gat	tat	tca	gat	ata	ttt	tgg	aat	gaa	gat	ctc	gat	ggg	tat	atc	576
Ile	Asp	Tyr	Ser	Asp	Ile	Phe	Trp	Asn	Glu	Asp	Leu	Asp	Gly	Tyr	Ile	
			180					185						190		
aat	aac	att	ata	aaa	atg	att	gat	aca	ttg	cca	gat	aat	gca	atg	ata	624
Asn	Asn	Ile	Ile	Lys	Met	Ile	Asp	Thr	Leu	Pro	Asp	Asn	Ala	Met	Ile	
		195					200					205				
ttg	aaa	tcc	gtt	ctg	gcc	gta	aaa	ctg	gtg	atg	caa	tta	aaa	ata	ctt	672
Leu	Lys	Ser	Val	Leu	Ala	Val	Lys	Leu	Val	Met	Gln	Leu	Lys	Ile	Leu	

210	215	220	
aat att gtt aat aaa aac ttt att gag aat atg aag aaa ata ttt agc			720
Asn Ile Val Asn Lys Asn Phe Ile Glu Asn Met Lys Lys Ile Phe Ser			
225	230	235	240
cat tgt cct tat ata aaa gat ccc att ata cgc agt tat atc cat tct			768
His Cys Pro Tyr Ile Lys Asp Pro Ile Ile Arg Ser Tyr Ile His Ser			
	245	250	255
gat gaa gat aac aag ttc gat gat ttt atg cgt caa cat cga ttc agt			816
Asp Glu Asp Asn Lys Phe Asp Asp Phe Met Arg Gln His Arg Phe Ser			
	260	265	270
gag gtg aat ttc gat acc caa cag atg atc gat ttt att aac aga ttt			864
Glu Val Asn Phe Asp Thr Gln Gln Met Ile Asp Phe Ile Asn Arg Phe			
	275	280	285
aat acg aat aaa tgg cta att gat aaa aat aac aat ttt ttt atc caa			912
Asn Thr Asn Lys Trp Leu Ile Asp Lys Asn Asn Asn Phe Phe Ile Gln			
	290	295	300
ctt atc gat cag gcc tta cga tca acg gat gat atg atc aaa gca aat			960
Leu Ile Asp Gln Ala Leu Arg Ser Thr Asp Asp Met Ile Lys Ala Asn			
	305	310	315
gtt tgg cat ctt tat aaa gag tgg att cgt agt gat gat gtt tca cct			1008
Val Trp His Leu Tyr Lys Glu Trp Ile Arg Ser Asp Asp Val Ser Pro			
	325	330	335
ata ttt ata gaa act gaa gat aat tta aga acc ttt aac acg aat gaa			1056
Ile Phe Ile Glu Thr Glu Asp Asn Leu Arg Thr Phe Asn Thr Asn Glu			
	340	345	350
tta aca cga aac gat aat atc ttt atc ctg ttc tcc tca gtc gat gat			1104
Leu Thr Arg Asn Asp Asn Ile Phe Ile Leu Phe Ser Ser Val Asp Asp			
	355	360	365
ggg cca gtt atg gtg gta agc tcc cag cgc tta cat gat atg ttg aat			1152
Gly Pro Val Met Val Val Ser Ser Gln Arg Leu His Asp Met Leu Asn			
	370	375	380
cct aca aaa gat acc aat tgg aat tcc acg tat atc tac aaa tcc aga			1200
Pro Thr Lys Asp Thr Asn Trp Asn Ser Thr Tyr Ile Tyr Lys Ser Arg			
	385	390	395
cat gag atg ttg cct gtt aat ctt act cag gaa aca ctt ttc agc tcc			1248
His Glu Met Leu Pro Val Asn Leu Thr Gln Glu Thr Leu Phe Ser Ser			
	405	410	415
aaa tct cat ggt aaa tat gcg ctt ttc ccc att ttt act gcg agt tgg			1296
Lys Ser His Gly Lys Tyr Ala Leu Phe Pro Ile Phe Thr Ala Ser Trp			
	420	425	430
cga gct cat cgt ata atg aat aag ggt gtt taa			1329
Arg Ala His Arg Ile Met Asn Lys Gly Val *			
	435	440	

<210> 205
 <211> 717
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(717)

<400> 205
 gtg gga cgt aaa tgg gcc aat att gtt gct aaa aaa acg gct aaa gac 48
 Met Gly Arg Lys Trp Ala Asn Ile Val Ala Lys Lys Thr Ala Lys Asp
 1 5 10 15
 ggt gca acg tct aaa att tat gca aaa ttc ggt gta gaa atc tat gct 96
 Gly Ala Thr Ser Lys Ile Tyr Ala Lys Phe Gly Val Glu Ile Tyr Ala
 20 25 30
 gct gct aaa caa ggt gaa ccc gat cca gaa tta aac aca tct tta aaa 144
 Ala Ala Lys Gln Gly Glu Pro Asp Pro Glu Leu Asn Thr Ser Leu Lys
 35 40 45
 ttc gtt att gaa cgt gca aag cag gca caa gtt cca aag cac gtt att 192
 Phe Val Ile Glu Arg Ala Lys Gln Ala Gln Val Pro Lys His Val Ile
 50 55 60
 gat aaa gca att gat aaa gcc aaa ggc ggc gga gat gaa acg ttc gtg 240
 Asp Lys Ala Ile Asp Lys Ala Lys Gly Gly Gly Asp Glu Thr Phe Val
 65 70 75 80
 cag gga cgt tat gaa ggc ttt ggt cct aat ggc tca atg att atc gcc 288
 Gln Gly Arg Tyr Glu Gly Phe Gly Pro Asn Gly Ser Met Ile Ile Ala
 85 90 95
 gag aca ttg act tca aat gtt aac cgt acg att gct aac gtt cgc aca 336
 Glu Thr Leu Thr Ser Asn Val Asn Arg Thr Ile Ala Asn Val Arg Thr
 100 105 110
 att ttc aat aaa aaa ggc ggc aat atc gga gcg gca ggt tct gtc agc 384
 Ile Phe Asn Lys Lys Gly Gly Asn Ile Gly Ala Ala Gly Ser Val Ser
 115 120 125
 tat atg ttt gac aat acg ggt gtg att gta ttt aaa ggg aca gac cct 432
 Tyr Met Phe Asp Asn Thr Gly Val Ile Val Phe Lys Gly Thr Asp Pro
 130 135 140
 gac cat att ttt gaa att tta ctt gaa gct gaa gtt gat gtt cgt gat 480
 Asp His Ile Phe Glu Ile Leu Leu Glu Ala Glu Val Asp Val Arg Asp
 145 150 155 160
 gtg act gaa gaa gaa ggt aac att gtt att tat act gaa cct act gac 528
 Val Thr Glu Glu Glu Gly Asn Ile Val Ile Tyr Thr Glu Pro Thr Asp
 165 170 175
 ctt cat aaa gga atc gcg gct cta aaa gca gct gga atc act gag ttc 576

Leu	His	Lys	Gly	Ile	Ala	Ala	Leu	Lys	Ala	Ala	Gly	Ile	Thr	Glu	Phe	
			180					185					190			
tca	aca	aca	gaa	tta	gaa	atg	att	gct	caa	tct	gaa	gtt	gag	ctt	tcc	624
Ser	Thr	Thr	Glu	Leu	Glu	Met	Ile	Ala	Gln	Ser	Glu	Val	Glu	Leu	Ser	
		195					200				205					
cca	gaa	gat	tta	gaa	atc	ttt	gaa	ggg	ctt	gtt	gat	gcc	ctt	gaa	gat	672
Pro	Glu	Asp	Leu	Glu	Ile	Phe	Glu	Gly	Leu	Val	Asp	Ala	Leu	Glu	Asp	
	210					215					220					
gac	gac	gat	gta	caa	aaa	gtt	tat	cat	aac	gtc	gca	aat	ctc	taa		717
Asp	Asp	Asp	Val	Gln	Lys	Val	Tyr	His	Asn	Val	Ala	Asn	Leu	*		
225					230					235						

<210> 206
 <211> 786
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(786)

<400> 206																
gtg	gtt	ctt	atg	tcc	gaa	aca	aaa	aac	gaa	ctt	gaa	gac	ctg	ctg	gaa	48
Met	Val	Leu	Met	Ser	Glu	Thr	Lys	Asn	Glu	Leu	Glu	Asp	Leu	Leu	Glu	
1				5				10					15			
aaa	gca	gca	act	gaa	ccg	gcg	cac	cgc	ccg	gcc	ttt	ttc	cgt	act	cta	96
Lys	Ala	Ala	Thr	Glu	Pro	Ala	His	Arg	Pro	Ala	Phe	Phe	Arg	Thr	Leu	
			20					25					30			
ctg	gaa	tcc	acc	gtc	tgg	gtg	cct	ggc	acg	gcg	gcg	cag	ggc	gag	gct	144
Leu	Glu	Ser	Thr	Val	Trp	Val	Pro	Gly	Thr	Ala	Ala	Gln	Gly	Glu	Ala	
		35					40					45				
gtg	gtt	gaa	gat	agc	gcg	ctt	gat	tta	cag	cac	tgg	gaa	aaa	gaa	gac	192
Val	Val	Glu	Asp	Ser	Ala	Leu	Asp	Leu	Gln	His	Trp	Glu	Lys	Glu	Asp	
	50					55					60					
ggc	acc	agc	gtc	att	cct	ttt	ttc	acc	tcg	tta	gaa	gca	ctt	caa	cag	240
Gly	Thr	Ser	Val	Ile	Pro	Phe	Phe	Thr	Ser	Leu	Glu	Ala	Leu	Gln	Gln	
	65				70					75				80		
gcg	gtt	gaa	gac	gaa	cag	gca	ttt	gtc	gta	atg	ccc	gtt	cgc	acg	ctg	288
Ala	Val	Glu	Asp	Glu	Gln	Ala	Phe	Val	Val	Met	Pro	Val	Arg	Thr	Leu	
				85				90						95		
ttt	gag	atg	aca	ctt	ggc	gaa	acg	ctc	ttc	ctt	aat	gcc	aaa	ctg	cca	336
Phe	Glu	Met	Thr	Leu	Gly	Glu	Thr	Leu	Phe	Leu	Asn	Ala	Lys	Leu	Pro	
			100					105					110			
acc	ggt	aaa	gaa	ttt	atg	ccg	cgt	gaa	atc	agt	ttg	ttg	att	ggt	gaa	384
Thr	Gly	Lys	Glu	Phe	Met	Pro	Arg	Glu	Ile	Ser	Leu	Leu	Ile	Gly	Glu	

115	120	125	
gag gga aat ccg ctg agc agc cag gaa atc ctg gaa ggc ggt gaa tcg			432
Glu Gly Asn Pro Leu Ser Ser Gln Glu Ile Leu Glu Gly Gly Glu Ser			
130	135	140	
ctg ata tta tcg gaa gtc gca gag ccg cca gca caa atg att gat tca			480
Leu Ile Leu Ser Glu Val Ala Glu Pro Pro Ala Gln Met Ile Asp Ser			
145	150	155	160
ctc acc acc tta ttt aaa acc att aag ccg gtg aag cgt gct ttt att			528
Leu Thr Thr Leu Phe Lys Thr Ile Lys Pro Val Lys Arg Ala Phe Ile			
165	170	175	
tgt tca att aaa gag aac gaa gag gca cag cct aat tta ctt att ggc			576
Cys Ser Ile Lys Glu Asn Glu Glu Ala Gln Pro Asn Leu Leu Ile Gly			
180	185	190	
att gaa gcc gat ggt gat atc gaa gaa att att cag gcg acg gga agt			624
Ile Glu Ala Asp Gly Asp Ile Glu Glu Ile Ile Gln Ala Thr Gly Ser			
195	200	205	
gta gcg acc gat aca tta cct ggc gat gaa cca atc gat att tgt cag			672
Val Ala Thr Asp Thr Leu Pro Gly Asp Glu Pro Ile Asp Ile Cys Gln			
210	215	220	
gtg aaa aaa ggg gaa aaa gga att agc cac ttt att acc gaa cat att			720
Val Lys Lys Gly Glu Lys Gly Ile Ser His Phe Ile Thr Glu His Ile			
225	230	235	240
gcg cca ttc tat gaa cgt cgc tgg ggt ggt ttt ttg cgt gac ttt aaa			768
Ala Pro Phe Tyr Glu Arg Arg Trp Gly Gly Phe Leu Arg Asp Phe Lys			
245	250	255	
cag aat cgg ata atc taa			786
Gln Asn Arg Ile Ile *			
260			

<210> 207
 <211> 1266
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1266)

<400> 207	
atg ctc acg aaa aag aaa tgg gcg tta ttt agt cta tta aca ctg tgt	48
Met Leu Thr Lys Lys Lys Trp Ala Leu Phe Ser Leu Leu Thr Leu Cys	
1	5 10 15

ggc ggt aca att tat aaa tta ccg tcg ctg aaa gat gcg ttt tat atc	96
Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile	
20	25 30

ccg atg cag gaa tat ttc cat ttg acc aat ggt caa att ggt aat gct	144
Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala	
35 40 45	
atg tcg gta aac tca ttt gtc acc aca gtg ggc ttt ttt ctg tct att	192
Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile	
50 55 60	
tat ttt gcc gat aaa cta ccg cgc aga tac acc atg tca ttc tca ctc	240
Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu	
65 70 75 80	
att gcg aca gga tta ctg ggt gtt tat ttg acg aca atg ccg ggg tat	288
Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr	
85 90 95	
tgg ggc atc ctc ttt gtc tgg gcg cta ttt ggc gtt act tgc gac atg	336
Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met	
100 105 110	
atg aac tgg ccg gtc ttg ctc aag tcg gta agt cga ttg ggc aat agc	384
Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser	
115 120 125	
gaa caa caa ggt cgg ttg ttt ggc ttc ttc gaa aca ggg cgt ggc att	432
Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile	
130 135 140	
gtc gat acc gtg gtg gca ttt tct gcg ttg gca gta ttt acc tgg ttt	480
Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe	
145 150 155 160	
ggc agt ggc tta tta ggt ttt aaa gca ggc atc tgg ttc tat tcc ctt	528
Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu	
165 170 175	
att gtg att gcc gta ggc att att att ttc ttt gtc ctg aat gac aaa	576
Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys	
180 185 190	
gaa gag gca ccg tcc gtt gag gtg aaa aaa gaa gac gga gca tcg aaa	624
Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys	
195 200 205	
aac acc agt atg acc tcg gtg ctg aaa gac aaa act atc tgg ctt atc	672
Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile	
210 215 220	
gct ttt aac gtc ttc ttc gtt tac gcg gtt tac tgt ggc ctg aca ttc	720
Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe	
225 230 235 240	
ttc att cca ttc ctg aaa aac atc tat cta ttg ccc gtt gcg ctg gtg	768
Phe Ile Pro Phe Leu Lys Asn Ile Tyr Leu Leu Pro Val Ala Leu Val	
245 250 255	
ggg gct tac ggc atc att aac caa tac tgt ctg aaa atg att ggt gga	816

agg gaa gaa ccc atc tgg ctg gcc ccc cga caa atg ccg caa ctg gca	768
Arg Glu Glu Pro Ile Trp Leu Ala Pro Arg Gln Met Pro Gln Leu Ala	
245 250 255	
ccg ctg ttt tgc cgc atg atg ctc ggt aaa agc aaa agc gac aaa atc	816
Pro Leu Phe Ser Arg Met Met Leu Gly Lys Ser Lys Ser Asp Lys Ile	
260 265 270	
act act acg ttg gat gcc ggt ctt caa cga cgt ctg gaa gaa ctg gcg	864
Thr Thr Thr Leu Asp Ala Gly Leu Gln Arg Arg Leu Glu Glu Leu Ala	
275 280 285	
caa aac tgg aaa ggg cgg ttg cca ccg cgc agc tca ctg gcg atg atc	912
Gln Asn Trp Lys Gly Arg Leu Pro Pro Arg Ser Ser Leu Ala Met Ile	
290 295 300	
gtg gtt gat cat acc gat atg cgt gtt cgc ggc tgg gtg gga tgc gtt	960
Val Val Asp His Thr Asp Met Arg Val Arg Gly Trp Val Gly Ser Val	
305 310 315 320	
gat ctc aac gat gat tca cgc ttt ggt cat gtt gat atg gtc aat tgc	1008
Asp Leu Asn Asp Asp Ser Arg Phe Gly His Val Asp Met Val Asn Ser	
325 330 335	
atc cga tgc cca gga tca gtg ctc aaa ccg ttt gtt tat ggt ctg gcg	1056
Ile Arg Ser Pro Gly Ser Val Leu Lys Pro Phe Val Tyr Gly Leu Ala	
340 345 350	
ctg gat gaa ggc ttg atc cac ccg gca tca ctg ctg caa gac gtc ccc	1104
Leu Asp Glu Gly Leu Ile His Pro Ala Ser Leu Leu Gln Asp Val Pro	
355 360 365	
cgg cgc acc ggt gat tat cga cca ggt aac ttt gat agc ggt ttt cat	1152
Arg Arg Thr Gly Asp Tyr Arg Pro Gly Asn Phe Asp Ser Gly Phe His	
370 375 380	
ggc ccg atc agc atg agc gag gcg ctg gtg cgc tgc ctg aac tta cct	1200
Gly Pro Ile Ser Met Ser Glu Ala Leu Val Arg Ser Leu Asn Leu Pro	
385 390 395 400	
gct gtg cag gtg ctg gaa gcc tat gga ccg aaa ccg ttt gcg gca aag	1248
Ala Val Gln Val Leu Glu Ala Tyr Gly Pro Lys Arg Phe Ala Ala Lys	
405 410 415	
tta cgc aat gtt gga ttg ccg tta tat ttg ccc aac ggt gct gcg ccg	1296
Leu Arg Asn Val Gly Leu Pro Leu Tyr Leu Pro Asn Gly Ala Ala Pro	
420 425 430	
aat ctt tca ctc att ctc ggc ggc gct ggt gca aaa ctg gaa gat atg	1344
Asn Leu Ser Leu Ile Leu Gly Gly Ala Gly Ala Lys Leu Glu Asp Met	
435 440 445	
gcg gca gcg tat acc gcg ttt gct cgc cac ggc aag gca ggc aaa ttg	1392
Ala Ala Ala Tyr Thr Ala Phe Ala Arg His Gly Lys Ala Gly Lys Leu	
450 455 460	
cgc tta cag cct gac gat ccg ctg ctt gaa cgg cct tta atg tgc tgc	1440

690	695	700	
cgt tta ccg ggc gca gcg gaa gcg act ttg ccg ttg caa tca agt gga			2160
Arg Leu Pro Gly Ala Ala Glu Ala Thr Leu Pro Leu Gln Ser Ser Gly			
705	710	715	720
ggg gca ggt gaa cgc tgg tgg ttt ctg aat ggc gaa ccg tta act gaa			2208
Gly Ala Gly Glu Arg Trp Trp Phe Leu Asn Gly Glu Pro Leu Thr Glu			
	725	730	735
cgc ggg cgc aac gtg acc ctg cat ttg acg gat aaa ggt gat tat caa			2256
Arg Gly Arg Asn Val Thr Leu His Leu Thr Asp Lys Gly Asp Tyr Gln			
	740	745	750
ttg ctg gtg atg gat gac gtg ggg caa atc gcg aca gtg aaa ttt gtc			2304
Leu Leu Val Met Asp Asp Val Gly Gln Ile Ala Thr Val Lys Phe Val			
	755	760	765
atg caa tag			2313
Met Gln *			
770			

<210> 209
 <211> 4962
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(4962)

<400> 209	
atg aaa aag tta cgc gta gcc gcc tgc atg cta atg ctg gcg ctg gca	48
Met Lys Lys Leu Arg Val Ala Ala Cys Met Leu Met Leu Ala Leu Ala	
1	5 10 15
ggg tgc gac aac aac gat aac gcg cca aca gcg gtg aaa aaa gat gcg	96
Gly Cys Asp Asn Asn Asp Asn Ala Pro Thr Ala Val Lys Lys Asp Ala	
	20 25 30
cct tct gaa gtt act aaa gcg gcc tct tca gaa aac gcg agt tca gca	144
Pro Ser Glu Val Thr Lys Ala Ala Ser Ser Glu Asn Ala Ser Ser Ala	
	35 40 45
aaa ctc tcc gtg ccg gag aga caa aaa ctg gcc caa cag agt gcc ggt	192
Lys Leu Ser Val Pro Glu Arg Gln Lys Leu Ala Gln Gln Ser Ala Gly	
	50 55 60
aag gtg ctg aca ttg ctg gat ctc tct gaa gtc caa ctt gat ggt gca	240
Lys Val Leu Thr Leu Leu Asp Leu Ser Glu Val Gln Leu Asp Gly Ala	
	65 70 75 80
gcc acg ctg gtg ctg acg ttc tcc atc cct ctc gac ccg gat cag gat	288
Ala Thr Leu Val Leu Thr Phe Ser Ile Pro Leu Asp Pro Asp Gln Asp	
	85 90 95

ttc tca cgc gtt att cat gtc gtc gat aaa aaa agc ggc aaa gtg gat	336
Phe Ser Arg Val Ile His Val Val Asp Lys Lys Ser Gly Lys Val Asp	
100 105 110	
ggt gcc tgg gag ctg tca gat aat ctt aaa gag tta cgt tta cgc cac	384
Gly Ala Trp Glu Leu Ser Asp Asn Leu Lys Glu Leu Arg Leu Arg His	
115 120 125	
ctc gaa ccg aaa cgt gat ttg atc gtt act att ggc aag gag gtc aaa	432
Leu Glu Pro Lys Arg Asp Leu Ile Val Thr Ile Gly Lys Glu Val Lys	
130 135 140	
gca ctc aac aac gca acc ttc agt aaa gat tac gaa aaa act ata act	480
Ala Leu Asn Asn Ala Thr Phe Ser Lys Asp Tyr Glu Lys Thr Ile Thr	
145 150 155 160	
acc cgc gac atc caa ccc agc gtc ggt ttt gcc agc cgt ggt tcg ctg	528
Thr Arg Asp Ile Gln Pro Ser Val Gly Phe Ala Ser Arg Gly Ser Leu	
165 170 175	
ctg cct ggc aaa gtc gtt gaa ggg ctg ccg gta atg gcg ctc aac gtt	576
Leu Pro Gly Lys Val Val Glu Gly Leu Pro Val Met Ala Leu Asn Val	
180 185 190	
aat aat gtc gat gtt aac ttc ttc cgc gtt aag cca gaa tct ctg cca	624
Asn Asn Val Asp Val Asn Phe Phe Arg Val Lys Pro Glu Ser Leu Pro	
195 200 205	
gca ttc att agc caa tgg gaa tac cgc aat tcg ctg gcg aac tgg cag	672
Ala Phe Ile Ser Gln Trp Glu Tyr Arg Asn Ser Leu Ala Asn Trp Gln	
210 215 220	
tca gac aaa ctg ctg cag atg gcg gat ctg gtc tac acc gga cgg ttt	720
Ser Asp Lys Leu Leu Gln Met Ala Asp Leu Val Tyr Thr Gly Arg Phe	
225 230 235 240	
gat ctc aat cct gcg cgt aac acc cgt gaa aaa tta ttg ctg ccg ctg	768
Asp Leu Asn Pro Ala Arg Asn Thr Arg Glu Lys Leu Leu Leu Pro Leu	
245 250 255	
ggc gat atc aaa ccg ctt cag cag gcg ggc gtg tat ctg gct gtg atg	816
Gly Asp Ile Lys Pro Leu Gln Gln Ala Gly Val Tyr Leu Ala Val Met	
260 265 270	
aat cag gct gga cgt tac gat tac agt aat ccc gcg acg ctg ttt acg	864
Asn Gln Ala Gly Arg Tyr Asp Tyr Ser Asn Pro Ala Thr Leu Phe Thr	
275 280 285	
tta agt gat atc ggc gtt tca gct cac cgt tat cac aat cgt ctg gat	912
Leu Ser Asp Ile Gly Val Ser Ala His Arg Tyr His Asn Arg Leu Asp	
290 295 300	
atc ttt acc caa agt ctg gaa aac ggc gcg gcc cag caa gga att gaa	960
Ile Phe Thr Gln Ser Leu Glu Asn Gly Ala Ala Gln Gln Gly Ile Glu	
305 310 315 320	
gtc tct tta tta aat gag aaa ggg cag act ctg act cag gca acc agt	1008

ggt tat gcg atg gtc gag tcc agt gaa ggg ccg ctg tgg tgg caa gag	2400
Gly Tyr Ala Met Val Glu Ser Ser Glu Gly Pro Leu Trp Trp Gln Glu	
785 790 795 800	
att gat gtt cgg gct caa ggg ctg gat ctg acg att ccg gtc gat aaa	2448
Ile Asp Val Arg Ala Gln Gly Leu Asp Leu Thr Ile Pro Val Asp Lys	
805 810 815	
acc tgg aat cgt cat gat ctg tat tta agt acg ctg gtg gta cgt cct	2496
Thr Trp Asn Arg His Asp Leu Tyr Leu Ser Thr Leu Val Val Arg Pro	
820 825 830	
ggc gat aaa tct cgc tcc gcg acg cca aaa cgc gcg gtt ggt gtg ttg	2544
Gly Asp Lys Ser Arg Ser Ala Thr Pro Lys Arg Ala Val Gly Val Leu	
835 840 845	
cat ctg ccg ctt ggc gat gaa aac cgt cgc ctc gat ctg gcg ctg gaa	2592
His Leu Pro Leu Gly Asp Glu Asn Arg Arg Leu Asp Leu Ala Leu Glu	
850 855 860	
aca cca gca aaa atg cgt ccc aat caa cca tta acc gtg aaa att aaa	2640
Thr Pro Ala Lys Met Arg Pro Asn Gln Pro Leu Thr Val Lys Ile Lys	
865 870 875 880	
gcc agc act aaa aat ggc gag aag cct aaa cag gtg aat gtg ctg gtg	2688
Ala Ser Thr Lys Asn Gly Glu Lys Pro Lys Gln Val Asn Val Leu Val	
885 890 895	
tct gcc gtt gat agt ggt gtg ctg aat att act gac tac gtc acg cca	2736
Ser Ala Val Asp Ser Gly Val Leu Asn Ile Thr Asp Tyr Val Thr Pro	
900 905 910	
gat ccg tgg cag gcg ttc ttt ggt cag aaa cgc tat ggc gca gac att	2784
Asp Pro Trp Gln Ala Phe Phe Gly Gln Lys Arg Tyr Gly Ala Asp Ile	
915 920 925	
tac gat att tac ggt cag gtt att gaa ggt cag ggg cgt ctg gca gct	2832
Tyr Asp Ile Tyr Gly Gln Val Ile Glu Gly Gln Gly Arg Leu Ala Ala	
930 935 940	
ctg cgt ttc ggt ggc gat ggt gat gag ctg aaa cgt ggt ggt aaa ccg	2880
Leu Arg Phe Gly Gly Asp Gly Asp Glu Leu Lys Arg Gly Gly Lys Pro	
945 950 955 960	
ccg gtc aat cac gtc aat att gtc gtg cag cag gcg ctg ccg gta acg	2928
Pro Val Asn His Val Asn Ile Val Val Gln Gln Ala Leu Pro Val Thr	
965 970 975	
ctc aac gaa cag ggc gaa ggc tcg gtt aca ctg ccg att ggc gat ttt	2976
Leu Asn Glu Gln Gly Glu Gly Ser Val Thr Leu Pro Ile Gly Asp Phe	
980 985 990	
aac ggt gaa ttg cgc gtc atg gcg caa gcc tgg acg gca gat gac ttc	3024
Asn Gly Glu Leu Arg Val Met Ala Gln Ala Trp Thr Ala Asp Asp Phe	
995 1000 1005	

<221> CDS
 <222> (1)...(795)

<400> 210

atg gat ctg ttg tac cgg gta aaa acg ctt tgg gcc gcg ctg cgc ggt	48
Met Asp Leu Leu Tyr Arg Val Lys Thr Leu Trp Ala Ala Leu Arg Gly	
1 5 10 15	
aat cat tac acc tgg cct gcc atc gat atc acc ctc ccc ggc aat cgc	96
Asn His Tyr Thr Trp Pro Ala Ile Asp Ile Thr Leu Pro Gly Asn Arg	
20 25 30	
cat ttt cat ctg att ggc agt att cat atg ggt agc cac gat atg gct	144
His Phe His Leu Ile Gly Ser Ile His Met Gly Ser His Asp Met Ala	
35 40 45	
ccc ctg ccc acc cgt ttg ctc aaa aag ctc aaa aac gcc gat gcg ctg	192
Pro Leu Pro Thr Arg Leu Leu Lys Lys Leu Lys Asn Ala Asp Ala Leu	
50 55 60	
atc gtc gag gcg gat gtt tcc acc agc gat acg cct ttt gct aat ttg	240
Ile Val Glu Ala Asp Val Ser Thr Ser Asp Thr Pro Phe Ala Asn Leu	
65 70 75 80	
cct gcc tgc gag gcg ctg gaa gag cgc att agc gag gag caa ctc caa	288
Pro Ala Cys Glu Ala Leu Glu Glu Arg Ile Ser Glu Glu Gln Leu Gln	
85 90 95	
aac ctg cag cac att agc cag gag atg ggc att tct ccc tca ctc ttt	336
Asn Leu Gln His Ile Ser Gln Glu Met Gly Ile Ser Pro Ser Leu Phe	
100 105 110	
tct acc caa ccg ctg tgg caa atc gcg atg gtt ctt cag gcg acg cag	384
Ser Thr Gln Pro Leu Trp Gln Ile Ala Met Val Leu Gln Ala Thr Gln	
115 120 125	
gca caa aaa ctg ggg ctg cgg gca gaa tac ggt atc gat tac cag cta	432
Ala Gln Lys Leu Gly Leu Arg Ala Glu Tyr Gly Ile Asp Tyr Gln Leu	
130 135 140	
ttg cag gcg gcg aag caa caa cat aaa ccc gtg att gaa ctg gaa ggg	480
Leu Gln Ala Ala Lys Gln Gln His Lys Pro Val Ile Glu Leu Glu Gly	
145 150 155 160	
gct gaa aac cag att gcc atg ttg ctc cag ctc cct gac aaa gga ctg	528
Ala Glu Asn Gln Ile Ala Met Leu Leu Gln Leu Pro Asp Lys Gly Leu	
165 170 175	
gcg ctg ctg gac gat acg ctg acc cac tgg cat acc aac gca cgg ttg	576
Ala Leu Leu Asp Asp Thr Leu Thr His Trp His Thr Asn Ala Arg Leu	
180 185 190	
ctg caa caa atg atg agc tgg tgg ctg aat gca ccg ccg caa aat aat	624
Leu Gln Gln Met Met Ser Trp Trp Leu Asn Ala Pro Pro Gln Asn Asn	
195 200 205	
gat ata acg ctg ccc aat acg ttc agt cag tcg ctg tac gat gtg ctg	672

Asp	Ile	Thr	Leu	Pro	Asn	Thr	Phe	Ser	Gln	Ser	Leu	Tyr	Asp	Val	Leu	
210						215					220					
atg	cat	cag	cga	aat	ctc	gcc	tgg	cgg	gat	aaa	tta	cgc	gcc	atg	ccg	720
Met	His	Gln	Arg	Asn	Leu	Ala	Trp	Arg	Asp	Lys	Leu	Arg	Ala	Met	Pro	
225					230					235					240	
ccg	ggg	cga	tat	gtg	gtc	gcg	gtc	ggg	gca	cta	cac	ctg	tat	gga	gaa	768
Pro	Gly	Arg	Tyr	Val	Val	Ala	Val	Gly	Ala	Leu	His	Leu	Tyr	Gly	Glu	
				245					250					255		
ggg	aat	ttg	ccg	caa	atg	ttg	cgc	taa								795
Gly	Asn	Leu	Pro	Gln	Met	Leu	Arg	*								
				260												

<210> 211
 <211> 969
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(969)

<400> 211																
atg	gat	aat	ttt	ctt	gct	ctg	acc	tta	acg	ggg	aaa	aaa	ccg	gtt	atc	48
Met	Asp	Asn	Phe	Leu	Ala	Leu	Thr	Leu	Thr	Gly	Lys	Lys	Pro	Val	Ile	
1				5					10					15		
acc	gag	cga	gaa	atc	aac	ggc	gtt	cgc	tgg	cgc	tgg	ctg	ggc	gat	ggg	96
Thr	Glu	Arg	Glu	Ile	Asn	Gly	Val	Arg	Trp	Arg	Trp	Leu	Gly	Asp	Gly	
			20					25					30			
gtg	ctg	gaa	ctg	acg	cca	tta	acg	cca	ccg	caa	ggc	gca	ctg	gtg	att	144
Val	Leu	Glu	Leu	Thr	Pro	Leu	Thr	Pro	Pro	Gln	Gly	Ala	Leu	Val	Ile	
			35				40					45				
tca	gcg	gga	ata	cac	ggg	aat	gag	acg	gca	cct	gtg	gag	atg	ctg	gac	192
Ser	Ala	Gly	Ile	His	Gly	Asn	Glu	Thr	Ala	Pro	Val	Glu	Met	Leu	Asp	
	50					55				60						
gcg	ttg	ctt	ggc	gcg	ata	tct	cac	ggc	gag	atc	ccg	tta	cgt	tgg	cgg	240
Ala	Leu	Leu	Gly	Ala	Ile	Ser	His	Gly	Glu	Ile	Pro	Leu	Arg	Trp	Arg	
65					70					75					80	
ttg	ctg	gtg	atc	ctc	ggg	aat	cct	cct	gcg	ctg	aag	caa	ggg	aaa	cgt	288
Leu	Leu	Val	Ile	Leu	Gly	Asn	Pro	Pro	Ala	Leu	Lys	Gln	Gly	Lys	Arg	
				85					90					95		
tat	tgc	cat	agc	gat	atg	aat	cga	atg	ttt	ggc	ggg	cgt	tgg	cag	cta	336
Tyr	Cys	His	Ser	Asp	Met	Asn	Arg	Met	Phe	Gly	Gly	Arg	Trp	Gln	Leu	
			100					105					110			
ttt	gct	gaa	agc	gga	gaa	acc	tgt	cgg	gcg	cgc	gaa	ctg	gaa	cag	tgc	384
Phe	Ala	Glu	Ser	Gly	Glu	Thr	Cys	Arg	Ala	Arg	Glu	Leu	Glu	Gln	Cys	
		115					120					125				

ctg gaa gat ttt tat gac cag ggc aaa gaa tct gtg cgc tgg cac ctt	432
Leu Glu Asp Phe Tyr Asp Gln Gly Lys Glu Ser Val Arg Trp His Leu	
130 135 140	
gat cta cat acc gca att cgt ggc tcc ttg cat ccg cag ttc ggt gta	480
Asp Leu His Thr Ala Ile Arg Gly Ser Leu His Pro Gln Phe Gly Val	
145 150 155 160	
tta ccg caa cgc gac att ccc tgg gac gag aaa ttt ctg acg tgg ctg	528
Leu Pro Gln Arg Asp Ile Pro Trp Asp Glu Lys Phe Leu Thr Trp Leu	
165 170 175	
ggg ggc ggc ggc ctg gag ggc ctg gtg ttc cat cag gaa cct ggt ggt	576
Gly Ala Ala Gly Leu Glu Ala Leu Val Phe His Gln Glu Pro Gly Gly	
180 185 190	
acg ttt acc cat ttc agc gcc aga cat ttt ggc ggc ctg gcc tgt acg	624
Thr Phe Thr His Phe Ser Ala Arg His Phe Gly Ala Leu Ala Cys Thr	
195 200 205	
ctg gaa ctt ggc aaa ggc ttg ccc ttt ggg caa aac gat ctt cgc cag	672
Leu Glu Leu Gly Lys Ala Leu Pro Phe Gly Gln Asn Asp Leu Arg Gln	
210 215 220	
ttt gca gta act gcc agc gca att gct ggc ctg cta tct ggt gag agt	720
Phe Ala Val Thr Ala Ser Ala Ile Ala Ala Leu Leu Ser Gly Glu Ser	
225 230 235 240	
gtc ggt atc gtg aga aca ccg ccg ctc cgt tat ccg gtg gtt tcg caa	768
Val Gly Ile Val Arg Thr Pro Pro Leu Arg Tyr Arg Val Val Ser Gln	
245 250 255	
att act cgc cac tcg ccg tcc ttc gaa atg cat atg gca agt gac acg	816
Ile Thr Arg His Ser Pro Ser Phe Glu Met His Met Ala Ser Asp Thr	
260 265 270	
ctg aat ttt atg ccg ttt gag aaa gga aca ttg ctg ggc cag gac gga	864
Leu Asn Phe Met Pro Phe Glu Lys Gly Thr Leu Leu Ala Gln Asp Gly	
275 280 285	
gag gaa cgt ttt acc gta acc cat gat gta gag tat gtg tta ttc cct	912
Glu Glu Arg Phe Thr Val Thr His Asp Val Glu Tyr Val Leu Phe Pro	
290 295 300	
aat ccg ttg gta ggc ttg gga tta cgc ggc gga tta atg ctc gaa aaa	960
Asn Pro Leu Val Ala Leu Gly Leu Arg Ala Gly Leu Met Leu Glu Lys	
305 310 315 320	
ata agc taa	969
Ile Ser *	

<210> 212
 <211> 1344
 <212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1344)

<400> 212

atg aac gcc tgg gaa gtc aat ttc gac ggg ctg gta ggg ctg acg cat	48
Met Asn Ala Trp Glu Val Asn Phe Asp Gly Leu Val Gly Leu Thr His	
1 5 10 15	
cat tac gcg ggc ctg tcg ttt ggt aat gaa gcc tct acc cgt cac cgt	96
His Tyr Ala Gly Leu Ser Phe Gly Asn Glu Ala Ser Thr Arg His Arg	
20 25 30	
ttt cag gtg tct aac ccg cga ctg gcg gcg aag cag ggc tta ctg aaa	144
Phe Gln Val Ser Asn Pro Arg Leu Ala Ala Lys Gln Gly Leu Leu Lys	
35 40 45	
atg aaa gcc ctt gcc gat gcg gga ttc ccc cag gcc gtg atc ccg ccg	192
Met Lys Ala Leu Ala Asp Ala Gly Phe Pro Gln Ala Val Ile Pro Pro	
50 55 60	
cac gag cgt ccg ttt att ccg gtg ctg cgt cag ttg gga ttc agt ggt	240
His Glu Arg Pro Phe Ile Pro Val Leu Arg Gln Leu Gly Phe Ser Gly	
65 70 75 80	
agc gat gag cag gta ctg gaa aaa gtt gca cgc cag gca ccg cac tgg	288
Ser Asp Glu Gln Val Leu Glu Lys Val Ala Arg Gln Ala Pro His Trp	
85 90 95	
ctt tcc agc gtc agt tcc gct tcg cca atg tgg gta gcc aat gcg gca	336
Leu Ser Ser Val Ser Ser Ala Ser Pro Met Trp Val Ala Asn Ala Ala	
100 105 110	
acg atc gcg cca tct gcc gat acg ctg gat ggc aaa gtg cat ctc acc	384
Thr Ile Ala Pro Ser Ala Asp Thr Leu Asp Gly Lys Val His Leu Thr	
115 120 125	
gtt gcc aac ctg aac aat aaa ttt cac cgt tcg ctg gaa gcg ccc gtc	432
Val Ala Asn Leu Asn Asn Lys Phe His Arg Ser Leu Glu Ala Pro Val	
130 135 140	
act gaa tcg ctg tta aaa gcg att ttt aac gac gaa gag aaa ttt agc	480
Thr Glu Ser Leu Leu Lys Ala Ile Phe Asn Asp Glu Glu Lys Phe Ser	
145 150 155 160	
gtc cat tcg gcg ttg cca cag gta gcg ttg ctc ggt gat gag ggg gcg	528
Val His Ser Ala Leu Pro Gln Val Ala Leu Leu Gly Asp Glu Gly Ala	
165 170 175	
gca aac cac aat cgt ctc ggc ggt cat tac ggt gaa ccg ggt atg caa	576
Ala Asn His Asn Arg Leu Gly Gly His Tyr Gly Glu Pro Gly Met Gln	
180 185 190	
ctt ttt gtc tac ggg cga gaa gaa ggc aat gat acc cgg cct tcc cgt	624
Leu Phe Val Tyr Gly Arg Glu Glu Gly Asn Asp Thr Arg Pro Ser Arg	

205

672

720

768

816

864

912

960

100

105

110

11.

12

12

12

207

ctc ggt tgc gtt tat ccg ttc cag cgc gag gga ggg ggc aat gga taa 1344
 Leu Gly Ser Val Tyr Pro Phe Gln Arg Glu Gly Gly Gly Asn Gly *
 435 440 445

<210> 213
 <211> 1479
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1479)

<400> 213
 atg act tta tgg att aac ggt gac tgg ata acg ggc cag ggc gca tgc 48
 Met Thr Leu Trp Ile Asn Gly Asp Trp Ile Thr Gly Gln Gly Ala Ser
 1 5 10 15

cgt gtg aag cgt aat ccg gta tgc ggc gag gtg tta tgg caa ggc aat 96
 Arg Val Lys Arg Asn Pro Val Ser Gly Glu Val Leu Trp Gln Gly Asn
 20 25 30

gat gcc gat gcc gct cag gtc gag cag gct tgt cgg gca gcc cgt gcg 144
 Asp Ala Asp Ala Ala Gln Val Glu Gln Ala Cys Arg Ala Ala Arg Ala
 35 40 45

gcg ttt ccg cgc tgg gcg cgg ctt tca ttt gct gaa cgt cat gcc gtt 192
 Ala Phe Pro Arg Trp Ala Arg Leu Ser Phe Ala Glu Arg His Ala Val
 50 55 60

gtc gaa cgc ttt gcc gca ctg ctg gaa agc aat aaa gcc gaa tta acc 240
 Val Glu Arg Phe Ala Ala Leu Leu Glu Ser Asn Lys Ala Glu Leu Thr
 65 70 75 80

gcg att att gcc aga gaa acg ggt aag ccg cgc tgg gaa gcg gca acc 288
 Ala Ile Ile Ala Arg Glu Thr Gly Lys Pro Arg Trp Glu Ala Ala Thr
 85 90 95

gaa gtg acg gcg atg atc aat aaa atc gcg ata tca att aag gcg tat 336
 Glu Val Thr Ala Met Ile Asn Lys Ile Ala Ile Ser Ile Lys Ala Tyr
 100 105 110

cac gtt cgt acc ggc gag cag cgt agt gaa atg ccg gac ggc gcg gcg 384
 His Val Arg Thr Gly Glu Gln Arg Ser Glu Met Pro Asp Gly Ala Ala
 115 120 125

agc ctg cga cat cgc ccg cac ggc gtg ctg gcg gtg ttt ggg ccg tat 432
 Ser Leu Arg His Arg Pro His Gly Val Leu Ala Val Phe Gly Pro Tyr
 130 135 140

aat ttc cct ggt cat ttg ccg aac gga cat atc gtt ccg gca ttg ctg 480
 Asn Phe Pro Gly His Leu Pro Asn Gly His Ile Val Pro Ala Leu Leu
 145 150 155 160

gca ggt aac acc att atc ttt aaa ccc agc gaa ctg aca ccg tgg agt	528
Ala Gly Asn Thr Ile Ile Phe Lys Pro Ser Glu Leu Thr Pro Trp Ser	
165 170 175	
ggc gaa gcg gta atg cgt tta tgg cag cag gct ggc ttg ccg cca ggc	576
Gly Glu Ala Val Met Arg Leu Trp Gln Gln Ala Gly Leu Pro Pro Gly	
180 185 190	
gtg ctg aac ctg gtg cag ggc ggg cgt gaa acg ggt cag gcg ctg agt	624
Val Leu Asn Leu Val Gln Gly Gly Arg Glu Thr Gly Gln Ala Leu Ser	
195 200 205	
gcg ctg gag gat ctc gac ggt ttg ctg ttt acc ggt agc gcc aat aca	672
Ala Leu Glu Asp Leu Asp Gly Leu Leu Phe Thr Gly Ser Ala Asn Thr	
210 215 220	
ggc tac cag ttg cat cgc cag ctc tcc ggt cag ccg gag aaa att ctc	720
Gly Tyr Gln Leu His Arg Gln Leu Ser Gly Gln Pro Glu Lys Ile Leu	
225 230 235 240	
gcc ctt gag atg ggc ggt aat aat ccg cta att atc gat gag gtg gcg	768
Ala Leu Glu Met Gly Gly Asn Asn Pro Leu Ile Ile Asp Glu Val Ala	
245 250 255	
gat atc gac gcg gct gtc cat ctg acc att cag tcg gcg ttt gtc aca	816
Asp Ile Asp Ala Ala Val His Leu Thr Ile Gln Ser Ala Phe Val Thr	
260 265 270	
gcc ggt caa cgc tgc acc tgc gcc cgc cgt tta ttg ctg aaa agc ggg	864
Ala Gly Gln Arg Cys Thr Cys Ala Arg Arg Leu Leu Leu Lys Ser Gly	
275 280 285	
gcg cag ggc gat gcg ttt ctt gct cgt ctg gtt gcc gtc agc cag cga	912
Ala Gln Gly Asp Ala Phe Leu Ala Arg Leu Val Ala Val Ser Gln Arg	
290 295 300	
tta acg ccg ggc aac tgg gat gac gaa ccg cag ccg ttt att ggc ggg	960
Leu Thr Pro Gly Asn Trp Asp Asp Glu Pro Gln Pro Phe Ile Gly Gly	
305 310 315 320	
ctg att tct gaa cag gcc gca cag cag gtg gtt act gca tgg cag caa	1008
Leu Ile Ser Glu Gln Ala Ala Gln Gln Val Val Thr Ala Trp Gln Gln	
325 330 335	
ctg gaa gcg atg ggc gga cga ccc ctg ctt gcg ccg cgc tta tta caa	1056
Leu Glu Ala Met Gly Gly Arg Pro Leu Leu Ala Pro Arg Leu Leu Gln	
340 345 350	
gca ggg aca tcg ttg ctg acg ccg ggg atc att gaa atg aca ggc gtt	1104
Ala Gly Thr Ser Leu Leu Thr Pro Gly Ile Ile Glu Met Thr Gly Val	
355 360 365	
gct ggc gta cca gat gaa gag gtg ttc gga ccg tta ttg cgc gtc tgg	1152
Ala Gly Val Pro Asp Glu Glu Val Phe Gly Pro Leu Leu Arg Val Trp	
370 375 380	
cgt tat gat act ttc gat gaa gcg att cga atg gcg aat aac act cgc	1200

Arg Tyr Asp Thr Phe Asp Glu Ala Ile Arg Met Ala Asn Asn Thr Arg	
385 390 395 400	
ttc gga ctc tct tgc ggt ctg gtt tcc ccc gag cgg gaa aag ttc gat	1248
Phe Gly Leu Ser Cys Gly Leu Val Ser Pro Glu Arg Glu Lys Phe Asp	
405 410 415	
caa ctg ttg ctg gag gcg cgg gcg ggg att gtt aac tgg aac aaa ccg	1296
Gln Leu Leu Leu Glu Ala Arg Ala Gly Ile Val Asn Trp Asn Lys Pro	
420 425 430	
ctt acc ggt gct gcc agt acc gcg cca ttc ggc ggc att ggt gct tcc	1344
Leu Thr Gly Ala Ala Ser Thr Ala Pro Phe Gly Gly Ile Gly Ala Ser	
435 440 445	
ggt aac cat cgc ccc agc gcc tgg tat gcc gca gat tac tgc gca tgg	1392
Gly Asn His Arg Pro Ser Ala Trp Tyr Ala Ala Asp Tyr Cys Ala Trp	
450 455 460	
ccg atg gcg agc ctg gag tgc gac tgc tta aca ttg ccc gcc acg ctt	1440
Pro Met Ala Ser Leu Glu Ser Asp Ser Leu Thr Leu Pro Ala Thr Leu	
465 470 475 480	
aac ccc ggg ctg gat ttt tcc gat gag gtg gtg cga tga	1479
Asn Pro Gly Leu Asp Phe Ser Asp Glu Val Val Arg *	
485 490	
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<211> 1035	
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<400> 214	
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Met Met Val Ile Arg Pro Val Glu Arg Ser Asp Val Ser Ala Leu Met	
1 5 10 15	
cag ctt gcc agc aaa acg ggc ggc ggc ctg acg tcg ctt ccc gcc aat	96
Gln Leu Ala Ser Lys Thr Gly Gly Leu Thr Ser Leu Pro Ala Asn	
20 25 30	
gaa gcc acg ctt tcg gcg cgt atc gaa agg gca atc aaa acc tgg caa	144
Glu Ala Thr Leu Ser Ala Arg Ile Glu Arg Ala Ile Lys Thr Trp Gln	
35 40 45	
ggc gaa ctg ccc aaa agt gag cag ggc tat gtg ttc gtg ctg gaa gat	192
Gly Glu Leu Pro Lys Ser Glu Gln Gly Tyr Val Phe Val Leu Glu Asp	
50 55 60	
agc gag aca ggc acc gtg gcg ggg att tgt gcc att gag gtg gcg gtt	240
Ser Glu Thr Gly Thr Val Ala Gly Ile Cys Ala Ile Glu Val Ala Val	
65 70 75 80	

gtg cgt acc gat ccg gca acc gag cgt ttg att tta acc gcc gca caa 960
 Val Arg Thr Asp Pro Ala Thr Glu Arg Leu Ile Leu Thr Ala Ala Gln
 305 310 315 320

ctg gat gcc ctc aaa tgc cac gcc ggg gat cgc gtt cgt ctg gtg cgc 1008
 Leu Asp Ala Leu Lys Cys His Ala Gly Asp Arg Val Arg Leu Val Arg
 325 330 335

ctg tgc gca gag gag aaa aca gca tga 1035
 Leu Cys Ala Glu Glu Lys Thr Ala *

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 <212> DNA
 <213> Escherichia coli

<220>
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 1 5 10 15

gtt tac gct ccg gca ccc ttt ata ccg gta cgt ggc gaa ggt tcg cgc 96
 Val Tyr Ala Pro Ala Pro Phe Ile Pro Val Arg Gly Glu Gly Ser Arg
 20 25 30

ttg tgg gat cag cag ggg aaa gag tat atc gac ttc gcg ggt ggc att 144
 Leu Trp Asp Gln Gln Gly Lys Glu Tyr Ile Asp Phe Ala Gly Gly Ile
 35 40 45

gcg gtg aac gcg ctg ggc cat gcg cat ccg gaa ctg cgt gaa gcg ctg 192
 Ala Val Asn Ala Leu Gly His Ala His Pro Glu Leu Arg Glu Ala Leu
 50 55 60

aac gaa cag gcg agt aag ttc tgg cat acc ggc aac ggt tac acc aac 240
 Asn Glu Gln Ala Ser Lys Phe Trp His Thr Gly Asn Gly Tyr Thr Asn
 65 70 75 80

gag ccg gta ctg cga ctg gcg aaa aaa ttg atc gac gcc acg ttt gcc 288
 Glu Pro Val Leu Arg Leu Ala Lys Lys Leu Ile Asp Ala Thr Phe Ala
 85 90 95

gat cgc gtc ttc ttt tgt aac tcc ggt gcg gaa gcc aac gaa gcg gcg 336
 Asp Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
 100 105 110

cta aaa ctg gcg cgt aaa ttc gct cac gac cgc tac ggc agc cat aag 384
 Leu Lys Leu Ala Arg Lys Phe Ala His Asp Arg Tyr Gly Ser His Lys
 115 120 125

agc ggc atc gtg gcg ttc aaa aat gcg ttt cat ggt cgc acg ctg ttt 432
 Ser Gly Ile Val Ala Phe Lys Asn Ala Phe His Gly Arg Thr Leu Phe

ggt ggc aac gtg gtg cgt ttt gcg cct gcg ctc aat gtc agc gaa gaa	1152
Gly Gly Asn Val Val Arg Phe Ala Pro Ala Leu Asn Val Ser Glu Glu	
370 375 380	

gag gtg acg acc gga ctg gat cgc ttt gca gct gct tgc gaa cac ttt	1200
Glu Val Thr Thr Gly Leu Asp Arg Phe Ala Ala Cys Glu His Phe	
385 390 395 400	

ggt agc cga ggt tca tca tga	1221
Val Ser Arg Gly Ser Ser *	
405	

<210> 216
 <211> 3147
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(3147)

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Met Lys Ile Leu Ser Leu Arg Leu Lys Asn Leu Asn Ser Leu Lys Gly	
1 5 10 15	

gaa tgg aag att gat ttc acc cgc gag ccg ttc gcc agc aac ggg ctg	96
Glu Trp Lys Ile Asp Phe Thr Arg Glu Pro Phe Ala Ser Asn Gly Leu	
20 25 30	

ttt gct att acc ggc cca aca ggt gcg ggg aaa acc acc ctg ctg gac	144
Phe Ala Ile Thr Gly Pro Thr Gly Ala Gly Lys Thr Thr Leu Leu Asp	
35 40 45	

gcc att tgt ctg gcg ctg tat cac gaa act ccg cgt ctc tct aac gtt	192
Ala Ile Cys Leu Ala Leu Tyr His Glu Thr Pro Arg Leu Ser Asn Val	
50 55 60	

tca caa tcg caa aat gat ctc atg acc cgc gat acc gcc gaa tgt ctg	240
Ser Gln Ser Gln Asn Asp Leu Met Thr Arg Asp Thr Ala Glu Cys Leu	
65 70 75 80	

gcg gag gtg gag ttt gaa gtg aaa ggt gaa gcg tac cgt gca ttc tgg	288
Ala Glu Val Glu Phe Glu Val Lys Gly Glu Ala Tyr Arg Ala Phe Trp	
85 90 95	

agc cag aat ccg gcg cgt aac caa ccc gac ggt aat ttg cag gtg cca	336
Ser Gln Asn Arg Ala Arg Asn Gln Pro Asp Gly Asn Leu Gln Val Pro	
100 105 110	

cgc gta gag ctg gcg cgc tgc gcc gac ggc aaa att ctc gcc gac aaa	384
Arg Val Glu Leu Ala Arg Cys Ala Asp Gly Lys Ile Leu Ala Asp Lys	
115 120 125	

gtg aaa gat aag ctg gaa ctg aca gcg acg tta acc ggg ctg gat tac	432
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006161691660

Leu Glu Ser Thr Phe Ala Val Lys *
1045

<210> 217
<211> 1203
<212> DNA
<213> Escherichia coli

<220>
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<222> (1)...(1203)

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1 5 10 15

agt aaa agc cgc gaa gct gaa cat cag gct ttt ctt gac tgg ctg ctg 96
Ser Lys Ser Arg Glu Ala Glu His Gln Ala Phe Leu Asp Trp Leu Leu
20 25 30

gag aca gca caa acc cat cag gtg gat gcg att att gtt gcc ggt gat 144
Glu Thr Ala Gln Thr His Gln Val Asp Ala Ile Ile Val Ala Gly Asp
35 40 45

gtt ttc gat acc ggc tcg ccg ccc agt tac gcc cgc acg tta tac aac 192
Val Phe Asp Thr Gly Ser Pro Pro Ser Tyr Ala Arg Thr Leu Tyr Asn
50 55 60

cgt ttt gtt gtc aat tta cag caa act ggc tgt cat ctg gtg gta ctg 240
Arg Phe Val Val Asn Leu Gln Gln Thr Gly Cys His Leu Val Val Leu
65 70 75 80

gca gga aac cat gac tcg gtc gcc acg ctg aat gaa tcg cgc gat atc 288
Ala Gly Asn His Asp Ser Val Ala Thr Leu Asn Glu Ser Arg Asp Ile
85 90 95

atg gcg ttc ctc aat act acc gtg gtc gcc agc gcc gga cat gcg ccg 336
Met Ala Phe Leu Asn Thr Thr Val Val Ala Ser Ala Gly His Ala Pro
100 105 110

caa atc ttg cct cgt cgc gac ggg acg cca ggc gca gtg ctg tgc ccc 384
Gln Ile Leu Pro Arg Arg Asp Gly Thr Pro Gly Ala Val Leu Cys Pro
115 120 125

att ccg ttt tta cgt ccg cgt gac att att acc agc cag gcg ggg ctt 432
Ile Pro Phe Leu Arg Pro Arg Asp Ile Ile Thr Ser Gln Ala Gly Leu
130 135 140

aac ggt att gaa aaa cag cag cat tta ctg gca gcg att acc gat tat 480
Asn Gly Ile Glu Lys Gln Gln His Leu Leu Ala Ala Ile Thr Asp Tyr
145 150 155 160

tac caa caa cac tat gcc gat gcc tgc aaa ctg cgc ggc gat cag cct 528
Tyr Gln Gln His Tyr Ala Asp Ala Cys Lys Leu Arg Gly Asp Gln Pro
165 170 175

ctg ccc atc atc gcc acg gga cat tta acg acc gtg ggg gcc agt aaa	576
Leu Pro Ile Ile Ala Thr Gly His Leu Thr Thr Val Gly Ala Ser Lys	
180 185 190	
agt gac gcc gtg cgt gac att tat att ggc acg ctg gac gcg ttt ccg	624
Ser Asp Ala Val Arg Asp Ile Tyr Ile Gly Thr Leu Asp Ala Phe Pro	
195 200 205	
gca caa aac ttt cca cca gcc gac tac atc gcg ctc ggg cat att cac	672
Ala Gln Asn Phe Pro Pro Ala Asp Tyr Ile Ala Leu Gly His Ile His	
210 215 220	
cgc gca cag att att ggc ggc atg gaa cat gtt cgc tat tgc ggc tcc	720
Arg Ala Gln Ile Ile Gly Gly Met Glu His Val Arg Tyr Cys Gly Ser	
225 230 235 240	
ccc att cca ctg agt ttt gat gaa tgc ggt aag agt aaa tat gtc cat	768
Pro Ile Pro Leu Ser Phe Asp Glu Cys Gly Lys Ser Lys Tyr Val His	
245 250 255	
ctg gtg aca ttt tca aac ggc aaa tta gag agc gtg gaa aac ctg aac	816
Leu Val Thr Phe Ser Asn Gly Lys Leu Glu Ser Val Glu Asn Leu Asn	
260 265 270	
gta ccg gta acg caa ccc atg gca gtg ctg aaa ggc gat ctg gcg tcg	864
Val Pro Val Thr Gln Pro Met Ala Val Leu Lys Gly Asp Leu Ala Ser	
275 280 285	
att acc gca cag ctg gaa cag tgg cgc gat gta tcg cag gag cca cct	912
Ile Thr Ala Gln Leu Glu Gln Trp Arg Asp Val Ser Gln Glu Pro Pro	
290 295 300	
gtc tgg ctg gat atc gaa atc act act gat gag tat ctg cat gat att	960
Val Trp Leu Asp Ile Glu Ile Thr Thr Asp Glu Tyr Leu His Asp Ile	
305 310 315 320	
cag cgc aaa atc cag gca tta acc gaa tca ttg cct gtc gaa gta ttg	1008
Gln Arg Lys Ile Gln Ala Leu Thr Glu Ser Leu Pro Val Glu Val Leu	
325 330 335	
ctg gta cgt cgg agt cgt gaa cag cgc gag cgt gtg tta gcc agc caa	1056
Leu Val Arg Arg Ser Arg Glu Gln Arg Glu Arg Val Leu Ala Ser Gln	
340 345 350	
cag cgt gaa acc ctc agc gaa ctc agc gtc gaa gag gtg ttc aat cgc	1104
Gln Arg Glu Thr Leu Ser Glu Leu Ser Val Glu Glu Val Phe Asn Arg	
355 360 365	
cgt ctg gca ctg gaa gaa ctg gat gaa tcg cag cag caa cgt ctg cag	1152
Arg Leu Ala Leu Glu Glu Leu Asp Glu Ser Gln Gln Gln Arg Leu Gln	
370 375 380	
cat ctt ttc acc acg acg ttg cat acc ctc gcc gga gaa cac gaa gca	1200
His Leu Phe Thr Thr Thr Leu His Thr Leu Ala Gly Glu His Glu Ala	
385 390 395 400	

tga
*

1203

<210> 218
<211> 765
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(765)

<400> 218

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Met Asn Asp Leu Phe Ser Leu Ala Gly Lys Asn Ile Leu Ile Thr Gly	
1 5 10 15	
tca gca cag ggc att ggc ttt tta ctg gca acc ggc ctg ggt aaa tat	96
Ser Ala Gln Gly Ile Gly Phe Leu Leu Ala Thr Gly Leu Gly Lys Tyr	
20 25 30	
ggc gca caa ata att att aat gat att act gcc gaa cgc gca gaa ctt	144
Gly Ala Gln Ile Ile Ile Asn Asp Ile Thr Ala Glu Arg Ala Glu Leu	
35 40 45	
gct gta gaa aaa ctc cac cag gag ggt att cag gcc gtt gcc gca cct	192
Ala Val Glu Lys Leu His Gln Glu Gly Ile Gln Ala Val Ala Ala Pro	
50 55 60	
ttt aat gtt act cat aaa cat gaa att gat gcc gcc gtt gaa cat atc	240
Phe Asn Val Thr His Lys His Glu Ile Asp Ala Ala Val Glu His Ile	
65 70 75 80	
gaa aag gac atc ggc ccc att gat gtg ctg gtg aat aac gcc ggt atc	288
Glu Lys Asp Ile Gly Pro Ile Asp Val Leu Val Asn Asn Ala Gly Ile	
85 90 95	
cag cgc cgt cat cct ttt act gag ttc cct gaa caa gag tgg aat gat	336
Gln Arg Arg His Pro Phe Thr Glu Phe Pro Glu Gln Glu Trp Asn Asp	
100 105 110	
gtg atc gca gta aac cag acc gcc gtg ttc ctg gta tcg caa gcg gta	384
Val Ile Ala Val Asn Gln Thr Ala Val Phe Leu Val Ser Gln Ala Val	
115 120 125	
act cgt cac atg gtt gaa cgc aag gca ggt aaa gtt att aat att tgc	432
Thr Arg His Met Val Glu Arg Lys Ala Gly Lys Val Ile Asn Ile Cys	
130 135 140	
tcg atg caa agc gaa ctg gga cgt gac acc atc acc cct tat gcc gca	480
Ser Met Gln Ser Glu Leu Gly Arg Asp Thr Ile Thr Pro Tyr Ala Ala	
145 150 155 160	
tcg aaa ggg gcg gta aaa atg ctc acc cgc ggc atg tgc gtc gag ctg	528
Ser Lys Gly Ala Val Lys Met Leu Thr Arg Gly Met Cys Val Glu Leu	

aaa tac tgc att gaa cat aac gag aat cag tgt aca gat atg cgt ttt	336
Lys Tyr Cys Ile Glu His Asn Glu Asn Gln Cys Thr Asp Met Arg Phe	
100 105 110	
ttt ggc agt gcc atg tat ttc cct cat gtt gat ggt ggt ttt acc cgt	384
Phe Gly Ser Ala Met Tyr Phe Pro His Val Asp Gly Gly Phe Thr Arg	
115 120 125	
tat aaa atg gtc gaa acg tcg caa tgt gtc cct tat ccg gcc aaa gct	432
Tyr Lys Met Val Glu Thr Ser Gln Cys Val Pro Tyr Pro Ala Lys Ala	
130 135 140	
gac gaa aag gtt atg gct ttt gcc gaa cct tta gcc gtc gcg att cat	480
Asp Glu Lys Val Met Ala Phe Ala Glu Pro Leu Ala Val Ala Ile His	
145 150 155 160	
gcc gca cat cag gcc ggc gag tta cag ggc aag cga gta ttt att tcc	528
Ala Ala His Gln Ala Gly Glu Leu Gln Gly Lys Arg Val Phe Ile Ser	
165 170 175	
ggg gtt gga ccc att ggc tgc ctg att gtc agt gca gtg aaa aca ctg	576
Gly Val Gly Pro Ile Gly Cys Leu Ile Val Ser Ala Val Lys Thr Leu	
180 185 190	
ggg gcc gcg gaa att gtc tgt gct gat gtg agt ccc cgt tcc ctt tcg	624
Gly Ala Ala Glu Ile Val Cys Ala Asp Val Ser Pro Arg Ser Leu Ser	
195 200 205	
ctg ggc aaa gag atg ggg gcg gat gtg ctc gta aac cca caa aac gac	672
Leu Gly Lys Glu Met Gly Ala Asp Val Leu Val Asn Pro Gln Asn Asp	
210 215 220	
gac atg gat cac tgg aaa gcg gaa aaa ggc tat ttc gat gtc agc ttt	720
Asp Met Asp His Trp Lys Ala Glu Lys Gly Tyr Phe Asp Val Ser Phe	
225 230 235 240	
gaa gtg tcc ggt cat cct tca tca gtg aat acc tgt ctg gag gtc act	768
Glu Val Ser Gly His Pro Ser Ser Val Asn Thr Cys Leu Glu Val Thr	
245 250 255	
cgt gca cgc ggc gta atg gtg cag gta ggt atg gga ggc gcg atg gca	816
Arg Ala Arg Gly Val Met Val Gln Val Gly Met Gly Gly Ala Met Ala	
260 265 270	
gaa ttc cca atg atg acg ttg att ggt aag gag att tca ctc aga ggc	864
Glu Phe Pro Met Met Thr Leu Ile Gly Lys Glu Ile Ser Leu Arg Gly	
275 280 285	
tct ttc cgt ttt acc agc gaa ttt aat acc gca gtg tca tgg ctg gcg	912
Ser Phe Arg Phe Thr Ser Glu Phe Asn Thr Ala Val Ser Trp Leu Ala	
290 295 300	
aat ggc gtt atc aat cca ctg cct tta ctg agt gct gaa tat ccc ttc	960
Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe	
305 310 315 320	

atg ttg cag ccg aag att cag gca atg cgt gag cgt ctg ggc gat gac	1200
Met Leu Gln Pro Lys Ile Gln Ala Met Arg Glu Arg Leu Gly Asp Asp	
385 390 395 400	
aaa cag cgt atc agc cag gaa atg atg gcg ctg tac aaa gct gag aag	1248
Lys Gln Arg Ile Ser Gln Glu Met Met Ala Leu Tyr Lys Ala Glu Lys	
405 410 415	
gtt aac ccg ctg ggc ggc tgc ttc ccg ctg ctg atc cag atg cca atc	1296
Val Asn Pro Leu Gly Gly Cys Phe Pro Leu Leu Ile Gln Met Pro Ile	
420 425 430	
ttc ctg gcg ttg tac tac atg ctg atg ggt tcc gtt gaa ctg cgt cag	1344
Phe Leu Ala Leu Tyr Tyr Met Leu Met Gly Ser Val Glu Leu Arg Gln	
435 440 445	
gca ccg ttt gca ctg tgg atc cac gac ctg tcg gca cag gac ccg tac	1392
Ala Pro Phe Ala Leu Trp Ile His Asp Leu Ser Ala Gln Asp Pro Tyr	
450 455 460	
tac atc ctg ccg atc ctg atg ggc gta acg atg ttc ttc att cag aag	1440
Tyr Ile Leu Pro Ile Leu Met Gly Val Thr Met Phe Phe Ile Gln Lys	
465 470 475 480	
atg tcg ccg acc aca gtg acc gac ccg atg cag cag aag atc atg acc	1488
Met Ser Pro Thr Thr Val Thr Asp Pro Met Gln Gln Lys Ile Met Thr	
485 490 495	
ttt atg ccg gtc atc ttc acc gtg ttc ttc ctg tgg ttc ccg tca ggt	1536
Phe Met Pro Val Ile Phe Thr Val Phe Phe Leu Trp Phe Pro Ser Gly	
500 505 510	
ctg gtg ctg tac tat atc gtc agc aac ctg gta acc att att cag cag	1584
Leu Val Leu Tyr Tyr Ile Val Ser Asn Leu Val Thr Ile Ile Gln Gln	
515 520 525	
cag ctg att tac cgt ggt ctg gaa aaa cgt ggc ctg cat agc cgc gag	1632
Gln Leu Ile Tyr Arg Gly Leu Glu Lys Arg Gly Leu His Ser Arg Glu	
530 535 540	
aag aaa aaa tcc tga	1647
Lys Lys Lys Ser *	
545	

<210> 221
 <211> 1629
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1629)

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1				5					10					15		
ggc	gca	acg	gga	gcc	ggg	att	gcc	cgc	gac	tgt	gcc	ctg	cgc	ggg	ctg	96
Gly	Ala	Thr	Gly	Ala	Gly	Ile	Ala	Arg	Asp	Cys	Ala	Leu	Arg	Gly	Leu	
			20				25					30				
cgc	gtg	att	ttg	gtt	gag	cgc	cac	gac	atc	gca	acc	ggt	gcc	acc	ggg	144
Arg	Val	Ile	Leu	Val	Glu	Arg	His	Asp	Ile	Ala	Thr	Gly	Ala	Thr	Gly	
		35				40					45					
cgt	aac	cac	ggc	ctg	ctg	cac	agc	ggt	gcg	cgc	tat	gcg	gta	acc	gat	192
Arg	Asn	His	Gly	Leu	Leu	His	Ser	Gly	Ala	Arg	Tyr	Ala	Val	Thr	Asp	
	50					55					60					
gcg	gaa	tcg	gcc	cgc	gaa	tgc	att	agt	gaa	aac	cag	atc	ctg	aaa	cgc	240
Ala	Glu	Ser	Ala	Arg	Glu	Cys	Ile	Ser	Glu	Asn	Gln	Ile	Leu	Lys	Arg	
65					70				75					80		
att	gca	cgt	cac	tgc	gtt	gaa	cca	acc	aac	ggc	ctg	ttt	atc	acc	ctg	288
Ile	Ala	Arg	His	Cys	Val	Glu	Pro	Thr	Asn	Gly	Leu	Phe	Ile	Thr	Leu	
			85					90				95				
ccg	gaa	gat	gac	ctc	tcc	ttc	cag	gcc	act	ttt	att	cgc	gcc	tgc	gaa	336
Pro	Glu	Asp	Asp	Leu	Ser	Phe	Gln	Ala	Thr	Phe	Ile	Arg	Ala	Cys	Glu	
			100				105					110				
gaa	gca	ggg	atc	agc	gca	gaa	gct	ata	gac	ccg	cag	caa	gcg	cgc	att	384
Glu	Ala	Gly	Ile	Ser	Ala	Glu	Ala	Ile	Asp	Pro	Gln	Gln	Ala	Arg	Ile	
		115				120					125					
atc	gaa	cct	gcc	gtt	aac	ccg	gca	ctg	att	ggc	gcg	gtg	aaa	gtt	ccg	432
Ile	Glu	Pro	Ala	Val	Asn	Pro	Ala	Leu	Ile	Gly	Ala	Val	Lys	Val	Pro	
	130				135					140						
gat	ggc	acc	gtt	gat	cca	ttt	cgt	ctg	acc	gca	gca	aac	atg	ctg	gat	480
Asp	Gly	Thr	Val	Asp	Pro	Phe	Arg	Leu	Thr	Ala	Ala	Asn	Met	Leu	Asp	
145				150					155					160		
gcc	aaa	gaa	cac	ggt	gcc	gtt	atc	ctt	acc	gct	cat	gaa	gtc	acg	ggg	528
Ala	Lys	Glu	His	Gly	Ala	Val	Ile	Leu	Thr	Ala	His	Glu	Val	Thr	Gly	
			165				170						175			
ctg	att	cgt	gaa	ggc	gcg	acg	gtg	tgc	ggt	gtt	cgt	gta	cgt	aac	cat	576
Leu	Ile	Arg	Glu	Gly	Ala	Thr	Val	Cys	Gly	Val	Arg	Val	Arg	Asn	His	
		180					185					190				
ctc	acc	ggc	gaa	act	cag	gcc	ctt	cat	gca	cct	gtc	gtg	gtt	aat	gcc	624
Leu	Thr	Gly	Glu	Thr	Gln	Ala	Leu	His	Ala	Pro	Val	Val	Val	Asn	Ala	
		195				200					205					
gct	ggg	atc	tgg	ggg	caa	cac	att	gcc	gaa	tat	gcc	gat	ctg	cgc	att	672
Ala	Gly	Ile	Trp	Gly	Gln	His	Ile	Ala	Glu	Tyr	Ala	Asp	Leu	Arg	Ile	
	210				215				220							
cgc	atg	ttc	ccg	gcg	aaa	gga	tcg	ctg	ctg	atc	atg	gat	cac	cgc	att	720
Arg	Met	Phe	Pro	Ala	Lys	Gly	Ser	Leu	Leu	Ile	Met	Asp	His	Arg	Ile	

gaa agc ggt gcg caa ttg cag ggc agc gta gaa ctt gct cac cag cgg	336
Glu Ser Gly Ala Gln Leu Gln Gly Ser Val Glu Leu Ala His Gln Arg	
100 105 110	
gtt acg ccg ctc ggc act ctg cgc tct acc tgg cta agt tcg cca gaa	384
Val Thr Pro Leu Gly Thr Leu Arg Ser Thr Trp Leu Ser Ser Pro Glu	
115 120 125	
gtc ccc gtc tgg ccg ctg ccc ggc aag aaa ata tgt gta gtg gga att	432
Val Pro Val Trp Pro Leu Pro Ala Lys Lys Ile Cys Val Val Gly Ile	
130 135 140	
agc ggc ctg atg gat ttt cag ggc cac ctt ggc gca gct tcg ttg cgt	480
Ser Gly Leu Met Asp Phe Gln Ala His Leu Ala Ala Ala Ser Leu Arg	
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gaa ctc ggc ctt gcc gtt gaa acc gca gaa ata gag ctg ccg gaa ctg	528
Glu Leu Gly Leu Ala Val Glu Thr Ala Glu Ile Glu Leu Pro Glu Leu	
165 170 175	
gat gtg ctg cgc aat aac gcc acc gaa ttt cgc ggc gtg aat atc gcc	576
Asp Val Leu Arg Asn Asn Ala Thr Glu Phe Arg Ala Val Asn Ile Ala	
180 185 190	
cgt ttc ctt gat aat gaa gaa aac tgg ccg ctg tta ctt gat gcg ctt	624
Arg Phe Leu Asp Asn Glu Glu Asn Trp Pro Leu Leu Leu Asp Ala Leu	
195 200 205	
att cct gtc gcc aat acc tgc gaa atg atc ctg atg ccc gcc tgc ttc	672
Ile Pro Val Ala Asn Thr Cys Glu Met Ile Leu Met Pro Ala Cys Phe	
210 215 220	
ggt ctg gcc gat gac aaa ctg tgg cgt tgg ttg aat gaa aaa cta cct	720
Gly Leu Ala Asp Asp Lys Leu Trp Arg Trp Leu Asn Glu Lys Leu Pro	
225 230 235 240	
tgt tca ctg atg ctt ttg cca acg ctg ccg cct tcc gtg ctg ggc att	768
Cys Ser Leu Met Leu Leu Pro Thr Leu Pro Pro Ser Val Leu Gly Ile	
245 250 255	
cgt ctg caa aac cag tta cag cgc cag ttt gtg cgc cag ggt ggc gtg	816
Arg Leu Gln Asn Gln Leu Gln Arg Gln Phe Val Arg Gln Gly Gly Val	
260 265 270	
tgg atg ccg ggc gat gaa gtg aaa aaa gtg acc tgt aaa aat ggc gta	864
Trp Met Pro Gly Asp Glu Val Lys Lys Val Thr Cys Lys Asn Gly Val	
275 280 285	
gtg aac gaa atc tgg acc cgc aat cac gcc gat att ccg cta cgt cca	912
Val Asn Glu Ile Trp Thr Arg Asn His Ala Asp Ile Pro Leu Arg Pro	
290 295 300	
cgt ttc gcg gtt ctc gcc agc ggc agt ttc ttt agt ggc gga ctg gta	960
Arg Phe Ala Val Leu Ala Ser Gly Ser Phe Phe Ser Gly Gly Leu Val	
305 310 315 320	
gcg gaa cgt aac ggc att cga gag ccg att ctc ggc ctt gat gtg cta	1008

gcg aaa tat gac acc acg cgc ccg tgc ctg cgt aat ttt gtg ttg agt	288
Ala Lys Tyr Asp Thr Thr Arg Pro Ser Leu Arg Asn Phe Val Leu Ser	
85 90 95	
cat acc gac ctg atg ggt agc gtt tcc acg ccg ttc gca cca atc gtc	336
His Thr Asp Leu Met Gly Ser Val Ser Thr Pro Phe Ala Pro Ile Val	
100 105 110	
aac acc gct acc tgc ctg aaa ccg gtg cgg cag ctg ctt gat gcg gcg	384
Asn Thr Ala Thr Ser Leu Lys Pro Val Arg Gln Leu Leu Asp Ala Ala	
115 120 125	
tta aaa atc gat cat cgc cgc acg cta ccg aaa tac tcc ttc ggc acg	432
Leu Lys Ile Asp His Arg Arg Thr Leu Pro Lys Tyr Ser Phe Gly Thr	
130 135 140	
ttc cgt cgc tgg tat cgc agc gtg gcg gct cag caa gca caa tat aaa	480
Phe Arg Arg Trp Tyr Arg Ser Val Ala Ala Gln Gln Ala Gln Tyr Lys	
145 150 155 160	
gac cag gtc gct ttc ttt cac ggc tgc ttc gtt aac tac aac cat ccg	528
Asp Gln Val Ala Phe Phe His Gly Cys Phe Val Asn Tyr Asn His Pro	
165 170 175	
cag tta ggt aaa gat tta att aaa gtg ctc aac gca atg ggt acc ggt	576
Gln Leu Gly Lys Asp Leu Ile Lys Val Leu Asn Ala Met Gly Thr Gly	
180 185 190	
gta caa ctg ctc agc aaa gaa aaa tgc tgc ggc gta ccg cta atc gcc	624
Val Gln Leu Leu Ser Lys Glu Lys Cys Cys Gly Val Pro Leu Ile Ala	
195 200 205	
aac ggc ttt acc gat aaa gca cgc aaa cag gca att acg aat gta gag	672
Asn Gly Phe Thr Asp Lys Ala Arg Lys Gln Ala Ile Thr Asn Val Glu	
210 215 220	
tgc atc cgc gaa gct gtg gga gta aaa ggc att ccg gtg att gcc acc	720
Ser Ile Arg Glu Ala Val Gly Val Lys Gly Ile Pro Val Ile Ala Thr	
225 230 235 240	
tcc tca acc tgt aca ttt gcc ctg cgc gac gaa tac ccg gaa gtg ctg	768
Ser Ser Thr Cys Thr Phe Ala Leu Arg Asp Glu Tyr Pro Glu Val Leu	
245 250 255	
aat gtc gac aac aaa ggc ttg cgc gat cat atc gaa ctg gca acc cgc	816
Asn Val Asp Asn Lys Gly Leu Arg Asp His Ile Glu Leu Ala Thr Arg	
260 265 270	
tgg ctg tgg cgc aag ctg gac gaa ggc aaa acg tta ccg ctg aaa ccg	864
Trp Leu Trp Arg Lys Leu Asp Glu Gly Lys Thr Leu Pro Leu Lys Pro	
275 280 285	
ctg ccg ctg aaa gtg gtt tat cac act ccg tgc cat atg gaa aaa atg	912
Leu Pro Leu Lys Val Val Tyr His Thr Pro Cys His Met Glu Lys Met	
290 295 300	

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 Gly Trp Thr Leu Tyr Thr Leu Glu Leu Leu Arg Asn Ile Pro Gly Leu
 305 310 315 320

gag tta acg gtg ctg gat tcc cag tgc tgc ggt att gcg ggt act tac 1008
 Glu Leu Thr Val Leu Asp Ser Gln Cys Cys Gly Ile Ala Gly Thr Tyr
 325 330 335

ggg ttc aaa aaa gag aac tac ccc acc tca caa gcc atc ggc gca cca 1056
 Gly Phe Lys Lys Glu Asn Tyr Pro Thr Ser Gln Ala Ile Gly Ala Pro
 340 345 350

ctg ttc cgc cag ata gaa gaa agc ggc gca gat ctg gtg gtc acc gac 1104
 Leu Phe Arg Gln Ile Glu Glu Ser Gly Ala Asp Leu Val Val Thr Asp
 355 360 365

tgc gaa acc tgt aaa tgg cag att gag atg tcc aca agt ctt cgc tgc 1152
 Cys Glu Thr Cys Lys Trp Gln Ile Glu Met Ser Thr Ser Leu Arg Cys
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 Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
 20 25 30

ctg gac aaa atc gcc aaa aac ggt gtg att gtc gtc ggt cac cgt gaa 144
 Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
 35 40 45

tct tca gtg cct ttc tct tat tac gac aat cag caa aaa gtg gtg ggt 192
 Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly
 50 55 60

tac tcg cag gat tac tcc aac gcc att gtt gaa gca gtg aaa aag aaa 240
 Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
 65 70 75 80

ctc aac aaa ccg gac ttg cag gta aaa ctg att ccg att acc tca caa 288
 Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln

	85	90	95	
aac cgt att cca ctg ctg caa aac ggc act ttc gat ttt gaa tgt ggt				336
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly	100	105	110	
tct acc acc aac aac gtc gaa cgc caa aaa cag gcg gct ttc tct gac				384
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp	115	120	125	
act att ttc gtg gtc ggt acg cgc ctg ttg acc aaa aag ggt ggc gat				432
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp	130	135	140	
atc aaa gat ttt gcc aac ctg aaa gac aaa gcc gta gtc gtc act tcc				480
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser	145	150	155	160
ggc act acc tct gaa gtt ttg ctc aac aaa ctg aat gaa gag caa aaa				528
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys	165	170	175	
atg aat atg cgc atc atc agc gcc aaa gat cac ggt gac tct ttc cgc				576
Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg	180	185	190	
acc ctg gaa agc ggt cgt gcc gtt gcc ttt atg atg gat gac gct ctg				624
Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu	195	200	205	
ctg gcc ggt gaa cgt gcg aaa gcg aag aaa cca gac aac tgg gaa atc				672
Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile	210	215	220	
gtc gcc aag ccg cag tct cag gag gcc tac ggt tgt atg ttg cgt aaa				720
Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys	225	230	235	240
gat gat ccg cag ttc aaa aag ctg atg gat gac acc atc gct cag gtg				768
Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val	245	250	255	
cag acc tcc ggt gaa gcg gaa aaa tgg ttt gat aag tgg ttc aaa aat				816
Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn	260	265	270	
cca att ccg ccg aaa aac ctg aac atg aat ttc gaa ctg tca gac gaa				864
Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu	275	280	285	
atg aaa gca ctg ttc aaa gaa ccg aat gac aag gca ctg aac taa				909
Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn *	290	295	300	

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[illegible]

235

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gtt Val	gcc Ala	tgt Cys	gtg Val	ccg Pro 85	tta Leu	tta Leu	ccc Pro	tgt Cys	ttt Phe 90	act Thr	tgt Cys	cca Pro	gag Glu	tgt Cys 95	ctg Leu	288
aaa Lys	ggg Gly	ttt Phe	tat Tyr 100	tcc Ser	cag Gln	tgc Cys	gca Ala	aaa Lys 105	tat Tyr	gat Asp	ttt Phe	att Ile	ggc Gly 110	tcg Ser	cgg Arg	336
cgt Arg	gat Asp	ggt Gly 115	gga Gly	ttt Phe	gct Ala	gaa Glu	tat Tyr 120	att Ile	gtc Val	gtt Val	aag Lys	cga Arg 125	aaa Lys	aat Asn	gtc Val	384
ttt Phe 130	gct Ala	cta Leu	ccc Pro	acg Thr	gat Asp	atg Met 135	cct Pro	att Ile	gag Glu	gat Asp	ggg Gly 140	gct Ala	ttt Phe	att Ile	gag Glu	432
ccg Pro 145	att Ile	acc Thr	gtt Val	ggt Gly	ctg Leu 150	cat His	gct Ala	ttt Phe	cat His	tta Leu 155	gcg Ala	caa Gln	ggt Gly	tgt Cys	gag Glu 160	480
aat Asn	aaa Lys	aac Asn	gtt Val	att Ile 165	att Ile	att Ile	ggt Gly	gcc Ala	gga Gly 170	acc Thr	att Ile	ggc Gly	ctg Leu	ctg Leu 175	gcc Ala	528
att Ile	cag Gln	tgc Cys	gct Ala 180	gtc Val	gcg Ala	ctg Leu	gga Gly	gca Ala 185	aag Lys	agt Ser	gtg Val	acg Thr	gcg Ala 190	atc Ile	gac Asp	576
att Ile	agt Ser	tca Ser 195	gaa Glu	aaa Lys	ctg Leu	gca Ala	ctg Leu 200	gca Ala	aaa Lys	tct Ser	ttc Phe	ggt Gly 205	gcg Ala	atg Met	caa Gln	624
aca Thr 210	ttt Phe	aac Asn	agt Ser	agc Ser	gaa Glu	atg Met 215	agc Ser	gcg Ala	ccg Pro	caa Gln	atg Met 220	cag Gln	agc Ser	gtt Val	tta Leu	672
cgc Arg 225	gaa Glu	ctg Leu	cgc Arg	ttt Phe	aat Asn 230	cag Gln	ctt Leu	atc Ile	ctc Leu	gag Glu 235	acg Thr	gct Ala	ggc Gly	gta Val	ccg Pro 240	720
caa Gln	act Thr	gtc Val	gaa Glu	ctg Leu 245	gcg Ala	gta Val	gag Glu	att Ile	gcc Ala	ggt Gly 250	cct Pro	cat His	gcc Ala	caa Gln 255	ctg Leu	768
gcg Ala	ctg Leu	gtg Val	ggc Gly 260	acg Thr	ttg Leu	cat His	cag Gln	gat Asp 265	ctg Leu	cat His	tta Leu	aca Thr	tcg Ser 270	gca Ala	acg Thr	816
ttt Phe	ggc Gly	aaa Lys 275	ata Ile	ttg Leu	cgt Arg	aaa Lys	gag Glu 280	ctg Leu	acg Thr	gtt Val	atc Ile	ggc Gly 285	agt Ser	tgg Trp	atg Met	864

aac tac tcc agc cct tgg ccg ggg cag gag tgg gaa acg gcg agc cgg 912
 Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
 290 295 300

 ttg ctg aca gaa cgt aag tta agc ctg gag cca tta atc gct cac cgt 960
 Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
 305 310 315 320

 gga agc ttt gaa agc ttc gcc cag gcg gtg cgt gac atc gct cgt aat 1008
 Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
 325 330 335

 gct atg ccg ggc aaa gtg ttg ctc att ccc tga 1041
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 340 345

<210> 229
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 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (1)...(1356)

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 1 5 10 15

 atg ctg ccg att gtc atc att att ttt tct aaa ata tta ggc atg aag 96
 Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
 20 25 30

 gca ggc gat tgc ttt aaa gcg ggt ctg cat atc ggg att ggc ttt gtt 144
 Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
 35 40 45

 ggc att ggc ctt gtg att ggc tta atg ctg gat tcc att ggc ccg gcg 192
 Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
 50 55 60

 gcg aaa gcg atg gcg gaa aat ttc gac ctg aat ctg cat gtg gtc gat 240
 Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
 65 70 75 80

 gtt ggc tgg ccg ggc tct tca cca atg acc tgg gcg tcg caa att gcg 288
 Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
 85 90 95

 ctg gtg gcg att ccg att gcg att ctg gtt aac gtg gcg atg tta ctg 336
 Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
 100 105 110

 acc cgt atg acg ccg gtg gta aat gtt gat atc tgg aat atc tgg cat 384

Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His
 115 120 125

atg acc ttc acc ggc gcg ttg ctg cat ctg gca acc ggt tca tgg atg 432
 Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met
 130 135 140

ata ggg atg gca ggt gtg gta att cac gcg gcg ttt gtt tat aag ctc 480
 Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu
 145 150 155 160

ggc gac tgg ttt gcc cgc gat acc cga aat ttc ttt gag ctg gaa ggt 528
 Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly
 165 170 175

att gct att ccg cac ggt acg tcg gcg tat atg ggg ccg att gcg gtg 576
 Ile Ala Ile Pro His Gly Thr Ser Ala Tyr Met Gly Pro Ile Ala Val
 180 185 190

ctg gtc gat gct atc atc gag aaa atc cca ggc gtt aac cga att aaa 624
 Leu Val Asp Ala Ile Ile Glu Lys Ile Pro Gly Val Asn Arg Ile Lys
 195 200 205

ttt agc gcc gac gat att cag cgc aaa ttt ggt cca ttt ggc gag cct 672
 Phe Ser Ala Asp Asp Ile Gln Arg Lys Phe Gly Pro Phe Gly Glu Pro
 210 215 220

gtc acc gtg ggt ttt gtg atg ggg ctg att atc ggc atc ctc gcg ggt 720
 Val Thr Val Gly Phe Val Met Gly Leu Ile Ile Gly Ile Leu Ala Gly
 225 230 235 240

tac gat gtc aaa ggt gta ttg cag ctg gcg gta aaa acg gcg gca gtg 768
 Tyr Asp Val Lys Gly Val Leu Gln Leu Ala Val Lys Thr Ala Ala Val
 245 250 255

atg ctg cta atg cca cgg gtg att aaa ccc atc atg gat ggt tta acg 816
 Met Leu Leu Met Pro Arg Val Ile Lys Pro Ile Met Asp Gly Leu Thr
 260 265 270

ccc atc gct aag cag gct cgt agt cgt tta cag gcg aag ttc ggc ggt 864
 Pro Ile Ala Lys Gln Ala Arg Ser Arg Leu Gln Ala Lys Phe Gly Gly
 275 280 285

cag gag ttc ctg att ggc ctt gat ccg gcg ttg ctg ctg gga cat acg 912
 Gln Glu Phe Leu Ile Gly Leu Asp Pro Ala Leu Leu Leu Gly His Thr
 290 295 300

gcg gtg gta tcg gca agc ctg att ttt atc cca ctc acc att tta att 960
 Ala Val Val Ser Ala Ser Leu Ile Phe Ile Pro Leu Thr Ile Leu Ile
 305 310 315 320

gct gtt tgt gtg ccg ggt aat cag gtg ctg ccg ttt ggc gat ctt gcc 1008
 Ala Val Cys Val Pro Gly Asn Gln Val Leu Pro Phe Gly Asp Leu Ala
 325 330 335

acc atc ggc ttc ttc gtg gcg atg gcg gtc gcc gtg cat cgt gga aat 1056
 Thr Ile Gly Phe Phe Val Ala Met Ala Val Ala Val His Arg Gly Asn

340						345						350						
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Leu	Phe	Arg	Thr	Leu	Ile	Ser	Gly	Val	Ile	Ile	Met	Ser	Ile	Thr	Leu			
355						360						365						
tgg	atc	gcg	acg	caa	act	att	ggt	ttg	cac	acc	caa	ctg	gcg	gct	aat	1152		
Trp	Ile	Ala	Thr	Gln	Thr	Ile	Gly	Leu	His	Thr	Gln	Leu	Ala	Ala	Asn			
370						375						380						
gct	ggg	gcg	tta	aaa	gcc	ggg	ggt	atg	gtg	gct	tca	atg	gat	cag	ggc	1200		
Ala	Gly	Ala	Leu	Lys	Ala	Gly	Gly	Met	Val	Ala	Ser	Met	Asp	Gln	Gly			
385						390						395				400		
ggt	tct	ccc	att	acc	tgg	tta	ctg	att	cag	gtt	ttc	tcc	ccg	caa	aat	1248		
Gly	Ser	Pro	Ile	Thr	Trp	Leu	Leu	Ile	Gln	Val	Phe	Ser	Pro	Gln	Asn			
405						410						415						
att	ccc	ggt	ttc	att	att	atc	ggt	gca	att	tat	ctg	acc	ggt	att	ttc	1296		
Ile	Pro	Gly	Phe	Ile	Ile	Ile	Gly	Ala	Ile	Tyr	Leu	Thr	Gly	Ile	Phe			
420						425						430						
atg	acc	tgg	cgt	aga	gcg	cgt	ggc	ttt	att	aaa	caa	gag	aaa	gtc	gtt	1344		
Met	Thr	Trp	Arg	Arg	Ala	Arg	Gly	Phe	Ile	Lys	Gln	Glu	Lys	Val	Val			
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Leu	Ala	Glu	*															
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1				5					10					15			
acg	atg	gcg	gcg	gaa	gaa	att	aaa	gag	ttg	tgt	cag	aat	cat	aat	att		96
Thr	Met	Ala	Ala	Glu	Glu	Ile	Lys	Glu	Leu	Cys	Gln	Asn	His	Asn	Ile		
			20					25					30				
cct	gtt	gaa	tta	atc	cag	tgt	cgg	gtt	aat	gaa	ata	gaa	acc	tat	atg		144
Pro	Val	Glu	Leu	Ile	Gln	Cys	Arg	Val	Asn	Glu	Ile	Glu	Thr	Tyr	Met		
		35					40					45					
gat	ggt	gtg	cat	ttg	ata	tgc	acc	act	gcc	aaa	gtg	gat	cgt	agt	ttt		192
Asp	Gly	Val	His	Leu	Ile	Cys	Thr	Thr	Ala	Lys	Val	Asp	Arg	Ser	Phe		
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Cys Ser Val Cys Ser Ala His Pro Leu Val Ile Glu Ala Ala Leu Ala
20 25 30

ttt gat cgc aac agc acg cgc aaa gtg ctg att gaa gca acg tca aac 144
Phe Asp Arg Asn Ser Thr Arg Lys Val Leu Ile Glu Ala Thr Ser Asn
35 40 45

cag gtc aat caa ttt ggc ggt tat acc gga atg aca ccg gca gac ttt 192
Gln Val Asn Gln Phe Gly Gly Tyr Thr Gly Met Thr Pro Ala Asp Phe
50 55 60

cgc gaa ttt gtt ttt acg att gcc gat aaa gtt ggg ttt gca cgc gaa 240
Arg Glu Phe Val Phe Thr Ile Ala Asp Lys Val Gly Phe Ala Arg Glu
65 70 75 80

cgc att att ctc ggc ggc gat cat ctg ggg cca aac tgc tgg cag caa 288
Arg Ile Ile Leu Gly Gly Asp His Leu Gly Pro Asn Cys Trp Gln Gln
85 90 95

gaa aat gcg gat gcg gcg atg gaa aaa tcc gtc gag ctg gta aag gaa 336
Glu Asn Ala Asp Ala Ala Met Glu Lys Ser Val Glu Leu Val Lys Glu
100 105 110

tat gtt cgt gcc ggc ttc agt aaa att cat ctt gat gcg tca atg tcc 384
Tyr Val Arg Ala Gly Phe Ser Lys Ile His Leu Asp Ala Ser Met Ser
115 120 125

tgc gcg ggg gat ccc ata ccg tta gca cca gaa acg gtt gcg gaa cga 432
Cys Ala Gly Asp Pro Ile Pro Leu Ala Pro Glu Thr Val Ala Glu Arg
130 135 140

gct gct gtg ctt tgc ttt gct gcg gaa agt gtg gcg aca gat tgc cag 480
Ala Ala Val Leu Cys Phe Ala Ala Glu Ser Val Ala Thr Asp Cys Gln
145 150 155 160

cgt gag caa ctg agc tat gtc att ggc acc gaa gtt ccg gtt ccg ggc 528
Arg Glu Gln Leu Ser Tyr Val Ile Gly Thr Glu Val Pro Val Pro Gly
165 170 175

agt tcg atg ctg tca tac tgt gtt act cag gaa ttt acc gca aac tgt 192
 Ser Ser Met Leu Ser Tyr Cys Val Thr Gln Glu Phe Thr Ala Asn Cys
 50 55 60

cga aaa ata tca caa aat tgt tat tcc act gcc ctt ttt acc att aac 240
 Arg Lys Ile Ser Gln Asn Cys Tyr Ser Thr Ala Leu Phe Thr Ile Asn
 65 70 75 80

ttt gcc act tca ccc atc cat aca gaa aat ata ctc att aca tta cac 288
 Phe Ala Thr Ser Pro Ile His Thr Glu Asn Ile Leu Ile Thr Leu His
 85 90 95

tat aaa aaa gaa atc att tcc tta tta ctg gaa acc acg cct att aaa 336
 Tyr Lys Lys Glu Ile Ile Ser Leu Leu Leu Glu Thr Thr Pro Ile Lys
 100 105 110

gct aac cat ttg cga agc ata ctg gat tat att gaa cag gaa cag tta 384
 Ala Asn His Leu Arg Ser Ile Leu Asp Tyr Ile Glu Gln Glu Gln Leu
 115 120 125

act gct gaa gat cgt aac cat tgt atg aaa ctg tct aaa aaa atc cat 432
 Thr Ala Glu Asp Arg Asn His Cys Met Lys Leu Ser Lys Lys Ile His
 130 135 140

aga gaa aaa aac tat aca ccc aac agt aaa tct caa tgg tag 474
 Arg Glu Lys Asn Tyr Thr Pro Asn Ser Lys Ser Gln Trp *
 145 150 155

<210> 235
 <211> 1416
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1416)

<400> 235
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 Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln
 1 5 10 15

tac gcc ctt gat tca ttg aga aat gga aaa ggc aaa gtc aac ctg att 96
 Tyr Ala Leu Asp Ser Leu Arg Asn Gly Lys Gly Lys Val Asn Leu Ile
 20 25 30

aaa cat tac tcc tcc gtt gaa tcc ata cag cag cat gtc ccc tta gtc 144
 Lys His Tyr Ser Ser Val Glu Ser Ile Gln Gln His Val Pro Leu Val
 35 40 45

cgg gac gcg gag ttc aga gca tta ctt cgc cat cct cct gca ggg agt 192
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 50 55 60


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<400> 236
atg cca tct gga tta ttt atg gac tta ttg cct ttt tta ctg gac gcg 48
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1 5 10 15

aac ctc agc gcg aca aac cca ccc gct att ccg cac tgg tgg aag cgt 96
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20 25 30

caa ccg ctt att ccc aac ctt ctg tca cag gaa ctg aaa aac tat ctg 144
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35 40 45

aag ctt aat gtt aaa gag aaa aat att cag att gca gac cag gta att 192
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50 55 60

att gat gaa act gca ggt gaa gtt gtt atc ggc gcg aat acc cgt att 240
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65 70 75 80

tgt cat ggt gcc gtt att cag ggt ccg gta gtg att ggc gca aac tgc 288
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85 90 95

ctg ata ggt aat tgg att tgc ccc tat att tcc aga cat ctg tta tca 336
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100 105 110

ctt aac cca tta caa gcc cgc tgc cgc aga tat tcc cgt ggc gag cga 384
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
115 120 125

taa 387
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<210> 237
<211> 1197
<212> DNA
<213> Escherichia coli
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<220>
<221> CDS
<222> (1)...(1197)
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<400> 237
atg aaa acc tgg ata ttt atc tgt atg tcc ata gca atg ttg cta tgg 48
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1 5 10 15

ttt tta agt acg cta aga cgt aaa ccc agt caa aag aaa ggc tgt att 96
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
20 25 30

gac gcc att ata cct gcg tat aac gaa ggc ccg tgt ctg gcg cag tca 144
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Asp	Ala	Ile	Ile	Pro	Ala	Tyr	Asn	Glu	Gly	Pro	Cys	Leu	Ala	Gln	Ser		
	35						40					45					
ctg	gat	aat	cta	ctg	cgt	aac	cct	tat	ttt	tgc	cgg	gta	att	tgc	gtt	192	
Leu	Asp	Asn	Leu	Leu	Arg	Asn	Pro	Tyr	Phe	Cys	Arg	Val	Ile	Cys	Val		
	50					55				60							
aac	gac	ggc	tcc	acg	gac	aat	acc	gaa	gcg	gtc	atg	gcg	gaa	gtc	aaa	240	
Asn	Asp	Gly	Ser	Thr	Asp	Asn	Thr	Glu	Ala	Val	Met	Ala	Glu	Val	Lys		
	65				70				75						80		
cgc	aaa	tgg	ggc	gac	cgc	ttt	gtt	gcc	gtc	acg	caa	aaa	aat	acc	ggc	288	
Arg	Lys	Trp	Gly	Asp	Arg	Phe	Val	Ala	Val	Thr	Gln	Lys	Asn	Thr	Gly		
				85				90						95			
aaa	ggc	ggc	gac	ctg	atg	aat	ggc	ctc	aat	tac	gcc	acc	tgc	gac	cag	336	
Lys	Gly	Gly	Ala	Leu	Met	Asn	Gly	Leu	Asn	Tyr	Ala	Thr	Cys	Asp	Gln		
			100					105					110				
gtt	ttt	tta	agt	gat	gcc	gac	acc	tat	gtt	ccg	ccc	gat	caa	gac	gga	384	
Val	Phe	Leu	Ser	Asp	Ala	Asp	Thr	Tyr	Val	Pro	Pro	Asp	Gln	Asp	Gly		
		115					120					125					
atg	ggc	tat	atg	ctg	gca	gaa	att	gag	cgc	ggc	gcc	gat	gcc	gta	ggc	432	
Met	Gly	Tyr	Met	Leu	Ala	Glu	Ile	Glu	Arg	Gly	Ala	Asp	Ala	Val	Gly		
	130					135				140							
ggc	att	ccc	tct	act	gac	ttg	aaa	ggc	gac	ggc	ctg	tta	ccg	cac	atc	480	
Gly	Ile	Pro	Ser	Thr	Ala	Leu	Lys	Gly	Ala	Gly	Leu	Leu	Pro	His	Ile		
	145				150			155						160			
cgc	gac	acc	gta	aag	ttg	ccg	atg	att	gtt	atg	aag	cgc	acg	cta	cag	528	
Arg	Ala	Thr	Val	Lys	Leu	Pro	Met	Ile	Val	Met	Lys	Arg	Thr	Leu	Gln		
				165				170						175			
cag	ctc	ctg	ggc	ggc	gca	ccg	ttt	att	atc	agc	ggc	gcc	tgc	ggg	atg	576	
Gln	Leu	Leu	Gly	Gly	Ala	Pro	Phe	Ile	Ile	Ser	Gly	Ala	Cys	Gly	Met		
			180				185					190					
ttc	cgt	act	gat	gta	ttg	cgt	aag	ttc	ggc	ttc	tgc	gat	cgt	act	aaa	624	
Phe	Arg	Thr	Asp	Val	Leu	Arg	Lys	Phe	Gly	Phe	Ser	Asp	Arg	Thr	Lys		
		195				200						205					
gtc	gaa	gac	ctt	gat	ctc	acc	tgg	aca	ttg	gtg	gca	aac	ggc	tac	cgt	672	
Val	Glu	Asp	Leu	Asp	Leu	Thr	Trp	Thr	Leu	Val	Ala	Asn	Gly	Tyr	Arg		
	210				215						220						
att	cgc	cag	gac	aat	cgc	tgc	atc	gta	tac	cca	cag	gaa	tgc	aac	agc	720	
Ile	Arg	Gln	Ala	Asn	Arg	Cys	Ile	Val	Tyr	Pro	Gln	Glu	Cys	Asn	Ser		
	225				230				235						240		
ccg	cgt	gag	gag	tgg	cgt	cgc	tgg	cgc	cgt	tgg	att	gtg	gga	tac	gac	768	
Pro	Arg	Glu	Glu	Trp	Arg	Arg	Trp	Arg	Arg	Trp	Ile	Val	Gly	Tyr	Ala		
				245			250							255			
gtc	tgt	atg	cgc	ctg	cat	aaa	aga	ctt	tta	ttt	agc	cgc	ttc	ggc	atc	816	
Val	Cys	Met	Arg	Leu	His	Lys	Arg	Leu	Leu	Phe	Ser	Arg	Phe	Gly	Ile		

260

265

270

ttc agt ata ttt cct atg ctg ttg gtt gtg ctt tat ggc gtt ggg att 864
 Phe Ser Ile Phe Pro Met Leu Leu Val Val Leu Tyr Gly Val Gly Ile
 275 280 285

tat ctc act acc tgg ttt aat gaa ttc atc acc acc ggg ccg cat gga 912
 Tyr Leu Thr Thr Trp Phe Asn Glu Phe Ile Thr Thr Gly Pro His Gly
 290 295 300

gtg gtg ttg gca atg ttt ccg ctt atc tgg gtc ggc gta gtt tgt gtt 960
 Val Val Leu Ala Met Phe Pro Leu Ile Trp Val Gly Val Val Cys Val
 305 310 315 320

att ggt gct ttt agc gcc tgg ttt cat cgt tgc tgg ttg ttg gtg cct 1008
 Ile Gly Ala Phe Ser Ala Trp Phe His Arg Cys Trp Leu Leu Val Pro
 325 330 335

tta gcg ccg ctt tcc gtt gtg tat gta tta tta gct tat gcc atc tgg 1056
 Leu Ala Pro Leu Ser Val Val Tyr Val Leu Leu Ala Tyr Ala Ile Trp
 340 345 350

att att tat gga ctt att gcc ttt ttt act gga cgc gaa cct cag cgc 1104
 Ile Ile Tyr Gly Leu Ile Ala Phe Phe Thr Gly Arg Glu Pro Gln Arg
 355 360 365

gac aaa ccc acc cgc tat tcc gca ctg gtg gaa gcg tca acc gct tat 1152
 Asp Lys Pro Thr Arg Tyr Ser Ala Leu Val Glu Ala Ser Thr Ala Tyr
 370 375 380

tcc caa cct tct gtc aca gga act gaa aaa cta tct gaa gct taa 1197
 Ser Gln Pro Ser Val Thr Gly Thr Glu Lys Leu Ser Glu Ala *
 385 390 395

<210> 238

<211> 1659

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1659)

<400> 238

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 Met Ile Leu Glu Arg Val Glu Ile Val Gly Phe Arg Gly Ile Asn Arg
 1 5 10 15

ttg tcg ttg atg ctg gaa caa aac aac gtc ctg att ggg gag aac gcg 96
 Leu Ser Leu Met Leu Glu Gln Asn Asn Val Leu Ile Gly Glu Asn Ala
 20 25 30

tgg ggt aaa tcc agc ttg ctg gac gcc tta act ctg ctg cta tcg cca 144
 Trp Gly Lys Ser Ser Leu Leu Asp Ala Leu Thr Leu Leu Leu Ser Pro
 35 40 45

Pro Met Asn Leu Arg Lys Ile Ile Ser Lys Ala Ile His Arg Ser Ser	
500 505 510	
aaa ccc gat ctt gcc att gaa gtg gca atg gag gca gga cgt cgt ggt	1584
Lys Pro Asp Leu Ala Ile Glu Val Ala Met Glu Ala Gly Arg Arg Gly	
515 520 525	
gtg gac tcc gta ccg acg ctg ctg aaa aaa atg ttc tca cgc gtg ctg	1632
Val Asp Ser Val Pro Thr Leu Leu Lys Lys Met Phe Ser Arg Val Leu	
530 535 540	
tgg ctg gcg cgc ggt cgc gcg gat taa	1659
Trp Leu Ala Arg Gly Arg Ala Asp *	
545 550	

<210> 239
 <211> 1059
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1059)

<400> 239	
atg cta cca tct att tca atc aac aat acc agc gca gct tac cca gaa	48
Met Leu Pro Ser Ile Ser Ile Asn Asn Thr Ser Ala Ala Tyr Pro Glu	
1 5 10 15	
tcc atc aat gaa aat aac aat gat gaa gtt aat gga tta gta caa gag	96
Ser Ile Asn Glu Asn Asn Asn Asp Glu Val Asn Gly Leu Val Gln Glu	
20 25 30	
ttc aaa aac ctt ttt aat ggt aag gaa gga ata agc acc tgt att aaa	144
Phe Lys Asn Leu Phe Asn Gly Lys Glu Gly Ile Ser Thr Cys Ile Lys	
35 40 45	
cat cta ctt gag ctt ata aaa aac gcc ata cga gta aac gac gat cct	192
His Leu Leu Glu Leu Ile Lys Asn Ala Ile Arg Val Asn Asp Asp Pro	
50 55 60	
tat aga ttt aat att aat aat tcc tca gtt act tat att gat att gac	240
Tyr Arg Phe Asn Ile Asn Asn Ser Ser Val Thr Tyr Ile Asp Ile Asp	
65 70 75 80	
tcc aat gat aca gac cat att act att ggt atc gac aac caa gaa cca	288
Ser Asn Asp Thr Asp His Ile Thr Ile Gly Ile Asp Asn Gln Glu Pro	
85 90 95	
ata gaa tta cct gcg aac tat aaa gac aaa gaa ctc gtc cgt act atc	336
Ile Glu Leu Pro Ala Asn Tyr Lys Asp Lys Glu Leu Val Arg Thr Ile	
100 105 110	
att aat gac aac ata gtt gag aag act cat gat atc aat aac aag gaa	384
Ile Asn Asp Asn Ile Val Glu Lys Thr His Asp Ile Asn Asn Lys Glu	
115 120 125	

taa
*

1059

<210> 240
<211> 1128
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)...(1128)

<400> 240
atg atg cgc cat tta cgc aat att ttt aat ctg ggt atc aaa gag ttg 48
Met Met Arg His Leu Arg Asn Ile Phe Asn Leu Gly Ile Lys Glu Leu
1 5 10 15

cgc agt ctg ctc ggt gat aaa gcg atg ctg acg ctg att gtc ttc tcg 96
Arg Ser Leu Leu Gly Asp Lys Ala Met Leu Thr Leu Ile Val Phe Ser
20 25 30

ttt acg gtg tcg gtg tat tcg tca gcg acc gtt acg cca gga tcg ttg 144
Phe Thr Val Ser Val Tyr Ser Ser Ala Thr Val Thr Pro Gly Ser Leu
35 40 45

aac ctc gcg ccg atc gcc att gcc gat atg gat caa tcg cag tta tcg 192
Asn Leu Ala Pro Ile Ala Ile Ala Asp Met Asp Gln Ser Gln Leu Ser
50 55 60

aac cgg atc gtt aac agc ttc tat cgt ccg tgg ttt ttg cca ccg gag 240
Asn Arg Ile Val Asn Ser Phe Tyr Arg Pro Trp Phe Leu Pro Pro Glu
65 70 75 80

atg atc acc gcc gat gag atg gat gcc gga ctg gac gcc gga cgc tat 288
Met Ile Thr Ala Asp Glu Met Asp Ala Gly Leu Asp Ala Gly Arg Tyr
85 90 95

acc ttc gcg ata aat att ccg cct aat ttt cag cgt gat gtc ctc gcc 336
Thr Phe Ala Ile Asn Ile Pro Pro Asn Phe Gln Arg Asp Val Leu Ala
100 105 110

gga cgc cag ccg gat att cag gtg aac gtc gat gcc acg cgc atg agc 384
Gly Arg Gln Pro Asp Ile Gln Val Asn Val Asp Ala Thr Arg Met Ser
115 120 125

cag gca ttt acc ggc aat ggg tat atc cag aat att atc aac ggt gaa 432
Gln Ala Phe Thr Gly Asn Gly Tyr Ile Gln Asn Ile Ile Asn Gly Glu
130 135 140

gtg aac agc ttt gtc gcg cgc tac cgt gat aac agc gaa ccg ttg gta 480
Val Asn Ser Phe Val Ala Arg Tyr Arg Asp Asn Ser Glu Pro Leu Val
145 150 155 160

tcg ctg gaa acc cgg atg cgc ttt aac ccg aac ctc gat ccc gcg tgg 528
Ser Leu Glu Thr Arg Met Arg Phe Asn Pro Asn Leu Asp Pro Ala Trp

<212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2685)

<400> 241

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Met Ser Gln His Tyr Gly Lys Thr Val Ala Leu Asn Asn Ile Thr Leu	
1 5 10 15	
gat att ccg gcc cgc tgt atg gtc ggg ctg att ggc ccg gac ggc gtc	96
Asp Ile Pro Ala Arg Cys Met Val Gly Leu Ile Gly Pro Asp Gly Val	
20 25 30	
ggg aag tcg agc ttg ttg tgc ttg att tcc ggt gcc cgc gtc att gaa	144
Gly Lys Ser Ser Leu Leu Ser Leu Ile Ser Gly Ala Arg Val Ile Glu	
35 40 45	
cag ggc aat gtg atg gtg ctg ggc ggc gat atg cgc gac ccg aag cat	192
Gln Gly Asn Val Met Val Leu Gly Gly Asp Met Arg Asp Pro Lys His	
50 55 60	
cgc cgc gac gtc tgc ccg cgc atc gcc tgg atg ccg cag ggg ctg ggc	240
Arg Arg Asp Val Cys Pro Arg Ile Ala Trp Met Pro Gln Gly Leu Gly	
65 70 75 80	
aaa aac ctc tac cac acc ttg tgc gtg tat gaa aac gtc gat ttt ttc	288
Lys Asn Leu Tyr His Thr Leu Ser Val Tyr Glu Asn Val Asp Phe Phe	
85 90 95	
gct cgc ctg ttc ggt cac gac aaa gcg gag cgg gaa gtg cga atc aat	336
Ala Arg Leu Phe Gly His Asp Lys Ala Glu Arg Glu Val Arg Ile Asn	
100 105 110	
gag ctg ctg acc agc acc ggg tta gca ccg ttt cgc gat cgt ccg gca	384
Glu Leu Leu Thr Ser Thr Gly Leu Ala Pro Phe Arg Asp Arg Pro Ala	
115 120 125	
ggg aaa ctc tcc ggc ggg atg aag caa aaa ctt ggg ctg tgc tgc gcg	432
Gly Lys Leu Ser Gly Gly Met Lys Gln Lys Leu Gly Leu Cys Cys Ala	
130 135 140	
tta atc cac gac ccg gaa ctg ttg atc ctt gat gag cca aca acg ggg	480
Leu Ile His Asp Pro Glu Leu Leu Ile Leu Asp Glu Pro Thr Thr Gly	
145 150 155 160	
gtt gac ccg ctc tcc cgc tcc cag ttc tgg gat ctg atc gac agt att	528
Val Asp Pro Leu Ser Arg Ser Gln Phe Trp Asp Leu Ile Asp Ser Ile	
165 170 175	
cgc cag cgg cag agc aat atg agc gtg ctg gtc gcc acc gcc tat atg	576
Arg Gln Arg Gln Ser Asn Met Ser Val Leu Val Ala Thr Ala Tyr Met	
180 185 190	
gaa gag gcc gaa cgc ttc gac tgg ctg gta gcg atg aat gcc gga gaa	624

gtg atg ggc tta agt atc ctg ctg ctg aaa aaa cag gag gga tga 2685
 Val Met Gly Leu Ser Ile Leu Leu Leu Lys Lys Gln Glu Gly *
 885 890

<210> 242
 <211> 1068
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1068)

<400> 242
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 Met Asp Lys Ser Lys Arg His Leu Ala Trp Trp Val Val Gly Leu Leu
 1 5 10 15
 gcg gtg gcg gct atc gtg gcg tgg tgg ctg ttg cgc ccg gca ggt gtg 96
 Ala Val Ala Ala Ile Val Ala Trp Trp Leu Leu Arg Pro Ala Gly Val
 20 25 30
 ccg gaa ggc ttt gct gtc agt aat ggg cgc att gaa gcg acg gaa gtg 144
 Pro Glu Gly Phe Ala Val Ser Asn Gly Arg Ile Glu Ala Thr Glu Val
 35 40 45
 gat att gcc agc aaa att gcc ggg cgt atc gac acc att ctg gtg aaa 192
 Asp Ile Ala Ser Lys Ile Ala Gly Arg Ile Asp Thr Ile Leu Val Lys
 50 55 60
 gaa ggc aag ttt gtt cgc gaa ggt gaa gtg ctg gcg aag atg gat act 240
 Glu Gly Lys Phe Val Arg Glu Gly Glu Val Leu Ala Lys Met Asp Thr
 65 70 75 80
 cgc gtg ttg cag gaa cag cga ctg gaa gcc atc gcg caa atc aaa gag 288
 Arg Val Leu Gln Glu Gln Arg Leu Glu Ala Ile Ala Gln Ile Lys Glu
 85 90 95
 gca caa agc gcc gtt gct gcc gcg cag gct ttg ctg gag caa cga caa 336
 Ala Gln Ser Ala Val Ala Ala Ala Gln Ala Leu Leu Glu Gln Arg Gln
 100 105 110
 agc gaa act cgt gcc gca cag tcg ctg gtt aat caa cgc cag gca gaa 384
 Ser Glu Thr Arg Ala Ala Gln Ser Leu Val Asn Gln Arg Gln Ala Glu
 115 120 125
 ctg gac tcc gta gca aaa cgt cat acg cgt tcc cgt tca ctg gcc caa 432
 Leu Asp Ser Val Ala Lys Arg His Thr Arg Ser Arg Ser Leu Ala Gln
 130 135 140
 cga ggg gct att tct gcg caa cag ctg gat gac gat cgc gcc gcc gct 480
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 145 150 155 160
 gag agc gcc cga gct gcg ctg gaa tcg gcg aaa gct cag gta tcg gct 528

<220>
 <221> CDS
 <222> (1)...(708)

<400> 243

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Met Tyr Arg Tyr Leu Ser Ile Ala Ala Val Val Leu Ser Ala Ala Phe	
1 5 10 15	
tcc ggc ccg gcg ttg gcc gaa ggt atc aat agt ttt tct cag gcg aaa	96
Ser Gly Pro Ala Leu Ala Glu Gly Ile Asn Ser Phe Ser Gln Ala Lys	
20 25 30	
gcc gcg gcg gta aaa gtc cac gct gac gcg ccc ggt acg ttt tat tgc	144
Ala Ala Ala Val Lys Val His Ala Asp Ala Pro Gly Thr Phe Tyr Cys	
35 40 45	
gga tgt aaa att aac tgg cag gcc aaa aaa gcc gtt gtt gat ctg caa	192
Gly Cys Lys Ile Asn Trp Gln Gly Lys Lys Gly Val Val Asp Leu Gln	
50 55 60	
tcg tgc ggc tat cag gtg cgc aaa aat gaa aac cgc gcc agc cgc gta	240
Ser Cys Gly Tyr Gln Val Arg Lys Asn Glu Asn Arg Ala Ser Arg Val	
65 70 75 80	
gag tgg gaa cat gtc gtt ccc gcc tgg cag ttc ggt cac cag cgc cag	288
Glu Trp Glu His Val Val Pro Ala Trp Gln Phe Gly His Gln Arg Gln	
85 90 95	
tgc tgg cag gac ggt gga cgt aaa aac tgc gct aaa gat ccg gtc tat	336
Cys Trp Gln Asp Gly Gly Arg Lys Asn Cys Ala Lys Asp Pro Val Tyr	
100 105 110	
cgc aag atg gaa agc gat atg cat aac ctg cag ccg tca gtc ggt gag	384
Arg Lys Met Glu Ser Asp Met His Asn Leu Gln Pro Ser Val Gly Glu	
115 120 125	
gtg aat ggc gat cgc gcc aac ttt atg tac agc cag tgg aat ggc ggt	432
Val Asn Gly Asp Arg Gly Asn Phe Met Tyr Ser Gln Trp Asn Gly Gly	
130 135 140	
gaa ggc cag tac ggt caa tgc gcc atg aag gtc gat ttc aaa gaa aaa	480
Glu Gly Gln Tyr Gly Gln Cys Ala Met Lys Val Asp Phe Lys Glu Lys	
145 150 155 160	
gct gcc gaa cca cca gcg cgt gca cgc ggt gcc att gcg cgc acc tac	528
Ala Ala Glu Pro Pro Ala Arg Ala Arg Gly Ala Ile Ala Arg Thr Tyr	
165 170 175	
ttc tat atg cgc gac caa tac aac ctg aca ctc tct cgc cag caa acg	576
Phe Tyr Met Arg Asp Gln Tyr Asn Leu Thr Leu Ser Arg Gln Gln Thr	
180 185 190	
cag ctg ttc aac gca tgg aac aag atg tat ccg gtt acc gac tgg gag	624
Gln Leu Phe Asn Ala Trp Asn Lys Met Tyr Pro Val Thr Asp Trp Glu	
195 200 205	

tgc gag cgc gat gaa cgc atc gcg aag gtg cag ggc aat cat aac ccg 672
 Cys Glu Arg Asp Glu Arg Ile Ala Lys Val Gln Gly Asn His Asn Pro
 210 215 220

tat gtg caa cgc gct tgc cag gcg cga aag agc taa 708
 Tyr Val Gln Arg Ala Cys Gln Ala Arg Lys Ser *
 225 230 235

<210> 244
 <211> 1443
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1443)

<400> 244
 atg tcc aga agg ctt cgc aga aca aaa atc gtt acc acg tta ggc cca 48
 Met Ser Arg Arg Leu Arg Arg Thr Lys Ile Val Thr Thr Leu Gly Pro
 1 5 10 15

gca aca gat cgc gat aat aat ctt gaa aaa gtt atc gcg gcg ggt gcc 96
 Ala Thr Asp Arg Asp Asn Asn Leu Glu Lys Val Ile Ala Ala Gly Ala
 20 25 30

aac gtt gta cgt atg aac ttt tct cac ggc tcg cct gaa gat cac aaa 144
 Asn Val Val Arg Met Asn Phe Ser His Gly Ser Pro Glu Asp His Lys
 35 40 45

atg cgc gcg gat aaa gtt cgt gag att gcc gca aaa ctg ggg cgt cat 192
 Met Arg Ala Asp Lys Val Arg Glu Ile Ala Ala Lys Leu Gly Arg His
 50 55 60

gtg gct att ctg ggt gac ctc cag ggg ccc aaa atc cgt gta tcc acc 240
 Val Ala Ile Leu Gly Asp Leu Gln Gly Pro Lys Ile Arg Val Ser Thr
 65 70 75 80

ttt aaa gaa ggc aaa gtt ttc ctc aat att ggg gat aaa ttc ctg ctc 288
 Phe Lys Glu Gly Lys Val Phe Leu Asn Ile Gly Asp Lys Phe Leu Leu
 85 90 95

gac gcc aac ctg ggt aaa ggt gaa ggc gac aaa gaa aaa gtc ggt atc 336
 Asp Ala Asn Leu Gly Lys Gly Glu Gly Asp Lys Glu Lys Val Gly Ile
 100 105 110

gac tac aaa ggc ctg cct gct gac gtc gtg cct ggt gac atc ctg ctg 384
 Asp Tyr Lys Gly Leu Pro Ala Asp Val Val Pro Gly Asp Ile Leu Leu
 115 120 125

ctg gac gat ggt cgc gtc cag tta aaa gta ctg gaa gtt cag ggc atg 432
 Leu Asp Asp Gly Arg Val Gln Leu Lys Val Leu Glu Val Gln Gly Met
 130 135 140

aaa gtg ttc acc gaa gtc acc gtc ggt ggt ccc ctc tcc aac aat aaa 480
 Lys Val Phe Thr Glu Val Thr Val Gly Gly Pro Leu Ser Asn Asn Lys

atg acc gaa tcg ggt cgt acc gcg ctg atg acc tcc cgt atc agc tct	1200
Met Thr Glu Ser Gly Arg Thr Ala Leu Met Thr Ser Arg Ile Ser Ser	
385 390 395 400	

ggt ctg cca att ttc gcc atg tcg cgc cat gaa cgt acg ctg aac ctg	1248
Gly Leu Pro Ile Phe Ala Met Ser Arg His Glu Arg Thr Leu Asn Leu	
405 410 415	

act gct ctc tat cgt ggc gtt acg ccg gtg cac ttt gat agc gct aat	1296
Thr Ala Leu Tyr Arg Gly Val Thr Pro Val His Phe Asp Ser Ala Asn	
420 425 430	

gac ggc gta gca gct gcc agc gaa gcg gtt aat ctg ctg cgc gat aaa	1344
Asp Gly Val Ala Ala Ala Ser Glu Ala Val Asn Leu Leu Arg Asp Lys	
435 440 445	

ggt tac ttg atg tct ggt gac ctg gtg att gtc acc cag ggc gac gtg	1392
Gly Tyr Leu Met Ser Gly Asp Leu Val Ile Val Thr Gln Gly Asp Val	
450 455 460	

atg agt acc gtg ggt tct act aat acc acg cgt att tta acg gta gag	1440
Met Ser Thr Val Gly Ser Thr Asn Thr Thr Arg Ile Leu Thr Val Glu	
465 470 475 480	

taa	1443
*	

<210> 245
 <211> 720
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(720)

<400> 245	
atg atc aat gta tta att atc gat gac gac gca atg gtc gcg gag ctg	48
Met Ile Asn Val Leu Ile Ile Asp Asp Ala Met Val Ala Glu Leu	
1 5 10 15	

aat cgc cga tac gta gca caa atc cca ggc ttt caa tgc tgt gga aca	96
Asn Arg Arg Tyr Val Ala Gln Ile Pro Gly Phe Gln Cys Cys Gly Thr	
20 25 30	

gcc tcg acg ctg gag aaa gcc aaa gag att atc ttc aat agc gat acg	144
Ala Ser Thr Leu Glu Lys Ala Lys Glu Ile Ile Phe Asn Ser Asp Thr	
35 40 45	

cct atc gac ctg ata ttg ctc gat atc tat atg caa aaa gag aac ggg	192
Pro Ile Asp Leu Ile Leu Leu Asp Ile Tyr Met Gln Lys Glu Asn Gly	
50 55 60	

ctc gat tta ctg cct gtc ctg cat aac gcg cgt tgc aaa agt gat gtg	240
---	-----

1	5	10	15	
ttg agt acc aca gtg atc tta atg gtc agt gcg gta ctg ttc tcg gtg				96
Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val				
20		25	30	
cta ttg gtg gtg cat ctg att tac ttc tcg caa atc agt gat atg acg				144
Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr				
35		40	45	
cga gat ggg cta gcc aac aag gca ctg gca gtg gcg cgt acc ctc gcc				192
Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala				
50		55	60	
gac tcg ccg gaa atc cgt cag gcc ttg cag aaa aaa ccg cag gag agt				240
Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser				
65		70	75	80
ggc atc cag gcc atc gcg gaa gcc gta cgc aaa cgc aac gat ctg ctg				288
Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu				
85		90	95	
ttt att gtc gtt acc gat atg caa agt ctt cgc tac tcg cat cct gaa				336
Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu				
100		105	110	
gcc cag cgt att ggt cag cca ttt aaa ggt gat gac atc ctt aaa gcg				384
Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala				
115		120	125	
ctg aat ggc gaa gaa aat gtc gct atc aat cgc ggt ttt ctg gcg cag				432
Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln				
130		135	140	
gct tta cgc gta ttt acc ccc atc tac gat gaa aat cat aaa caa att				480
Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile				
145		150	155	160
ggc gtg gtg gcg atc ggc ctt gag tta agc cgt gtg acc caa cag atc				528
Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile				
165		170	175	
aat gac agt cgc tgg agc att atc tgg tcg gta tta ttt ggc atg ctg				576
Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu				
180		185	190	
gtc gga ctg att ggc acc tgc att ctg gtt aag gta ctg aaa aaa atc				624
Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile				
195		200	205	
ctt ttc ggc ctg gaa ccc tac gaa atc tcc acg ctg ttt gag caa cgc				672
Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg				
210		215	220	
cag gcc atg ttg cag tct atc aaa gaa ggc gtc gtt gcc gtg gac gat				720
Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp				
225		230	235	240

cgt cac ggc tgg ctg cac tgt gaa gtt aat gat gat gga ccg ggg atc	1440
Arg His Gly Trp Leu His Cys Glu Val Asn Asp Asp Gly Pro Gly Ile	
465 470 475 480	
gca ccc gat aaa atc gat cac att ttt gac aaa ggt gtc tcg aca aaa	1488
Ala Pro Asp Lys Ile Asp His Ile Phe Asp Lys Gly Val Ser Thr Lys	
485 490 495	
gga agc gag cga ggc gtc ggt tta gca ctt gtc aaa caa cag gta gaa	1536
Gly Ser Glu Arg Gly Val Gly Leu Ala Leu Val Lys Gln Gln Val Glu	
500 505 510	
aat ctc ggc ggc agc atc gcc gtg gaa tcg gaa ccc ggg att ttc aca	1584
Asn Leu Gly Gly Ser Ile Ala Val Glu Ser Glu Pro Gly Ile Phe Thr	
515 520 525	
caa ttt ttt gtc cag ata ccc tgg gac ggg gag agg tcg aac aga tga	1632
Gln Phe Phe Val Gln Ile Pro Trp Asp Gly Glu Arg Ser Asn Arg *	
530 535 540	

<210> 247
 <211> 987
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(987)

<400> 247	
ttg agt gta ccg ctg tcg aca tgg aat ctt ctg cga tac aac aat tcg	48
Met Ser Val Pro Leu Ser Thr Trp Asn Leu Leu Arg Tyr Asn Asn Ser	
1 5 10 15	
tat cta cag aag gta act atg ttt cca caa tgc aaa ttt tcc cgc gag	96
Tyr Leu Gln Lys Val Thr Met Phe Pro Gln Cys Lys Phe Ser Arg Glu	
20 25 30	
ttt cta cat cct cgc tac tgg ctc aca tgg ttt ggg ctt ggt gta ctc	144
Phe Leu His Pro Arg Tyr Trp Leu Thr Trp Phe Gly Leu Gly Val Leu	
35 40 45	
tgg ctt tgg gta cag ctt cct tat cct gtt ctc tgc ttt ctc ggc acg	192
Trp Leu Trp Val Gln Leu Pro Tyr Pro Val Leu Cys Phe Leu Gly Thr	
50 55 60	
cgt att ggc gca atg gcg cga cca ttc ctg aaa cgt cgt gaa tct atc	240
Arg Ile Gly Ala Met Ala Arg Pro Phe Leu Lys Arg Arg Glu Ser Ile	
65 70 75 80	
gcc cgt aaa aac ctg gaa ctt tgt ttc ccg cag cat tct gcg gaa gaa	288
Ala Arg Lys Asn Leu Glu Leu Cys Phe Pro Gln His Ser Ala Glu Glu	
85 90 95	
cgc gag aag atg att gcc gaa aac ttt cgt tca ctc ggc atg gcg ctg	336

<210> 248
 <211> 264
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(264)

<400> 248
 ttg gct aat atc aaa tca gct aag aag cgc gcc att cag tct gaa aag 48
 Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1 5 10 15
 gct cgt aag cac aac gca agc cgt cgc tct atg atg cgt act ttc atc 96
 Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
 20 25 30
 aag aaa gta tac gca gct atc gaa gct ggc gac aaa gct gct gca cag 144
 Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
 35 40 45
 aaa gca ttt aac gaa atg caa ccg atc gtg gac cgt cag gct gct aaa 192
 Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
 50 55 60
 ggt ctg atc cac aaa aac aaa gct gca cgt cat aag gct aac ctg act 240
 Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
 65 70 75 80
 gca cag atc aac aaa ctg gct taa 264
 Ala Gln Ile Asn Lys Leu Ala *
 85

<210> 249
 <211> 1293
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1293)

<400> 249
 atg cgc tat aat ggt tta aat aat atg ttt ttc cct ctt tgc ctg att 48
 Met Arg Tyr Asn Gly Leu Asn Asn Met Phe Phe Pro Leu Cys Leu Ile
 1 5 10 15
 aac gat aac cac tct gtc aca agt cca tca cat aca aag aaa aca aaa 96
 Asn Asp Asn His Ser Val Thr Ser Pro Ser His Thr Lys Lys Thr Lys
 20 25 30
 tca gat aat tac agc aaa cat cat aaa aac acg tta att gac aat aaa 144

Ser	Asp	Asn	Tyr	Ser	Lys	His	His	Lys	Asn	Thr	Leu	Ile	Asp	Asn	Lys		
		35					40					45					
gcc	ctc	tct	ctt	ttc	aaa	atg	gat	gat	cat	gaa	aaa	gtg	ata	ggc	ttg	192	
Ala	Leu	Ser	Leu	Phe	Lys	Met	Asp	Asp	His	Glu	Lys	Val	Ile	Gly	Leu		
	50					55				60							
att	cag	aaa	atg	aaa	aga	att	tat	gat	agt	tta	cca	tca	gga	aaa	atc	240	
Ile	Gln	Lys	Met	Lys	Arg	Ile	Tyr	Asp	Ser	Leu	Pro	Ser	Gly	Lys	Ile		
	65				70				75						80		
acg	aaa	gaa	acg	gac	agg	aaa	ata	cat	aaa	tat	ttt	ata	gat	ata	gct	288	
Thr	Lys	Glu	Thr	Asp	Arg	Lys	Ile	His	Lys	Tyr	Phe	Ile	Asp	Ile	Ala		
				85					90					95			
tca	cat	gca	aat	aat	aaa	tgt	gac	gat	aga	att	acg	aga	aga	ggt	tac	336	
Ser	His	Ala	Asn	Asn	Lys	Cys	Asp	Asp	Arg	Ile	Thr	Arg	Arg	Val	Tyr		
			100					105						110			
ctt	aat	aaa	gat	aag	gaa	gtg	tca	att	aag	gtg	gta	tat	ttt	ata	aat	384	
Leu	Asn	Lys	Asp	Lys	Glu	Val	Ser	Ile	Lys	Val	Val	Tyr	Phe	Ile	Asn		
		115					120					125					
aat	gtc	acc	gtc	cat	aat	aat	act	atc	gaa	atc	cca	cag	aca	gta	aat	432	
Asn	Val	Thr	Val	His	Asn	Asn	Thr	Ile	Glu	Ile	Pro	Gln	Thr	Val	Asn		
	130					135					140						
ggt	ggt	tac	gat	ttt	tca	cac	ctt	agc	ctg	aaa	ggt	atc	gtg	att	aaa	480	
Gly	Gly	Tyr	Asp	Phe	Ser	His	Leu	Ser	Leu	Lys	Gly	Ile	Val	Ile	Lys		
	145				150					155					160		
gat	gaa	gat	tta	tcc	aat	tcg	aat	ttt	gca	ggt	tgc	aga	cta	caa	aac	528	
Asp	Glu	Asp	Leu	Ser	Asn	Ser	Asn	Phe	Ala	Gly	Cys	Arg	Leu	Gln	Asn		
				165					170					175			
gct	att	ttt	cag	gac	tgt	aat	atg	tat	aaa	acg	aat	ttt	aat	ttc	gcc	576	
Ala	Ile	Phe	Gln	Asp	Cys	Asn	Met	Tyr	Lys	Thr	Asn	Phe	Asn	Phe	Ala		
			180					185					190				
ata	atg	gaa	aaa	ata	ctt	ttt	gat	aat	tgt	att	ctc	gat	gac	tca	aat	624	
Ile	Met	Glu	Lys	Ile	Leu	Phe	Asp	Asn	Cys	Ile	Leu	Asp	Asp	Ser	Asn		
		195					200					205					
ttc	gct	cag	ata	aaa	atg	act	gac	gga	act	cta	aat	tca	tgt	tcc	gct	672	
Phe	Ala	Gln	Ile	Lys	Met	Thr	Asp	Gly	Thr	Leu	Asn	Ser	Cys	Ser	Ala		
	210					215					220						
atg	cat	gtt	caa	ttc	tac	aat	gca	aca	atg	aat	aga	gcc	aat	att	aaa	720	
Met	His	Val	Gln	Phe	Tyr	Asn	Ala	Thr	Met	Asn	Arg	Ala	Asn	Ile	Lys		
	225				230					235					240		
aat	acc	ttc	ctt	gat	tat	tca	aat	ttt	tat	atg	gca	tac	atg	gct	gag	768	
Asn	Thr	Phe	Leu	Asp	Tyr	Ser	Asn	Phe	Tyr	Met	Ala	Tyr	Met	Ala	Glu		
				245					250					255			
gta	aat	ctt	tat	aaa	gta	ata	gcg	cca	tat	att	aat	tta	ttt	aga	gcc	816	
Val	Asn	Leu	Tyr	Lys	Val	Ile	Ala	Pro	Tyr	Ile	Asn	Leu	Phe	Arg	Ala		

<221> CDS
 <222> (1)...(1992)

<400> 251

atg tcc tca cgt aaa gag ctt gcc aat gct att cgt gcg ctg agc atg	48
Met Ser Ser Arg Lys Glu Leu Ala Asn Ala Ile Arg Ala Leu Ser Met	
1 5 10 15	
 gac gca gta cag aaa gcc aaa tcc ggt cac ccg ggt gcc cct atg ggt	96
Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly	
20 25 30	
 atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac	144
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn	
35 40 45	
 ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac	192
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn	
50 55 60	
 ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac	240
Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr	
65 70 75 80	
 gat ctg ccg atg gaa gaa ctg aaa aac ttc cgt cag ctg cac tct aaa	288
Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys	
85 90 95	
 act ccg ggt cac ccg gaa gtg ggt tac acc gct ggt gtg gaa acc acc	336
Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr	
100 105 110	
 acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att	384
Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile	
115 120 125	
 gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att	432
Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile	
130 135 140	
 gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa	480
Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu	
145 150 155 160	
 ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt	528
Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly	
165 170 175	
 aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac	576
Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His	
180 185 190	
 gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac	624
Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr	
195 200 205	
 ggc tgg cac gtt att cgc gac atc gac ggt cat gac gcg gca tct atc	672

<210> 252
 <211> 459
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(459)

<400> 252
 atg ttc cgg gga gca acg tta gtc aat ctc gac agc aaa ggg cgc tta 48
 Met Phe Arg Gly Ala Thr Leu Val Asn Leu Asp Ser Lys Gly Arg Leu
 1 5 10 15
 tca gtg cct acc cgt tat cgg gaa cag ctg ctt gag aac gct gcc ggt 96
 Ser Val Pro Thr Arg Tyr Arg Glu Gln Leu Leu Glu Asn Ala Ala Gly
 20 25 30
 caa atg gtt tgc acc att gac att tat cac ccg tgc ctg ctg ctt tac 144
 Gln Met Val Cys Thr Ile Asp Ile Tyr His Pro Cys Leu Leu Leu Tyr
 35 40 45
 ccc ctg cct gaa tgg gaa att atc gag caa aaa tta tcg cgt ctg tcg 192
 Pro Leu Pro Glu Trp Glu Ile Ile Glu Gln Lys Leu Ser Arg Leu Ser
 50 55 60
 agc atg aac ccg gtt gag cgc cgt gtg cag cgc cta ctg tta ggt cat 240
 Ser Met Asn Pro Val Glu Arg Arg Val Gln Arg Leu Leu Leu Gly His
 65 70 75 80
 gcc agc gaa tgt cag atg gat ggc gca ggt cga ttg tta atc gcg cca 288
 Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
 85 90 95
 gta ctg cgg caa cat gcc ggg ctg aca aaa gaa gtg atg ctg gtt gga 336
 Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
 100 105 110
 cag ttc aac aag ttt gag ctg tgg gat gaa aca acc tgg cat caa cag 384
 Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
 115 120 125
 gtc aag gaa gat atc gac gca gag cag ttg gct acc gga gac tta tcg 432
 Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
 130 135 140
 gag cga ctg cag gac ttg tct cta taa 459
 Glu Arg Leu Gln Asp Leu Ser Leu *
 145 150

<210> 253
 <211> 942
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(942)

<400> 253

atg atg gaa aac tat aaa cat act acg gtg ctg ctg gat gaa gcc gtt	48
Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val	
1 5 10 15	
aat ggc ctc aat atc cgt cct gat ggc atc tac att gat ggg act ttt	96
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe	
20 25 30	
ggg cgc ggt ggt cac tca cgt ctg atc ctc tcg cag ctt ggc gaa gag	144
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu	
35 40 45	
ggg cgt ttg ctg gcg atc gat cgc gac ccg cag gct atc gcc gtt gcg	192
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala	
50 55 60	
aag act att gat gat ccg cgc ttc tcc atc atc cac gga cct ttc tcc	240
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser	
65 70 75 80	
gcg ctg ggc gaa tac gtt gcc gag cgc gat ctt atc ggc aag atc gac	288
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp	
85 90 95	
ggc att ctc ctc gat ctt ggc gtc tct tca ccg caa ctt gat gat gct	336
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala	
100 105 110	
gaa cgt ggc ttt tcc ttt atg cgc gat ggt ccg ctg gac atg cgt atg	384
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met	
115 120 125	
gac cca acc cgt ggg cag tca gcc gct gaa tgg cta caa acc gca gaa	432
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu	
130 135 140	
gaa gcc gat atc gcc tgg gta ttg aaa acc tat ggt gaa gag cgt ttt	480
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe	
145 150 155 160	
gcc aaa cgc att gcc cgc gcc att gtc gag cgt aac cgc gaa cag ccg	528
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro	
165 170 175	
atg acc cgc acc aaa gaa ctg gcg gaa gtc gtg gct gct gca acg ccg	576
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro	
180 185 190	
gtg aaa gat aag ttt aaa cat ccc gcg acc cgt acc ttc cag gcg gtg	624
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val	
195 200 205	

cgc att tgg gta aac agt gaa ctg gag gag ata gag cag gcg cta aaa 672
 Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
 210 215 220

agc tcg ctc aac gtg ctg gcc ccg ggt ggg cgg ctt tcg atc atc agc 720
 Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
 225 230 235 240

ttc cac tcg ctg gaa gac cgt att gtg aaa cgt ttt atg cgt gaa aac 768
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
245 250 255

agc cgc ggt ccg caa gtt ccg gca ggg tta ccg atg act gaa gag cag 816
 Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
 260 265 270

ctc aaa aaa ctg ggt ggc cgt cag ctg cga gca cta ggc aag tta atg 864
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285

cgc ggc gaa gaa gag gtg gct gag aac cct cgt gcc cgt agt tca gtt 912
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
290 295 300

ctg cgt att gca gag agg acg aat gca tga 942
Leu Arg Ile Ala Glu Arg Thr Asn Ala *
305 310

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<210> 254
<211> 366
<212> DNA
<213> Escherichia coli
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<220> .
<221> CDS
<222> (1) ... (366)
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<400> 254
atg atc agc aga gtg aca gaa gct cta agc aaa gtt aaa gga tgc atg 48
Met Ile Ser Arg Val Thr Glu Ala Leu Ser Lys Val Lys Gly Ser Met
1 5 10 15

gga agc cac gag cgc cat gca ttg cct ggt gtt atc ggt gac gat ctt 96
Gly Ser His Glu Arg His Ala Leu Pro Gly Val Ile Gly Asp Asp Leu
20 25 30

ttg	cga	ttt	ggg	aag	ctg	cca	ctc	tgc	ctg	ttc	att	tgc	att	att	ttg	144
Leu	Arg	Phe	Gly	Lys	Leu	Pro	Leu	Cys	Leu	Phe	Ile	Cys	Ile	Ile	Leu	
		35					40					45				

acg gcg gtg act gtg gta acc acg gcg cac cat acc cgt tta ctg acc 192
Thr Ala Val Thr Val Val Thr Thr Ala His His Thr Arg Leu Leu Thr
50 55 60

gct cag cgc gaa caa ctg gtg ctg gag cga gat gct tta gac att gaa 240

Ala	Gln	Arg	Glu	Gln	Leu	Val	Leu	Glu	Arg	Asp	Ala	Leu	Asp	Ile	Glu	
65					70					75					80	
tgg	cgc	aac	ctg	atc	ctt	gaa	gag	aat	gcg	ctc	ggc	gac	cat	agc	cgg	288
Trp	Arg	Asn	Leu	Ile	Leu	Glu	Glu	Asn	Ala	Leu	Gly	Asp	His	Ser	Arg	
			85						90					95		
gtg	gaa	agg	atc	gcc	acg	gaa	aag	ctg	caa	atg	cag	cat	gtt	gat	ccg	336
Val	Glu	Arg	Ile	Ala	Thr	Glu	Lys	Leu	Gln	Met	Gln	His	Val	Asp	Pro	
			100					105					110			
tca	caa	gaa	aat	atc	gta	gtg	caa	aaa	taa							366
Ser	Gln	Glu	Asn	Ile	Val	Val	Gln	Lys	*							
		115					120									

<210> 255
 <211> 1767
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1767)

<400> 255																
atg	aaa	gca	gcg	gcg	aaa	acg	cag	aaa	cca	aaa	cgt	cag	gaa	gaa	cat	48
Met	Lys	Ala	Ala	Ala	Lys	Thr	Gln	Lys	Pro	Lys	Arg	Gln	Glu	Glu	His	
1				5					10					15		
gcc	aac	ttt	atc	agt	tgg	cgt	ttt	gcg	ttg	tta	tgc	ggc	tgt	att	ctc	96
Ala	Asn	Phe	Ile	Ser	Trp	Arg	Phe	Ala	Leu	Leu	Cys	Gly	Cys	Ile	Leu	
			20					25					30			
ctg	gcg	ctg	gct	ttt	ctg	ctc	gga	cgc	gta	gcg	tgg	tta	caa	gtt	atc	144
Leu	Ala	Leu	Ala	Phe	Leu	Leu	Gly	Arg	Val	Ala	Trp	Leu	Gln	Val	Ile	
		35					40					45				
tcc	ccg	gat	atg	ctg	gtg	aaa	gag	ggc	gac	atg	cgt	tct	ctt	cgc	gtt	192
Ser	Pro	Asp	Met	Leu	Val	Lys	Glu	Gly	Asp	Met	Arg	Ser	Leu	Arg	Val	
	50					55				60						
cag	caa	gtt	tcc	acc	tcc	cgc	ggc	atg	att	act	gac	cgt	tct	ggc	cgc	240
Gln	Gln	Val	Ser	Thr	Ser	Arg	Gly	Met	Ile	Thr	Asp	Arg	Ser	Gly	Arg	
65					70					75					80	
ccg	tta	gcg	gtg	agc	gtg	ccg	gta	aaa	gcg	att	tgg	gct	gac	ccg	aaa	288
Pro	Leu	Ala	Val	Ser	Val	Pro	Val	Lys	Ala	Ile	Trp	Ala	Asp	Pro	Lys	
			85					90					95			
gaa	gtg	cat	gac	gct	ggc	ggt	atc	agc	gtc	ggt	gac	cgc	tgg	aag	gcg	336
Glu	Val	His	Asp	Ala	Gly	Gly	Ile	Ser	Val	Gly	Asp	Arg	Trp	Lys	Ala	
			100				105						110			
ctg	gct	aac	gcg	ctc	aat	att	ccg	ctg	gat	cag	ctt	tca	gcc	cgc	att	384
Leu	Ala	Asn	Ala	Leu	Asn	Ile	Pro	Leu	Asp	Gln	Leu	Ser	Ala	Arg	Ile	
		115					120					125				

acc ggg gta tta cag aag tcg agt aac gtc ggt gtt tcc aag ctg gcg	1104
Thr Gly Val Leu Gln Lys Ser Ser Asn Val Gly Val Ser Lys Leu Ala	
355 360 365	
tta gcg atg ccg tcc tca gcg tta gta gat act tac tca cgt ttt gga	1152
Leu Ala Met Pro Ser Ser Ala Leu Val Asp Thr Tyr Ser Arg Phe Gly	
370 375 380	
ctg gga aaa gcg acc aat ttg ggg ttg gtc gga gaa cgc agt ggc tta	1200
Leu Gly Lys Ala Thr Asn Leu Gly Leu Val Gly Glu Arg Ser Gly Leu	
385 390 395 400	
tat cct caa aaa caa ccg tgg tct gac ata gag agg gcc acc ttc tct	1248
Tyr Pro Gln Lys Gln Arg Trp Ser Asp Ile Glu Arg Ala Thr Phe Ser	
405 410 415	
ttc ggc tac ggg cta atg gta aca cca tta cag tta gcg cga gtc tac	1296
Phe Gly Tyr Gly Leu Met Val Thr Pro Leu Gln Leu Ala Arg Val Tyr	
420 425 430	
gca act atc ggc agc tac ggc att tat cgc cca ctg tcg att acc aaa	1344
Ala Thr Ile Gly Ser Tyr Gly Ile Tyr Arg Pro Leu Ser Ile Thr Lys	
435 440 445	
gtt gac ccc ccg gtt ccc ggt gaa cgt gtc ttc ccg gaa tcc att gtc	1392
Val Asp Pro Pro Val Pro Gly Glu Arg Val Phe Pro Glu Ser Ile Val	
450 455 460	
cgc act gtg gtg cat atg atg gaa agc gtg gcg cta cca ggc ggc ggc	1440
Arg Thr Val Val His Met Met Glu Ser Val Ala Leu Pro Gly Gly Gly	
465 470 475 480	
ggc gtg aag gcg gcg att aaa ggc tat cgt atc gcc att aaa acc ggt	1488
Gly Val Lys Ala Ala Ile Lys Gly Tyr Arg Ile Ala Ile Lys Thr Gly	
485 490 495	
acc gcg aaa aag gtc ggg ccg gac ggt cgc tac atc aat aaa tat att	1536
Thr Ala Lys Lys Val Gly Pro Asp Gly Arg Tyr Ile Asn Lys Tyr Ile	
500 505 510	
gct tat acc gca ggc gtt gcg cct gcg agt cag ccg cgc ttc gcg ctg	1584
Ala Tyr Thr Ala Gly Val Ala Pro Ala Ser Gln Pro Arg Phe Ala Leu	
515 520 525	
gtt gtt gtt atc aac gat ccg cag gcg ggt aaa tac tac ggc ggc gcc	1632
Val Val Val Ile Asn Asp Pro Gln Ala Gly Lys Tyr Tyr Gly Gly Ala	
530 535 540	
gtt tcc gcg ccg gtc ttt ggt gcc atc atg ggc ggc gta ttg cgt acc	1680
Val Ser Ala Pro Val Phe Gly Ala Ile Met Gly Gly Val Leu Arg Thr	
545 550 555 560	
atg aac atc gag ccg gat gcg ctg aca acg ggc gat aaa aat gaa ttt	1728
Met Asn Ile Glu Pro Asp Ala Leu Thr Thr Gly Asp Lys Asn Glu Phe	
565 570 575	
gtg att aat caa ggc gag ggg aca ggt ggc aga tcg taa	1767

Val Ile Asn Gln Gly Glu Gly Thr Gly Gly Arg Ser *
 580 585

<210> 256
 <211> 1488
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1488)

<400> 256
 gtg gca gat cgt aat ttg cgc gac ctt ctt gct ccg tgg gtg cca gac 48
 Met Ala Asp Arg Asn Leu Arg Asp Leu Leu Ala Pro Trp Val Pro Asp
 1 5 10 15
 gca cct tcg cga gca ctg cga gag atg aca ctc gac agc cgt gtg gct 96
 Ala Pro Ser Arg Ala Leu Arg Glu Met Thr Leu Asp Ser Arg Val Ala
 20 25 30
 gcg gcg ggc gat ctc ttt gta gct gta gta ggt cat cag gcg gac ggg 144
 Ala Ala Gly Asp Leu Phe Val Ala Val Val Gly His Gln Ala Asp Gly
 35 40 45
 cgt cga tat atc ccg cag gcg ata gcg caa ggt gtg gct gcc att att 192
 Arg Arg Tyr Ile Pro Gln Ala Ile Ala Gln Gly Val Ala Ala Ile Ile
 50 55 60
 gca gag gcg aaa gat gag gcg acc gat ggt gaa atc cgt gaa atg cac 240
 Ala Glu Ala Lys Asp Glu Ala Thr Asp Gly Glu Ile Arg Glu Met His
 65 70 75 80
 ggc gta ccg gtc atc tat ctc agc cag ctc aac gag cgt tta tct gca 288
 Gly Val Pro Val Ile Tyr Leu Ser Gln Leu Asn Glu Arg Leu Ser Ala
 85 90 95
 ctg gcg ggc cgc ttt tac cat gaa ccc tct gac aat tta cgt ctc gtg 336
 Leu Ala Gly Arg Phe Tyr His Glu Pro Ser Asp Asn Leu Arg Leu Val
 100 105 110
 ggc gta acg ggc acc aac ggc aaa acc acg act acc cag ctg ttg gcg 384
 Gly Val Thr Gly Thr Asn Gly Lys Thr Thr Thr Thr Gln Leu Leu Ala
 115 120 125
 cag tgg agc caa ctg ctt ggc gaa atc agc gcg gta atg ggc acc gtt 432
 Gln Trp Ser Gln Leu Leu Gly Glu Ile Ser Ala Val Met Gly Thr Val
 130 135 140
 ggt aac ggc ctg ctg ggg aaa gtg atc ccg aca gaa aat aca acc ggt 480
 Gly Asn Gly Leu Leu Gly Lys Val Ile Pro Thr Glu Asn Thr Thr Gly
 145 150 155 160
 tcg gca gtc gat gtt cag cat gag ctg gcg ggg ctg gtg gat cag ggc 528
 Ser Ala Val Asp Val Gln His Glu Leu Ala Gly Leu Val Asp Gln Gly
 165 170 175

305	310	315	320	
caa ctg gca gaa aac cag ttg ctg ctc gac gac tcc tac aac gcc aat				1008
Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn				
	325	330	335	
gtc ggt tca atg act gca gca gtc cag gta ctg gct gaa atg ccg ggc				1056
Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly				
	340	345	350	
tac cgc gtg ctg gtg gtg ggc gat atg gcg gaa ctg ggc gct gaa agc				1104
Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser				
	355	360	365	
gaa gcc tgc cat gta cag gtg ggc gag gcg gca aaa gct gct ggt att				1152
Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile				
	370	375	380	
gac cgc gtg tta agc gtg ggt aaa caa agc cat gct atc agc acc gcc				1200
Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala				
	385	390	395	400
agc ggc gtt ggc gaa cat ttt gct gat aaa act gcg tta att acg cgt				1248
Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg				
	405	410	415	
ctt aaa tta ctg att gct gag caa cag gta att acg att tta gtt aag				1296
Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys				
	420	425	430	
ggc tca cgt agt gcc gcc atg gaa gag gta gta cgc gct tta cag gag				1344
Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu				
	435	440	445	
aat ggg aca tgt tag				1359
Asn Gly Thr Cys *				
	450			

<210> 258
 <211> 1083
 <212> DNA
 <213> Escherichia coli
 <220>
 <221> CDS
 <222> (1)...(1083)

<400> 258	
atg tta gtt tgg ctg gcc gaa cat ttg gtc aaa tat tat tcc ggc ttt	48
Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe	
1 5 10 15	
aac gtc ttt tcc tat ctg acg ttt cgc gcc atc gtc agc ctg ctg acc	96
Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr	
20 25 30	

gcg Ala	ctg Leu	ttc Phe 35	atc Ile	tca Ser	ttg Leu	tgg Trp	atg Met 40	ggc Gly	ccg Pro	cgt Arg	atg Met	att Ile 45	gct Ala	cat His	ttg Leu	144
caa Gln	aaa Lys 50	ctt Leu	tcc Ser	ttt Phe	ggg Gly 55	cag Gln	gtg Val	gtg Val	cgt Arg	aac Asn	gac Asp 60	ggg Gly	cct Pro	gaa Glu	tca Ser	192
cac His 65	ttc Phe	agc Ser	aag Lys	cgc Arg	ggg Gly 70	acg Thr	ccg Pro	acc Thr	atg Met	ggc Gly 75	ggg Gly	att Ile	atg Met	atc Ile	ctg Leu 80	240
acg Thr	gcg Ala	att Ile	gtg Val	atc Ile 85	tcc Ser	gta Val	ctg Leu	ctg Leu	tgg Trp 90	gct Ala	tac Tyr	ccg Pro	tcc Ser	aat Asn 95	ccg Pro	288
tac Tyr	gtc Val	tgg Trp 100	tgc Cys	gtg Val	ttg Leu	gtg Val	gtg Val	ctg Leu 105	gta Val	ggg Gly	tac Tyr	ggg Gly	gtt Val 110	att Ile	ggc Gly	336
ttt Phe	gtt Val	gat Asp 115	gat Asp	tat Tyr	cgc Arg	aaa Lys	gtg Val 120	gtg Val	cgt Arg	aaa Lys	gac Asp	acc Thr 125	aaa Lys	ggg Gly	ttg Leu	384
atc Ile 130	gct Ala	cgt Arg	tgg Trp	aag Lys	tat Tyr	ttc Phe 135	tgg Trp	atg Met	tcg Ser	gtc Val	att Ile 140	gcg Ala	ctg Leu	ggg Gly	gtc Val	432
gcc Ala 145	ttc Phe	gcc Ala	ctg Leu	tac Tyr	ctt Leu 150	gcc Ala	ggc Gly	aaa Lys	gac Asp	acg Thr 155	ccc Pro	gca Ala	acg Thr	cag Gln	ctg Leu 160	480
gtg Val	gtc Val	cca Pro	ttc Phe	ttt Phe 165	aaa Lys	gat Asp	gtg Val	atg Met	ccg Pro 170	cag Gln	ctg Leu	ggg Gly	ctg Leu	ttc Phe 175	tac Tyr	528
att Ile	ctg Leu	ctg Leu	gct Ala 180	tac Tyr	ttc Phe	gtc Val	att Ile	gtg Val 185	ggg Gly	act Thr	ggc Gly	aac Asn 190	gcg Ala	gta Val	aac Asn	576
ctg Leu	acc Thr 195	gat Asp	ggg Gly	ctc Leu	gac Asp	ggc Gly	ctg Leu 200	gca Ala	att Ile	atg Met	ccg Pro 205	acc Thr	gta Val	ttt Phe	gtc Val	624
gcc Ala 210	ggg Gly	ggg Gly	ttt Phe	gcg Ala	ctg Leu	gtg Val 215	gcg Ala	tgg Trp	gcg Ala	acc Thr	ggc Gly 220	aac Asn	atg Met	aac Asn	ttt Phe	672
gcc Ala 225	agc Ser	tac Tyr	ttg Leu	cat His	ata Ile 230	ccg Pro	tat Tyr	ctg Leu	cga Arg	cac His 235	gcc Ala	ggg Gly	gaa Glu	ctg Leu	gtt Val 240	720
att Ile	gtc Val	tgt Cys	acc Thr	gcg Ala 245	ata Ile	gtc Val	ggg Gly	gca Ala	gga Gly 250	ctg Leu	ggc Gly	ttc Phe	ctg Leu	tgg Trp 255	ttt Phe	768
aac	acc	tat	ccg	gcg	cag	gtc	ttt	atg	ggc	gat	gta	ggg	tcg	ctg	gcg	816

gaa gtt gtg ctg gag cat aac ggc gta cgt tgg att aac gat tcg aaa	960
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys	
305 310 315 320	
gcg acc aac gtc ggc agt acg gaa gcg gcg ctg aat ggc ctg cac gta	1008
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val	
325 330 335	
gac ggc aca ctg cat ttg ttg ctg ggt ggc gat ggt aaa tcg gcg gac	1056
Asp Gly Thr Leu His Leu Leu Leu Gly Gly Asp Gly Lys Ser Ala Asp	
340 345 350	
ttt agc cca ctg gcg cgt tac ctg aat ggc gat aac gta cgt ctg tat	1104
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr	
355 360 365	
tgt ttc ggt cgt gac ggc gcg cag ctg gcg gcg cta cgc ccg gaa gtg	1152
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val	
370 375 380	
gca gaa caa acc gaa act atg gaa cag gcg atg cgc ttg ctg gct ccg	1200
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro	
385 390 395 400	
cgt gtt cag ccg ggc gat atg gtt ctg ctc tcc cca gcc tgt gcc agc	1248
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser	
405 410 415	
ctt gat cag ttc aag aac ttt gaa caa cga ggc aat gag ttt gcc cgt	1296
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg	
420 425 430	
ctg gcg aag gag tta ggt tga	1317
Leu Ala Lys Glu Leu Gly *	
435	

<210> 260

<211> 1245

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(1245)

<400> 260

atg cgt tta tct ctc cct cgc ctg aaa atg ccg cgc ctg cca gga ttc	48
Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe	
1 5 10 15	

agt atc ctg gtc tgg atc tcc acg gcg cta aag ggc tgg gtg atg ggc	96
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly	
20 25 30	

tcg cgg gaa aaa gat acc gac agc ctg atc atg tac gat cgc acc tta	144
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu	

Val	Val	Cys	Arg	Ser	Gly	Ala	Leu	Thr	Val	Ser	Glu	Ile	Ala	Ala	Ala		
			260					265					270				
gga	cta	ccg	gcg	ttg	ttt	gtg	ccg	ttt	caa	cat	aaa	gac	cgc	cag	caa	864	
Gly	Leu	Pro	Ala	Leu	Phe	Val	Pro	Phe	Gln	His	Lys	Asp	Arg	Gln	Gln		
		275					280					285					
tac	tgg	aat	gcg	cta	ccg	ctg	gaa	aaa	gcg	ggc	gca	gcc	aaa	att	atc	912	
Tyr	Trp	Asn	Ala	Leu	Pro	Leu	Glu	Lys	Ala	Gly	Ala	Ala	Lys	Ile	Ile		
	290					295					300						
gag	cag	cca	cag	ctt	agc	gtg	gat	gct	gtc	gcc	aac	acc	ctg	gcc	ggg	960	
Glu	Gln	Pro	Gln	Leu	Ser	Val	Asp	Ala	Val	Ala	Asn	Thr	Leu	Ala	Gly		
305					310					315					320		
tgg	tcg	cga	gaa	acc	tta	tta	acc	atg	gca	gaa	cgc	gcc	cgc	gct	gca	1008	
Trp	Ser	Arg	Glu	Thr	Leu	Leu	Thr	Met	Ala	Glu	Arg	Ala	Arg	Ala	Ala		
			325						330					335			
tcc	att	ccg	gat	gcc	acc	gag	cga	gtg	gca	aat	gaa	gtg	agc	cgg	gtt	1056	
Ser	Ile	Pro	Asp	Ala	Thr	Glu	Arg	Val	Ala	Asn	Glu	Val	Ser	Arg	Val		
			340					345					350				
gcc	cgg	gcg	taa													1068	
Ala	Arg	Ala	*														
		355															
<210>	262																
<211>	1476																
<212>	DNA																
<213>	Escherichia coli																
<220>																	
<221>	CDS																
<222>	(1)...(1476)																
<400>	262																
atg	aat	aca	caa	caa	ttg	gca	aaa	ctg	cgt	tcc	atc	gtg	ccc	gaa	atg	48	
Met	Asn	Thr	Gln	Gln	Leu	Ala	Lys	Leu	Arg	Ser	Ile	Val	Pro	Glu	Met		
1				5				10					15				
cgt	cgc	gtt	cgg	cac	ata	cat	ttt	gtc	ggc	att	ggg	ggg	gcc	ggg	atg	96	
Arg	Arg	Val	Arg	His	Ile	His	Phe	Val	Gly	Ile	Gly	Gly	Ala	Gly	Met		
			20					25					30				
ggc	ggg	att	gcc	gaa	gtt	ctg	gcc	aat	gaa	ggg	tat	cag	atc	agt	ggg	144	
Gly	Gly	Ile	Ala	Glu	Val	Leu	Ala	Asn	Glu	Gly	Tyr	Gln	Ile	Ser	Gly		
		35				40						45					
tcc	gat	tta	gcg	cca	aat	ccg	gtc	acg	cag	cag	tta	atg	aat	ctg	ggg	192	
Ser	Asp	Leu	Ala	Pro	Asn	Pro	Val	Thr	Gln	Gln	Leu	Met	Asn	Leu	Gly		
	50					55					60						
gcg	acg	att	tat	ttc	aac	cat	cgc	ccg	gaa	aac	gta	cgt	gat	gcc	agc	240	
Ala	Thr	Ile	Tyr	Phe	Asn	His	Arg	Pro	Glu	Asn	Val	Arg	Asp	Ala	Ser		
65				70				75							80		

acg gaa gag ggc att gac gac gag gct att ttg cgg gcg ctt gaa agc	960
Thr Glu Glu Gly Ile Asp Asp Glu Ala Ile Leu Arg Ala Leu Glu Ser	
305 310 315 320	
ttc cag ggg act ggt cgc cgt ttt gat ttc ctc ggt gaa ttc ccg ctg	1008
Phe Gln Gly Thr Gly Arg Arg Phe Asp Phe Leu Gly Glu Phe Pro Leu	
325 330 335	
gag cca gtg aat ggt aaa agc ggt acg gca atg ctg gtc gat gac tac	1056
Glu Pro Val Asn Gly Lys Ser Gly Thr Ala Met Leu Val Asp Asp Tyr	
340 345 350	
ggc cac cac ccg acg gaa gtg gac gcc acc att aaa gcg gcg cgc gca	1104
Gly His His Pro Thr Glu Val Asp Ala Thr Ile Lys Ala Ala Arg Ala	
355 360 365	
ggc tgg ccg gat aaa aac ctg gta atg ctg ttt cag ccg cac cgt ttt	1152
Gly Trp Pro Asp Lys Asn Leu Val Met Leu Phe Gln Pro His Arg Phe	
370 375 380	
acc cgt acg cgc gac ctg tat gat gat ttc gcc aat gtg ctg acg cag	1200
Thr Arg Thr Arg Asp Leu Tyr Asp Asp Phe Ala Asn Val Leu Thr Gln	
385 390 395 400	
gtt gat acc ctg ttg atg ctg gaa gtg tat ccg gct ggc gaa gcg cca	1248
Val Asp Thr Leu Leu Met Leu Glu Val Tyr Pro Ala Gly Glu Ala Pro	
405 410 415	
att ccg gga gcg gac agc cgt tgc ctg tgt cgc aca att cgt gga cgt	1296
Ile Pro Gly Ala Asp Ser Arg Ser Leu Cys Arg Thr Ile Arg Gly Arg	
420 425 430	
ggg aaa att gat ccc att ctg gtg ccg gat ccg gcg cgg gta gcc gag	1344
Gly Lys Ile Asp Pro Ile Leu Val Pro Asp Pro Ala Arg Val Ala Glu	
435 440 445	
atg ctg gca ccg gta tta acc ggt aac gac ctg att ctc gtt cag ggg	1392
Met Leu Ala Pro Val Leu Thr Gly Asn Asp Leu Ile Leu Val Gln Gly	
450 455 460	
gct ggt aat att gga aaa att gcc cgt tct tta gct gaa atc aaa ctg	1440
Ala Gly Asn Ile Gly Lys Ile Ala Arg Ser Leu Ala Glu Ile Lys Leu	
465 470 475 480	
aag ccg caa act ccg gag gaa gaa caa cat gac tga	1476
Lys Pro Gln Thr Pro Glu Glu Glu Gln His Asp *	
485 490	

<210> 263
 <211> 921
 <212> DNA
 <213> Escherichia coli

 <220>
 <221> CDS
 <222> (1)...(921)

<400> 263

atg act gat aaa atc gcg gtc ctg ttg ggt ggg acc tcc gct gag cgg	48
Met Thr Asp Lys Ile Ala Val Leu Leu Gly Gly Thr Ser Ala Glu Arg	
1 5 10 15	
gaa gtt tct ctg aat tct ggc gca gcg gtg tta gcc gga ctg cgt gaa	96
Glu Val Ser Leu Asn Ser Gly Ala Val Leu Ala Gly Leu Arg Glu	
20 25 30	
ggc ggt att gac gcg tat cct gtc gac ccg aaa gaa gtc gac gtg acg	144
Gly Gly Ile Asp Ala Tyr Pro Val Asp Pro Lys Glu Val Asp Val Thr	
35 40 45	
caa ctg aag tcg atg ggc ttt cag aaa gtg ttt atc gcg cta cac ggt	192
Gln Leu Lys Ser Met Gly Phe Gln Lys Val Phe Ile Ala Leu His Gly	
50 55 60	
cgc ggc ggt gaa gat ggt acg ctg cag ggg atg ctc gag ctg atg ggc	240
Arg Gly Gly Glu Asp Gly Thr Leu Gln Gly Met Leu Glu Leu Met Gly	
65 70 75 80	
ttg cct tat acc gga agc gga gtg atg gca tct gcg ctt tca atg gat	288
Leu Pro Tyr Thr Gly Ser Gly Val Met Ala Ser Ala Leu Ser Met Asp	
85 90 95	
aaa cta cgc agc aaa ctt cta tgg caa ggt gcc ggt tta ccg gtc gcg	336
Lys Leu Arg Ser Lys Leu Leu Trp Gln Gly Ala Gly Leu Pro Val Ala	
100 105 110	
ccg tgg gta gcg tta acc cgc gca gag ttt gaa aaa ggc ctg agc gat	384
Pro Trp Val Ala Leu Thr Arg Ala Glu Phe Glu Lys Gly Leu Ser Asp	
115 120 125	
aag cag tta gca gaa att tct gct ctg ggt ttg ccg gtt atc gtt aag	432
Lys Gln Leu Ala Glu Ile Ser Ala Leu Gly Leu Pro Val Ile Val Lys	
130 135 140	
ccg agc cgc gaa ggt tcc agt gtg gga atg tca aaa gta gta gca gaa	480
Pro Ser Arg Glu Gly Ser Ser Val Gly Met Ser Lys Val Val Ala Glu	
145 150 155 160	
aat gct cta caa gat gca tta aga ttg gca ttt cag cac gat gaa gaa	528
Asn Ala Leu Gln Asp Ala Leu Arg Leu Ala Phe Gln His Asp Glu Glu	
165 170 175	
gta ttg att gaa aaa tgg cta agt ggg ccg gag ttc acg gtt gcg ata	576
Val Leu Ile Glu Lys Trp Leu Ser Gly Pro Glu Phe Thr Val Ala Ile	
180 185 190	
ctc ggt gaa gaa att tta ccg tca ata cgt att caa ccg tcc gga acc	624
Leu Gly Glu Glu Ile Leu Pro Ser Ile Arg Ile Gln Pro Ser Gly Thr	
195 200 205	
ttc tat gat tat gag gcg aag tat ctc tct gat gag aca cag tat ttc	672
Phe Tyr Asp Tyr Glu Ala Lys Tyr Leu Ser Asp Glu Thr Gln Tyr Phe	
210 215 220	

gac agt aag cgt cac ggc acc cag ggc gaa aag ctg gat ctg gct ctg	240
Asp Ser Lys Arg His Gly Thr Gln Gly Glu Lys Leu Asp Leu Ala Leu	
65 70 75 80	
ctg gtg gac ggc ctg caa gct gag cgc gaa cag ggc atc acc att gac	288
Leu Val Asp Gly Leu Gln Ala Glu Arg Glu Gln Gly Ile Thr Ile Asp	
85 90 95	
gtg gcc tac cgc tat ttc tct acc gag aag cgt aaa ttt att atc gcc	336
Val Ala Tyr Arg Tyr Phe Ser Thr Glu Lys Arg Lys Phe Ile Ile Ala	
100 105 110	
gac acc cca ggg cac gag cag tac acc cgc aat atg gcg act ggc gca	384
Asp Thr Pro Gly His Glu Gln Tyr Thr Arg Asn Met Ala Thr Gly Ala	
115 120 125	
tcg aca tgt gaa ctg gcg atc tta ctg atc gat gcc cgt aaa ggc gtg	432
Ser Thr Cys Glu Leu Ala Ile Leu Leu Ile Asp Ala Arg Lys Gly Val	
130 135 140	
ctc gat caa acc cgt cgt cac agt ttt atc tcc aca ctg ttg ggg atc	480
Leu Asp Gln Thr Arg Arg His Ser Phe Ile Ser Thr Leu Leu Gly Ile	
145 150 155 160	
aaa cat ctg gtc gtg gcg atc aac aaa atg gat ctg gtg gat tac agt	528
Lys His Leu Val Val Ala Ile Asn Lys Met Asp Leu Val Asp Tyr Ser	
165 170 175	
gaa gag acg ttc acc cgt att cgt gaa gat tat ttg acc ttt gcc ggg	576
Glu Glu Thr Phe Thr Arg Ile Arg Glu Asp Tyr Leu Thr Phe Ala Gly	
180 185 190	
cag ctg ccg ggt aat ctg gat atc cgc ttt gtg ccg ctc tct gca ctg	624
Gln Leu Pro Gly Asn Leu Asp Ile Arg Phe Val Pro Leu Ser Ala Leu	
195 200 205	
gaa ggc gac aac gtg gca tcg caa agt gaa agt atg ccg tgg tac agc	672
Glu Gly Asp Asn Val Ala Ser Gln Ser Glu Ser Met Pro Trp Tyr Ser	
210 215 220	
ggt ccg aca ctg ctc gaa gtg ctg gaa acc gtg gag atc cag cga gtg	720
Gly Pro Thr Leu Leu Glu Val Leu Glu Thr Val Glu Ile Gln Arg Val	
225 230 235 240	
gtg gat gct cag cca atg cgc ttc ccg gtg cag tac gtt aat cgc ccg	768
Val Asp Ala Gln Pro Met Arg Phe Pro Val Gln Tyr Val Asn Arg Pro	
245 250 255	
aat ctc gat ttt cgt ggt tac gcc gga acg ctg gca tcc ggt cgc gtg	816
Asn Leu Asp Phe Arg Gly Tyr Ala Gly Thr Leu Ala Ser Gly Arg Val	
260 265 270	
gaa gtc ggg caa cgt gtc aaa gtg ctg ccc tct ggt gtg gaa tca aac	864
Glu Val Gly Gln Arg Val Lys Val Leu Pro Ser Gly Val Glu Ser Asn	
275 280 285	

<400> 266

atg	cgc	cat	cgt	aag	agt	ggt	cgt	caa	ctg	aac	cgc	aac	agc	agc	cat	48
Met	Arg	His	Arg	Lys	Ser	Gly	Arg	Gln	Leu	Asn	Arg	Asn	Ser	Ser	His	
1				5					10					15		

cgc	cag	gct	atg	ttc	cgc	aat	atg	gca	ggt	tca	ctg	ggt	cgt	cat	gaa	96
Arg	Gln	Ala	Met	Phe	Arg	Asn	Met	Ala	Gly	Ser	Leu	Val	Arg	His	Glu	
		20						25					30			

atc	atc	aag	acg	act	ctg	cct	aaa	gcg	aaa	gag	ctg	cgc	cgc	gta	ggt	144
Ile	Ile	Lys	Thr	Thr	Leu	Pro	Lys	Ala	Lys	Glu	Leu	Arg	Arg	Val	Val	
		35					40					45				

gag	ccg	ctg	att	act	ctt	gcc	aag	act	gat	agc	ggt	gct	aat	cgt	cgt	192
Glu	Pro	Leu	Ile	Thr	Leu	Ala	Lys	Thr	Asp	Ser	Val	Ala	Asn	Arg	Arg	
	50					55					60					

ctg	gca	ttc	gcc	cgt	act	cgt	gat	aac	gag	atc	gtg	gca	aaa	ctg	ttt	240
Leu	Ala	Phe	Ala	Arg	Thr	Arg	Asp	Asn	Glu	Ile	Val	Ala	Lys	Leu	Phe	
65					70					75					80	

aac	gaa	ctg	ggc	ccg	cgt	ttc	gcg	agc	cgt	gcc	ggt	ggt	tac	act	cgt	288
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Ala	Ser	Arg	Ala	Gly	Gly	Tyr	Thr	Arg	
				85					90					95		

att	ctg	aag	tgt	ggc	ttc	cgt	gca	ggc	gac	aac	gcg	ccg	atg	gct	tac	336
Ile	Leu	Lys	Cys	Gly	Phe	Arg	Ala	Gly	Asp	Asn	Ala	Pro	Met	Ala	Tyr	
		100						105					110			

atc	gag	ctg	ggt	gat	cgt	tca	gag	aaa	gca	gaa	gct	gct	gca	gag	taa	384
Ile	Glu	Leu	Val	Asp	Arg	Ser	Glu	Lys	Ala	Glu	Ala	Ala	Ala	Glu	*	
		115					120					125				

<210> 267

<211> 990

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(990)

<400> 267

atg	cag	ggt	tct	gtg	aca	gag	ttt	cta	aaa	ccg	cgc	ctg	ggt	gat	atc	48
Met	Gln	Gly	Ser	Val	Thr	Glu	Phe	Leu	Lys	Pro	Arg	Leu	Val	Asp	Ile	
1				5					10					15		

gag	caa	gtg	agt	tcg	acg	cac	gcc	aag	gtg	acc	ctt	gag	cct	tta	gag	96
Glu	Gln	Val	Ser	Ser	Thr	His	Ala	Lys	Val	Thr	Leu	Glu	Pro	Leu	Glu	
		20					25					30				

cgt	ggc	ttt	ggc	cat	act	ctg	ggt	aac	gca	ctg	cgc	cgt	att	ctg	ctc	144
Arg	Gly	Phe	Gly	His	Thr	Leu	Gly	Asn	Ala	Leu	Arg	Arg	Ile	Leu	Leu	
		35					40					45				

tca tgc atg ccg ggt tgc gcg gtg acc gag gtt gag att gat ggt gta	192
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val	
50 55 60	
cta cat gag tac agc acc aaa gaa ggc gtt cag gaa gat atc ctg gaa	240
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu	
65 70 75 80	
atc ctg ctc aac ctg aaa ggg ctg gcg gtg aga gtt cag ggc aaa gat	288
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp	
85 90 95	
gaa gtt att ctt acc ttg aat aaa tct ggc att ggc cct gtg act gca	336
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala	
100 105 110	
gcc gat atc acc cac gac ggt gat gtc gaa atc gtc aag ccg cag cac	384
Ala Asp Ile Thr His Asp Gly Asp Val Glu Ile Val Lys Pro Gln His	
115 120 125	
gtg atc tgc cac ctg acc gat gag aac gcg tct att agc atg cgt atc	432
Val Ile Cys His Leu Thr Asp Glu Asn Ala Ser Ile Ser Met Arg Ile	
130 135 140	
aaa gtt cag cgc ggt cgt ggt tat gtg ccg gct tct acc cga att cat	480
Lys Val Gln Arg Gly Arg Gly Tyr Val Pro Ala Ser Thr Arg Ile His	
145 150 155 160	
tgc gaa gaa gat gag cgc cca atc ggc cgt ctg ctg gtc gac gca tgc	528
Ser Glu Glu Asp Glu Arg Pro Ile Gly Arg Leu Leu Val Asp Ala Cys	
165 170 175	
tac agc cct gtg gag cgt att gcc tac aat gtt gaa gca gcg cgt gta	576
Tyr Ser Pro Val Glu Arg Ile Ala Tyr Asn Val Glu Ala Ala Arg Val	
180 185 190	
gaa cag cgt acc gac ctg gac aag ctg gtc atc gaa atg gaa acc aac	624
Glu Gln Arg Thr Asp Leu Asp Lys Leu Val Ile Glu Met Glu Thr Asn	
195 200 205	
ggc aca atc gat cct gaa gag gcg att cgt cgt gcg gca acc att ctg	672
Gly Thr Ile Asp Pro Glu Glu Ala Ile Arg Arg Ala Ala Thr Ile Leu	
210 215 220	
gct gaa caa ctg gaa gct ttc gtt gac tta cgt gat gta cgt cag cct	720
Ala Glu Gln Leu Glu Ala Phe Val Asp Leu Arg Asp Val Arg Gln Pro	
225 230 235 240	
gaa gtg aaa gaa gag aaa cca gag ttc gat ccg atc ctg ctg cgc cct	768
Glu Val Lys Glu Glu Lys Pro Glu Phe Asp Pro Ile Leu Leu Arg Pro	
245 250 255	
gtt gac gat ctg gaa ttg act gtc cgc tct gct aac tgc ctt aaa gca	816
Val Asp Asp Leu Glu Leu Thr Val Arg Ser Ala Asn Cys Leu Lys Ala	
260 265 270	

gaa gct atc cac tat atc ggt gat ctg gta cag cgt acc gag gtt gag	864
Glu Ala Ile His Tyr Ile Gly Asp Leu Val Gln Arg Thr Glu Val Glu	
275 280 285	
ctc ctt aaa acg cct aac ctt ggt aaa aaa tct ctt act gag att aaa	912
Leu Leu Lys Thr Pro Asn Leu Gly Lys Lys Ser Leu Thr Glu Ile Lys	
290 295 300	
gac gtg ctg gct tcc cgt gga ctg tct ctg ggc atg cgc ctg gaa aac	960
Asp Val Leu Ala Ser Arg Gly Leu Ser Leu Gly Met Arg Leu Glu Asn	
305 310 315 320	
tgg cca ccg gca agc atc gct gac gag taa	990
Trp Pro Pro Ala Ser Ile Ala Asp Glu *	
325	

<210> 268
 <211> 621
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(621)

<400> 268	
atg gca aga tat ttg ggt cct aag ctg aag ctg agc cgt cgt gag ggc	48
Met Ala Arg Tyr Leu Gly Pro Lys Leu Lys Leu Ser Arg Arg Glu Gly	
1 5 10 15	
acc gac tta ttc ctt aag tct ggc gtt cgc gcg atc gat acc aag tgt	96
Thr Asp Leu Phe Leu Lys Ser Gly Val Arg Ala Ile Asp Thr Lys Cys	
20 25 30	
aaa att gaa caa gct cct ggc cag cac ggt gcg cgt aaa ccg cgt ctg	144
Lys Ile Glu Gln Ala Pro Gly Gln His Gly Ala Arg Lys Pro Arg Leu	
35 40 45	
tct gac tat ggt gtg cag ttg cgt gaa aag caa aaa gtt cgc cgt atc	192
Ser Asp Tyr Gly Val Gln Leu Arg Glu Lys Gln Lys Val Arg Arg Ile	
50 55 60	
tat ggt gtg ctg gag cgt cag ttc cgt aac tac tac aaa gaa gca gca	240
Tyr Gly Val Leu Glu Arg Gln Phe Arg Asn Tyr Tyr Lys Glu Ala Ala	
65 70 75 80	
cgt ctg aaa ggc aac acc ggt gaa aac ctg ttg gct ctg ctg gaa ggt	288
Arg Leu Lys Gly Asn Thr Gly Glu Asn Leu Leu Ala Leu Leu Glu Gly	
85 90 95	
cgt ctg gac aac gtt gta tac cgt atg ggc ttc ggt gcc act cgt gca	336
Arg Leu Asp Asn Val Val Tyr Arg Met Gly Phe Gly Ala Thr Arg Ala	
100 105 110	
gaa gca cgt cag ctg gtt agc cat aaa gca att atg gta aac ggt cgt	384
Glu Ala Arg Gln Leu Val Ser His Lys Ala Ile Met Val Asn Gly Arg	

115	120	125	
gtt gtt aac atc gct tct tat cag gtt agt ccg aat gac gtt gta agc			432
Val Val Asn Ile Ala Ser Tyr Gln Val Ser Pro Asn Asp Val Val Ser			
130	135	140	
att cgt gag aaa gcg aag aag cag tct cgc gtg aaa gcc gct ctg gag			480
Ile Arg Glu Lys Ala Lys Lys Gln Ser Arg Val Lys Ala Ala Leu Glu			
145	150	155	160
ctg gct gag cag cgt gaa aag cca acc tgg ctg gaa gtt gat gct ggc			528
Leu Ala Glu Gln Arg Glu Lys Pro Thr Trp Leu Glu Val Asp Ala Gly			
165	170	175	
aag atg gaa ggt acg ttt aag cgt aag ccg gag cgt tct gat ctg tct			576
Lys Met Glu Gly Thr Phe Lys Arg Lys Pro Glu Arg Ser Asp Leu Ser			
180	185	190	
gcg gac att aac gaa cac ctg atc gtc gag ctt tac tcc aag taa			621
Ala Asp Ile Asn Glu His Leu Ile Val Glu Leu Tyr Ser Lys *			
195	200	205	

<210> 269
 <211> 390
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(390)

<400> 269	
atg gca aag gca cca att cgt gca cgt aaa cgt gta aga aaa caa gtc	48
Met Ala Lys Ala Pro Ile Arg Ala Arg Lys Arg Val Arg Lys Gln Val	
1 5 10 15	
tct gac ggc gtg gct cat atc cat gct tct ttc aac aac acc atc gtg	96
Ser Asp Gly Val Ala His Ile His Ala Ser Phe Asn Asn Thr Ile Val	
20 25 30	
act atc act gat cgt cag ggt aac gcg ttg ggt tgg gca aca gcc ggt	144
Thr Ile Thr Asp Arg Gln Gly Asn Ala Leu Gly Trp Ala Thr Ala Gly	
35 40 45	
ggt tcc ggt ttc cgt ggt tct cgc aaa tcc act ccg ttt gca gct cag	192
Gly Ser Gly Phe Arg Gly Ser Arg Lys Ser Thr Pro Phe Ala Ala Gln	
50 55 60	
gtt gca gca gag cgt tgc gct gac gcc gtg aaa gaa tac ggc atc aag	240
Val Ala Ala Glu Arg Cys Ala Asp Ala Val Lys Glu Tyr Gly Ile Lys	
65 70 75 80	
aat ctg gaa gtt atg gtt aaa ggt ccg ggt cca ggc cgc gaa tct act	288
Asn Leu Glu Val Met Val Lys Gly Pro Gly Pro Gly Arg Glu Ser Thr	
85 90 95	

att cgt gct ctg aac gcc gca ggt ttc cgc atc act aac att act gat	336
Ile Arg Ala Leu Asn Ala Ala Gly Phe Arg Ile Thr Asn Ile Thr Asp	
100 105 110	
gtg act ccg atc cct cat aac ggt tgt cgt ccg ccg aaa aaa cgt cgc	384
Val Thr Pro Ile Pro His Asn Gly Cys Arg Pro Pro Lys Lys Arg Arg	
115 120 125	
gta taa	390
Val *	

<210> 270
 <211> 357
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(357)

<400> 270	
gtg gcc cgt ata gca ggc att aac att cct gat cat aag cat gcc gta	48
Met Ala Arg Ile Ala Gly Ile Asn Ile Pro Asp His Lys His Ala Val	
1 5 10 15	
atc gca tta act tcg att tat ggc gtc ggc aag acc cgt tct aaa gcc	96
Ile Ala Leu Thr Ser Ile Tyr Gly Val Gly Lys Thr Arg Ser Lys Ala	
20 25 30	
atc ctg gct gca gcg ggt atc gct gaa gat gtt aag atc agt gag ctg	144
Ile Leu Ala Ala Ala Gly Ile Ala Glu Asp Val Lys Ile Ser Glu Leu	
35 40 45	
tct gaa gga caa atc gac acg ctg cgt gac gaa gtt gcc aaa ttt gtc	192
Ser Glu Gly Gln Ile Asp Thr Leu Arg Asp Glu Val Ala Lys Phe Val	
50 55 60	
gtt gaa ggt gat ctg cgc cgt gaa atc agc atg agc atc aag cgc ctg	240
Val Glu Gly Asp Leu Arg Arg Glu Ile Ser Met Ser Ile Lys Arg Leu	
65 70 75 80	
atg gat ctt ggt tgc tat cgc ggt ttg cgt cat cgt cgt ggt ctc ccg	288
Met Asp Leu Gly Cys Tyr Arg Gly Leu Arg His Arg Arg Gly Leu Pro	
85 90 95	
gtt cgc ggt cag cgt acc aag acc aac gca cgt acc cgt aag ggt ccg	336
Val Arg Gly Gln Arg Thr Lys Thr Asn Ala Arg Thr Arg Lys Gly Pro	
100 105 110	
cgc aaa ccg atc aag aaa taa	357
Arg Lys Pro Ile Lys Lys *	
115	

<210> 271
 <211> 1383
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1383)

<400> 271
 atg acg caa tta acc atg aaa gac aaa att ggc tac ggg ctg gga gac 48
 Met Thr Gln Leu Thr Met Lys Asp Lys Ile Gly Tyr Gly Leu Gly Asp
 1 5 10 15
 acc gcc tgc ggc ttc gtc tgg cag gcc acg atg ttc ctg ctg gcc tat 96
 Thr Ala Cys Gly Phe Val Trp Gln Ala Thr Met Phe Leu Leu Ala Tyr
 20 25 30
 ttc tac acc gac gtc ttc ggc ctg tcg gcg ggg att atg ggc acg ctg 144
 Phe Tyr Thr Asp Val Phe Gly Leu Ser Ala Gly Ile Met Gly Thr Leu
 35 40 45
 ttt ttg gtc tcc cgc gtg ctc gac gcc gtc acc gac ccg ctg atg ggg 192
 Phe Leu Val Ser Arg Val Leu Asp Ala Val Thr Asp Pro Leu Met Gly
 50 55 60
 ctg ctg gta gac cgc acc cgc acg ccg cac ggc cag ttc cgc ccg ttc 240
 Leu Leu Val Asp Arg Thr Arg Thr Arg His Gly Gln Phe Arg Pro Phe
 65 70 75 80
 ctg ctg tgg ggg gcc atc ccg ttc ggc atc gtc tgc gtg ctg acc ttc 288
 Leu Leu Trp Gly Ala Ile Pro Phe Gly Ile Val Cys Val Leu Thr Phe
 85 90 95
 tac acg ccg gac ttc tcc gca cag ggc aag atc atc tac gcc tgc gtg 336
 Tyr Thr Pro Asp Phe Ser Ala Gln Gly Lys Ile Ile Tyr Ala Cys Val
 100 105 110
 acc tac att ctc ctg acc ctg gtc tac acc ttc gtt aac gtg ccg tac 384
 Thr Tyr Ile Leu Leu Thr Leu Val Tyr Thr Phe Val Asn Val Pro Tyr
 115 120 125
 tgc gcc atg ccg ggc gtc atc acc gcc gac ccg aaa gag cgt cac gcc 432
 Cys Ala Met Pro Gly Val Ile Thr Ala Asp Pro Lys Glu Arg His Ala
 130 135 140
 ctg cag tcc tgg cgc ttc ttc ctg gcg gcg gcg ggc tcg ctc gct atc 480
 Leu Gln Ser Trp Arg Phe Phe Leu Ala Ala Ala Gly Ser Leu Ala Ile
 145 150 155 160
 agc ggc atc gcg ctg ccg ctg gtg agc atc atc ggc aaa ggg gac gag 528
 Ser Gly Ile Ala Leu Pro Leu Val Ser Ile Ile Gly Lys Gly Asp Glu
 165 170 175
 cag gtg ggc tac ttc ggc gcc atg tgc gtg ctg ggg ctg agc ggc gtg 576
 Gln Val Gly Tyr Phe Gly Ala Met Cys Val Leu Gly Leu Ser Gly Val
 180 185 190

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gcg ggc atg ttc atc atg ctg tgc ctc tac aag ctc acc gat gcc cgc	1296
Ala Gly Met Phe Ile Met Leu Ser Leu Tyr Lys Leu Thr Asp Ala Arg	
420 425 430	
gtg gag gcc atc agc cgg cag ctg att aag cac cgc gcg gcg cag ggc	1344
Val Glu Ala Ile Ser Arg Gln Leu Ile Lys His Arg Ala Ala Gln Gly	
435 440 445	
gag gcc gtt ccc gac gcc gcg aca gcc gca tcc cat taa	1383
Glu Ala Val Pro Asp Ala Ala Thr Ala Ala Ser His *	
450 455 460	

<210> 272
 <211> 1611
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1611)

<400> 272	
atg gaa atc act aac ccg ata ctc acc ggc ttc aac ccg gac ccg tcc	48
Met Glu Ile Thr Asn Pro Ile Leu Thr Gly Phe Asn Pro Asp Pro Ser	
1 5 10 15	
ctg tgc cgc cag ggc gag gac tac tac atc gcc acc tcg acc ttc gag	96
Leu Cys Arg Gln Gly Glu Asp Tyr Tyr Ile Ala Thr Ser Thr Phe Glu	
20 25 30	
tgg ttc ccg ggc gtg cgc atc tac cac tcc cgt gac ctg aaa aac tgg	144
Trp Phe Pro Gly Val Arg Ile Tyr His Ser Arg Asp Leu Lys Asn Trp	
35 40 45	
tcg ctg gtc agc acc ccg ttg gac cgc gtg tcg atg ctg gac atg aag	192
Ser Leu Val Ser Thr Pro Leu Asp Arg Val Ser Met Leu Asp Met Lys	
50 55 60	
ggc aac ccg gac tcc ggc ggc atc tgg gcg ccg tgc ctg agc tac gcc	240
Gly Asn Pro Asp Ser Gly Gly Ile Trp Ala Pro Cys Leu Ser Tyr Ala	
65 70 75 80	
gac ggt aaa ttc tgg ctg ctc tac acc gac gtg aag att gtc gac tcg	288
Asp Gly Lys Phe Trp Leu Leu Tyr Thr Asp Val Lys Ile Val Asp Ser	
85 90 95	
ccg tgg aaa aac ggc cgc aac ttc ctc gtc acc gcg ccc tcc atc gag	336
Pro Trp Lys Asn Gly Arg Asn Phe Leu Val Thr Ala Pro Ser Ile Glu	
100 105 110	
ggg cca tgg agc gag cca atc ccg atg ggc aac ggc ggg ttt gac ccg	384
Gly Pro Trp Ser Glu Pro Ile Pro Met Gly Asn Gly Gly Phe Asp Pro	
115 120 125	
tcc ctg ttc cac gac gac gat ggc cgc aaa tac tat atc tac cgc ccg	432
Ser Leu Phe His Asp Asp Asp Gly Arg Lys Tyr Tyr Ile Tyr Arg Pro	

225	230	235	240	
cag gta aaa gcg gca ttg ttg tca tct	cag gat tta tct gtt tat tct	768		
Gln Val Lys Ala Leu Leu Ser Ser	Gln Asp Leu Ser Val Tyr Ser			
245	250	255		
atg aat acc cca ggg ttt att ccc ggt att gat ttc tct gac cac ctg	816			
Met Asn Thr Pro Gly Phe Ile Pro Gly Ile Asp Phe Ser Asp His Leu				
260	265	270		
aat tat tgg caa cac gat att ccc gcc ata atg att act gac acc gct	864			
Asn Tyr Trp Gln His Asp Ile Pro Ala Ile Met Ile Thr Asp Thr Ala				
275	280	285		
ttt tat cgt aat aaa caa tac cac ttg ccc ggt gat acc gca gac aga	912			
Phe Tyr Arg Asn Lys Gln Tyr His Leu Pro Gly Asp Thr Ala Asp Arg				
290	295	300		
ttg aat tat cag aaa atg gct cag gta gtg gat ggt gtt ata act ttg	960			
Leu Asn Tyr Gln Lys Met Ala Gln Val Val Asp Gly Val Ile Thr Leu				
305	310	315	320	
tta tac aac agt aaa taa	978			
Leu Tyr Asn Ser Lys *				
325				
<210> 274				
<211> 963				
<212> DNA				
<213> Escherichia coli				
<220>				
<221> CDS				
<222> (1)...(963)				
<400> 274				
gtg atg atc aaa acg cgt ttt tct cgc tgg cta acg ttt ttt acg ttc	48			
Met Met Ile Lys Thr Arg Phe Ser Arg Trp Leu Thr Phe Phe				
1 5 10 15				
gcc gct gcc gtg gcg ctg gcg cta ccg gca aaa gcc aac acc tgg ccg	96			
Ala Ala Ala Val Ala Leu Ala Leu Pro Ala Lys Ala Asn Thr Trp Pro				
20 25 30				
ctg ccg cca gcg ggc agt cgt ctg gtt ggc gaa aac aaa ttt cat gtg	144			
Leu Pro Pro Ala Gly Ser Arg Leu Val Gly Glu Asn Lys Phe His Val				
35 40 45				
gtg gaa aat gac ggt ggt tct ctg gaa gcc atc gcc aaa aaa tac aac	192			
Val Glu Asn Asp Gly Gly Ser Leu Glu Ala Ile Ala Lys Lys Tyr Asn				
50 55 60				
gtc ggc ttt ctc gct ctg tta cag gct aac ccc ggc gtt gat cct tac	240			
Val Gly Phe Leu Ala Leu Leu Gln Ala Asn Pro Gly Val Asp Pro Tyr				
65 70 75 80				

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gta ccg cgc gcg ggc agc gtg tta acg atc ccg ttg caa acc cta ctt	288
Val Pro Arg Ala Gly Ser Val Leu Thr Ile Pro Leu Gln Thr Leu Leu	
85 90 95	
cca gat gcg ccg cgc gaa ggc att gtg atc aac att gcg gag ctg cgt	336
Pro Asp Ala Pro Arg Glu Gly Ile Val Ile Asn Ile Ala Glu Leu Arg	
100 105 110	
ctc tat tac tac ccg ccg ggt aaa aat tgc gta acc gtg tat cca ata	384
Leu Tyr Tyr Tyr Pro Pro Gly Lys Asn Ser Val Thr Val Tyr Pro Ile	
115 120 125	
ggg att ggt cag tta ggt ggt gac acg ctg aca ccg aca atg gtg acc	432
Gly Ile Gly Gln Leu Gly Gly Asp Thr Leu Thr Pro Thr Met Val Thr	
130 135 140	
acc gtt tca gac aaa cgt gca aac cca acc tgg acg cca acg gca aac	480
Thr Val Ser Asp Lys Arg Ala Asn Pro Thr Trp Thr Pro Thr Ala Asn	
145 150 155 160	
atc cgc gcc cgt tat aaa gca cag gga att gag ttg cct gcg gta gtg	528
Ile Arg Ala Arg Tyr Lys Ala Gln Gly Ile Glu Leu Pro Ala Val Val	
165 170 175	
ccg gct gga ctg gat aac cca atg ggc cat cat gcg att cgt ctg gcg	576
Pro Ala Gly Leu Asp Asn Pro Met Gly His His Ala Ile Arg Leu Ala	
180 185 190	
gcc tat ggc ggc gtt tat ttg ctt cat ggt acg aac gcc gat ttc ggc	624
Ala Tyr Gly Gly Val Tyr Leu Leu His Gly Thr Asn Ala Asp Phe Gly	
195 200 205	
att ggc atg cgg gta agt tct ggc tgt att cgt ctg cgg gat gac gat	672
Ile Gly Met Arg Val Ser Ser Gly Cys Ile Arg Leu Arg Asp Asp Asp	
210 215 220	
atc aaa aca ctc ttt agc cag gtc acc cca ggc acc aaa gtg aat atc	720
Ile Lys Thr Leu Phe Ser Gln Val Thr Pro Gly Thr Lys Val Asn Ile	
225 230 235 240	
atc aac act ccg ata aaa gtc tct gcc gaa cca aac ggt gcg cgt ctg	768
Ile Asn Thr Pro Ile Lys Val Ser Ala Glu Pro Asn Gly Ala Arg Leu	
245 250 255	
gtt gaa gta cat cag ccg ctg tca gag aag att gat gac gat ccg cag	816
Val Glu Val His Gln Pro Leu Ser Glu Lys Ile Asp Asp Pro Gln	
260 265 270	
ctg ctg cca att acg ctg aat agc gca atg caa tca ttt aaa gat gca	864
Leu Leu Pro Ile Thr Leu Asn Ser Ala Met Gln Ser Phe Lys Asp Ala	
275 280 285	
gca caa act gac gct gaa gtg atg caa cat gtg atg gat gtc cgt tcc	912
Ala Gln Thr Asp Ala Glu Val Met Gln His Val Met Asp Val Arg Ser	
290 295 300	
ggg atg ccg gtg gat gtc cgc cgt cat caa gtg agc cca caa acg ctg	960

Gly Met Pro Val Asp Val Arg Arg His Gln Val Ser Pro Gln Thr Leu
 305 310 315 320

taa 963
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<210> 275
 <211> 1485
 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (1)...(1485)

<400> 275
 gtg gtc gca atc cat ctt ttg ccg gtt agt tac aat tct gcg aca tcc 48
 Met Val Ala Ile His Leu Leu Pro Val Ser Tyr Asn Ser Ala Thr Ser
 1 5 10 15
 acc gtg aat atc agt gct aga atc ata ccc ctg ttg att att cac caa 96
 Thr Val Asn Ile Ser Ala Arg Ile Ile Pro Leu Leu Ile Ile His Gln
 20 25 30
 aga tat aaa att cct atg cca aaa gtt cag gcc gac ggc ctg cca ttg 144
 Arg Tyr Lys Ile Pro Met Pro Lys Val Gln Ala Asp Gly Leu Pro Leu
 35 40 45
 ccc cag cga tac ggt gcg ata tta acc att gtg att ggt att tcg atg 192
 Pro Gln Arg Tyr Gly Ala Ile Leu Thr Ile Val Ile Gly Ile Ser Met
 50 55 60
 gcc gtc ctt gac ggc gca atc gcc aac gtc gcc ctg cca aca atc gcc 240
 Ala Val Leu Asp Gly Ala Ile Ala Asn Val Ala Leu Pro Thr Ile Ala
 65 70 75 80
 acg gac ctt cat gcc acg cca gcc agt tcc atc tgg gta gtg aac gcc 288
 Thr Asp Leu His Ala Thr Pro Ala Ser Ser Ile Trp Val Val Asn Ala
 85 90 95
 tat caa atc gcc att gtc atc tcc ctg ctc tcg ttt tcg ttt ctg ggc 336
 Tyr Gln Ile Ala Ile Val Ile Ser Leu Leu Ser Phe Ser Phe Leu Gly
 100 105 110
 gat atg ttt ggc tat cga cgt att tat aaa tgc ggt ctg gtc gtt ttt 384
 Asp Met Phe Gly Tyr Arg Arg Ile Tyr Lys Cys Gly Leu Val Val Phe
 115 120 125
 ctg ttg tct tca ctg ttc tgc gcc ctt tct gat tcg ctg caa atg ctc 432
 Leu Leu Ser Ser Leu Phe Cys Ala Leu Ser Asp Ser Leu Gln Met Leu
 130 135 140
 acc ctt gcg cgt gtc ata caa ggt ttc ggc ggt gca gcg ttg atg agc 480
 Thr Leu Ala Arg Val Ile Gln Gly Phe Gly Ala Ala Leu Met Ser
 145 150 155 160

290	295	300	
ccg atc gag ctg gaa aat gct gta cgt gga cgt gca gat aca ggc ttt			960
Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe			
305	310	315	320
ggc gtg atg acc gaa gag gaa ctg aag ctg gcc gta gcg gca gcg cgt			1008
Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg			
	325	330	335
aaa cgt ggt gaa aaa gtg gtg atg acc aac ggt gtc ttt gac atc ctg			1056
Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu			
	340	345	350
cac gcc ggg cac gtc tct tat ctg gca aat gcc cgc aag ctg ggt gac			1104
His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp			
	355	360	365
cgc ttg att gtt gcc gtc aac agc gat gcc tcc acc aaa cgg ctg aaa			1152
Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys			
	370	375	380
ggg gat tcc cgc ccg gta aac cca ctc gaa cag cgt atg att gtg ctg			1200
Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu			
	385	390	400
ggc gca ctg gaa gcg gtc gac tgg gta gtg tcg ttt gaa gag gac acg			1248
Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr			
	405	410	415
ccg cag cgc ttg atc gcc ggg atc ttg cca gat ctg ctg gtg aaa ggc			1296
Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly			
	420	425	430
ggc gac tat aaa cca gaa gag att gcc ggg agt aaa gaa gtc tgg gcc			1344
Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala			
	435	440	445
aac ggt ggc gaa gtg ttg gtg ctc aac ttt gaa gac ggt tgc tcg acg			1392
Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr			
	450	455	460
acc aac atc atc aag aag atc caa cag gat aaa aaa ggc taa			1434
Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly *			
465	470	475	

<210> 277
 <211> 2841
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(2841)

cat	ctg	gca	tta	cag	gaa	ttg	ccg	ggc	cat	gtg	tcg	gag	gat	tgc	ttc	2784
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe	
		915					920					925				

acc	gca	gag	cgt	gaa	ctg	gtg	cgg	gca	agc	tgg	cag	aag	tgg	ctg	gtg	2832
Thr	Ala	Glu	Arg	Glu	Leu	Val	Arg	Ala	Ser	Trp	Gln	Lys	Trp	Leu	Val	
		930				935						940				

gaa	gaa	tga														2841
Glu	Glu	*														
		945														

<210> 278
 <211> 1302
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1302)

<400>	278																
atg	gct	cag	gaa	atc	gaa	tta	aag	ttt	att	gtt	aat	cac	agt	gcc	gtt	48	
Met	Ala	Gln	Glu	Ile	Glu	Leu	Lys	Phe	Ile	Val	Asn	His	Ser	Ala	Val		
	1			5					10					15			

gag	gcg	ttg	cgt	gac	cat	ctc	aat	acg	ctg	ggc	ggc	gag	cac	cat	gac	96
Glu	Ala	Leu	Arg	Asp	His	Leu	Asn	Thr	Leu	Gly	Gly	Glu	His	His	Asp	
			20					25					30			

ccc	gtg	cag	ttg	ctg	aat	att	tac	tac	gaa	acg	ccg	gat	aac	tgg	ctg	144
Pro	Val	Gln	Leu	Leu	Asn	Ile	Tyr	Tyr	Glu	Thr	Pro	Asp	Asn	Trp	Leu	
		35				40						45				

cgt	ggg	cac	gat	atg	ggc	tta	cgt	att	cgt	ggc	gaa	aac	ggg	cgc	tat	192
Arg	Gly	His	Asp	Met	Gly	Leu	Arg	Ile	Arg	Gly	Glu	Asn	Gly	Arg	Tyr	
	50					55					60					

gag	atg	acc	atg	aaa	gtt	gca	gga	aga	gtg	aca	ggc	ggc	tta	cat	cag	240
Glu	Met	Thr	Met	Lys	Val	Ala	Gly	Arg	Val	Thr	Gly	Gly	Leu	His	Gln	
	65				70				75						80	

cgc	ccg	gaa	tat	aac	gtg	gcg	ttg	agc	gaa	ccg	acg	ctc	gac	ctg	gcg	288
Arg	Pro	Glu	Tyr	Asn	Val	Ala	Leu	Ser	Glu	Pro	Thr	Leu	Asp	Leu	Ala	
				85					90					95		

cag	tta	ccg	acg	gaa	gtc	tgg	ccg	aac	ggc	gaa	ttg	ccc	gcc	gat	ctc	336
Gln	Leu	Pro	Thr	Glu	Val	Trp	Pro	Asn	Gly	Glu	Leu	Pro	Ala	Asp	Leu	
		100					105						110			

gcc	tcc	cgc	gtg	cag	ccg	ctg	ttc	agc	acc	gat	ttt	tat	cgc	gaa	aaa	384
Ala	Ser	Arg	Val	Gln	Pro	Leu	Phe	Ser	Thr	Asp	Phe	Tyr	Arg	Glu	Lys	
		115				120						125				

tgg	ctg	gtg	gcg	gtc	gat	ggg	agc	caa	att	gaa	atc	gcc	ctc	gac	cag	432
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ttg cca cgc ctg acg cgt gat att gac tca ata ctg ttg ctg gcg ggt 1152
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly
 370 375 380

tac tat gat cct gtc gtc gcg caa gcc tgg ctg gag aac tgg cag ggg 1200
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
 385 390 395 400

ctg cat cac gct att gcg acc ggg caa cgc atc gaa att gaa cat ttc 1248
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
 405 410 415

cgt aat gag gca aac aat cag gaa ccg ttc tgg ttg cac agc gga aaa 1296
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
 420 425 430

cgt taa 1302
 Arg *

<210> 279
 <211> 624
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(624)

<400> 279
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 Met Leu Asn Lys Leu Ser Leu Leu Leu Lys Asp Ala Gly Ile Ser Leu
 1 5 10 15

acc gat cac cag aaa aac cag ctt att gcc tac gtg aat atg ctg cat 96
 Thr Asp His Gln Lys Asn Gln Leu Ile Ala Tyr Val Asn Met Leu His
 20 25 30

aaa tgg aac aaa gcg tac aac ctg act tcg gtc cgc gat cct aat gag 144
 Lys Trp Asn Lys Ala Tyr Asn Leu Thr Ser Val Arg Asp Pro Asn Glu
 35 40 45

atg ctg gta cgc cat att ctc gat agc att gtg gtg gca ccg tat ctg 192
 Met Leu Val Arg His Ile Leu Asp Ser Ile Val Val Ala Pro Tyr Leu
 50 55 60

caa ggt gaa cgg ttt atc gat gtc ggc acc gga cca gga ctg cca ggc 240
 Gln Gly Glu Arg Phe Ile Asp Val Gly Thr Gly Pro Gly Leu Pro Gly
 65 70 75 80

att cca ctc tct atc gtg cgt cct gaa gcc cat ttc act ctg ttg gat 288
 Ile Pro Leu Ser Ile Val Arg Pro Glu Ala His Phe Thr Leu Leu Asp
 85 90 95

ttt gcc cct gcg ttg aca gac gaa cag gcg gcg gaa cag gtt gag att	1632
Phe Ala Pro Ala Leu Thr Asp Glu Gln Ala Ala Glu Gln Val Glu Ile	
530 535 540	
cag gtt aaa tac gaa ggt tat atc gcg cgc cag caa gat gag atc gaa	1680
Gln Val Lys Tyr Glu Gly Tyr Ile Ala Arg Gln Gln Asp Glu Ile Glu	
545 550 555 560	
aag cag ctg cgt aac gag aac acc ctg cta ccc gcg aca ctg gat tac	1728
Lys Gln Leu Arg Asn Glu Asn Thr Leu Leu Pro Ala Thr Leu Asp Tyr	
565 570 575	
cgc cag gta tcc ggt ctt tct aac gaa gtg atc gcc aaa ctt aac gat	1776
Arg Gln Val Ser Gly Leu Ser Asn Glu Val Ile Ala Lys Leu Asn Asp	
580 585 590	
cac aaa cca gcc tct atc ggc caa gct tcg cgt att tct ggc gtc acg	1824
His Lys Pro Ala Ser Ile Gly Gln Ala Ser Arg Ile Ser Gly Val Thr	
595 600 605	
cct gcg gcc atc tcc att ctg ctg gtg tgg ctg aaa aaa cag ggt atg	1872
Pro Ala Ala Ile Ser Ile Leu Leu Val Trp Leu Lys Lys Gln Gly Met	
610 615 620	
ctg cgt cgt agc gca taa	1890
Leu Arg Arg Ser Ala *	
625	
<210> 281	
<211> 444	
<212> DNA	
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<222> (1)...(444)	
<400> 281	
atg gca gat atc act ctt atc agc ggc agc acc ctc ggc ggt gcc gaa	48
Met Ala Asp Ile Thr Leu Ile Ser Gly Ser Thr Leu Gly Gly Ala Glu	
1 5 10 15	
tat gta gca gaa cac ctg gct gaa aag ctg gaa gag gcg ggt ttt acc	96
Tyr Val Ala Glu His Leu Ala Glu Lys Leu Glu Glu Ala Gly Phe Thr	
20 25 30	
acc gaa acg ctg cac ggt ccg ctg tta gaa gat tta cct gcc tca ggg	144
Thr Glu Thr Leu His Gly Pro Leu Leu Glu Asp Leu Pro Ala Ser Gly	
35 40 45	
atc tgg ctg gtt atc agc tcc acc cac ggt gcc gga gat att ccg gac	192
Ile Trp Leu Val Ile Ser Ser Thr His Gly Ala Gly Asp Ile Pro Asp	
50 55 60	
aac ctt tct cct ttc tat gaa gca ttg cag gaa cag aag ccc gat ctt	240

ctc act cac ctt gag cag ctg caa aaa cac cag gga aat acc att gaa	336
Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu	
100 105 110	
att cgt tac acc acg cat gaa caa ttc aaa caa caa acc gca gaa agt	384
Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser	
115 120 125	
cag gcg gta att cgc agc gga gaa tgt tct ccg tat gcg aat atc att	432
Gln Ala Val Ile Arg Ser Gly Glu Cys Ser Pro Tyr Ala Asn Ile Ile	
130 135 140	
ctc tgt gct ggc gtg acg ttc tga	456
Leu Cys Ala Gly Val Thr Phe *	
145 150	

<210> 283
 <211> 1506
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(1506)

<400> 283	
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Met Glu Ala Leu Leu Gln Leu Lys Gly Ile Asp Lys Ala Phe Pro Gly	
1 5 10 15	
gta aaa gcc ctc tcg ggc gca gcg tta aat gtc tat ccg ggc cgc gtg	96
Val Lys Ala Leu Ser Gly Ala Ala Leu Asn Val Tyr Pro Gly Arg Val	
20 25 30	
atg gcg ctg gtg ggc gaa aac ggc gcg ggt aaa tcc acc atg atg aaa	144
Met Ala Leu Val Gly Glu Asn Gly Ala Gly Lys Ser Thr Met Met Lys	
35 40 45	
gtg ctt act ggc atc tat act cgc gat gcc ggt acg ctt tta tgg ctg	192
Val Leu Thr Gly Ile Tyr Thr Arg Asp Ala Gly Thr Leu Leu Trp Leu	
50 55 60	
ggg aaa gaa acg aca ttt acc ggg cca aaa tct tcc cag gaa gcc ggg	240
Gly Lys Glu Thr Thr Phe Thr Gly Pro Lys Ser Ser Gln Glu Ala Gly	
65 70 75 80	
att ggg att atc cat cag gaa ctg aac ctg atc ccg cag ttg acc att	288
Ile Gly Ile Ile His Gln Glu Leu Asn Leu Ile Pro Gln Leu Thr Ile	
85 90 95	
gcc gaa aac att ttc ctc ggt cgt gag ttt gtt aat cgc ttt ggc aaa	336
Ala Glu Asn Ile Phe Leu Gly Arg Glu Phe Val Asn Arg Phe Gly Lys	
100 105 110	
att gac tgg aaa acc atg tat gcc gaa gcg gat aaa ttg ctg gct aaa	384

Arg	Leu	Ser	Ser	Ala	Gln	Pro	Thr	Ala	Gly	Thr	Gly	Tyr	Glu	Leu	Asp	
				245					250					255		
gct	att	gct	gcg	gtg	gtt	ctg	ggc	ggt	acg	agt	ctg	gcg	ggc	gga	aaa	816
Ala	Ile	Ala	Ala	Val	Val	Leu	Gly	Gly	Thr	Ser	Leu	Ala	Gly	Gly	Lys	
			260				265					270				
ggt	cgc	att	gtt	ggg	acg	ttg	atc	ggc	gca	tta	att	ctt	ggc	ttc	ctt	864
Gly	Arg	Ile	Val	Gly	Thr	Leu	Ile	Gly	Ala	Leu	Ile	Leu	Gly	Phe	Leu	
		275				280						285				
aat	aat	gga	ttg	aat	ttg	tta	ggt	gtt	tcc	tcc	tat	tac	cag	atg	atc	912
Asn	Asn	Gly	Leu	Asn	Leu	Leu	Gly	Val	Ser	Ser	Tyr	Tyr	Gln	Met	Ile	
	290					295					300					
gtc	aaa	gcg	gtg	gtg	att	ttg	ctg	gcg	gtg	ctg	gta	gac	aac	aaa	aag	960
Val	Lys	Ala	Val	Val	Ile	Leu	Leu	Ala	Val	Leu	Val	Asp	Asn	Lys	Lys	
305					310					315					320	
cag	taa															966
Gln	*															

<210> 285
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)...(891)

<400>	285															
atg	aac	atg	aaa	aaa	ctg	gct	acc	ctg	gtt	tcc	gct	gtt	gcg	cta	agc	48
Met	Asn	Met	Lys	Lys	Leu	Ala	Thr	Leu	Val	Ser	Ala	Val	Ala	Leu	Ser	
1				5					10					15		
gcc	acc	gtc	agt	gcg	aat	gcg	atg	gca	aaa	gac	acc	atc	gcg	ctg	gtg	96
Ala	Thr	Val	Ser	Ala	Asn	Ala	Met	Ala	Lys	Asp	Thr	Ile	Ala	Leu	Val	
			20				25						30			
gtc	tcc	acg	ctt	aac	aac	ccg	ttc	ttt	gta	tcg	ctg	aaa	gat	ggc	gcg	144
Val	Ser	Thr	Leu	Asn	Asn	Pro	Phe	Phe	Val	Ser	Leu	Lys	Asp	Gly	Ala	
			35				40					45				
cag	aaa	gag	gcg	gat	aaa	ctt	ggc	tat	aac	ctg	gtg	gtg	ctg	gac	tcc	192
Gln	Lys	Glu	Ala	Asp	Lys	Leu	Gly	Tyr	Asn	Leu	Val	Val	Leu	Asp	Ser	
	50					55					60					
cag	aac	aac	ccg	gcg	aaa	gag	ctg	gcg	aac	gtg	cag	gac	tta	acc	gtt	240
Gln	Asn	Asn	Pro	Ala	Lys	Glu	Leu	Ala	Asn	Val	Gln	Asp	Leu	Thr	Val	
	65				70				75					80		
cgc	ggc	aca	aaa	att	ctg	ctg	att	aac	ccg	acc	gac	tcc	gac	gca	gtg	288
Arg	Gly	Thr	Lys	Ile	Leu	Leu	Ile	Asn	Pro	Thr	Asp	Ser	Asp	Ala	Val	
				85					90					95		

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(930)

<400> 286

atg	caa	aac	gca	ggc	agc	ctc	gtt	gtt	ctt	ggc	agc	att	aat	gct	gac	48
Met	Gln	Asn	Ala	Gly	Ser	Leu	Val	Val	Leu	Gly	Ser	Ile	Asn	Ala	Asp	
1				5					10					15		
cac	att	ctt	aat	ctt	caa	tct	ttt	cct	act	cca	ggc	gaa	acc	gta	acc	96
His	Ile	Leu	Asn	Leu	Gln	Ser	Phe	Pro	Thr	Pro	Gly	Glu	Thr	Val	Thr	
			20					25					30			
ggt	aac	cac	tat	cag	gtt	gca	ttt	ggc	ggc	aaa	ggc	gcg	aat	cag	gct	144
Gly	Asn	His	Tyr	Gln	Val	Ala	Phe	Gly	Gly	Lys	Gly	Ala	Asn	Gln	Ala	
		35					40					45				
gtg	gct	gct	ggg	cgt	agc	ggt	gcg	aat	atc	gcg	ttt	att	gcc	tgt	acg	192
Val	Ala	Ala	Gly	Arg	Ser	Gly	Ala	Asn	Ile	Ala	Phe	Ile	Ala	Cys	Thr	
	50					55				60						
ggt	gat	gac	agc	att	ggt	gag	agc	gtt	cgc	cag	cag	ctc	gcc	act	gat	240
Gly	Asp	Asp	Ser	Ile	Gly	Glu	Ser	Val	Arg	Gln	Gln	Leu	Ala	Thr	Asp	
65					70				75					80		
aac	att	gat	att	act	ccg	gtc	agc	gtg	atc	aaa	ggc	gaa	tca	aca	ggt	288
Asn	Ile	Asp	Ile	Thr	Pro	Val	Ser	Val	Ile	Lys	Gly	Glu	Ser	Thr	Gly	
				85					90					95		
gtg	gcg	ctg	att	ttt	gtt	aat	ggc	gaa	ggt	gag	aat	gtc	atc	ggt	att	336
Val	Ala	Leu	Ile	Phe	Val	Asn	Gly	Glu	Gly	Glu	Asn	Val	Ile	Gly	Ile	
			100					105					110			
cat	gcc	ggc	gct	aat	gct	gcc	ctt	tcc	ccg	gcg	ctg	gtg	gaa	gcg	caa	384
His	Ala	Gly	Ala	Asn	Ala	Ala	Leu	Ser	Pro	Ala	Leu	Val	Glu	Ala	Gln	
		115					120						125			
cgt	gag	cgt	att	gcc	aac	gcg	tca	gca	tta	tta	atg	cag	ctg	gaa	tca	432
Arg	Glu	Arg	Ile	Ala	Asn	Ala	Ser	Ala	Leu	Leu	Met	Gln	Leu	Glu	Ser	
	130					135					140					
cca	ctc	gaa	agt	gtg	atg	gca	gcg	gcg	aaa	atc	gcc	cat	caa	aat	aag	480
Pro	Leu	Glu	Ser	Val	Met	Ala	Ala	Ala	Lys	Ile	Ala	His	Gln	Asn	Lys	
	145				150					155					160	
act	atc	gtt	gcg	ctt	aac	ccg	gct	ccg	gct	cgc	gaa	ctt	cct	gac	gaa	528
Thr	Ile	Val	Ala	Leu	Asn	Pro	Ala	Pro	Ala	Arg	Glu	Leu	Pro	Asp	Glu	
				165					170					175		
ctg	ctg	gcg	ctg	gtg	gac	att	att	acg	cca	aac	gaa	acg	gaa	gca	gaa	576
Leu	Leu	Ala	Leu	Val	Asp	Ile	Ile	Thr	Pro	Asn	Glu	Thr	Glu	Ala	Glu	
			180					185					190			
aag	ctc	acc	ggt	att	cgt	gtt	gaa	aat	gat	gaa	gat	gca	gcg	aag	gcg	624
Lys	Leu	Thr	Gly	Ile	Arg	Val	Glu	Asn	Asp	Glu	Asp	Ala	Ala	Lys	Ala	

195

200

205

gcg cag gta ctg cat gaa aaa ggt atc cgt act gta ctg att act tta 672
 Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu
 210 215 220

gga agt cgt ggt gta tgg gct agc gtg aat ggt gaa ggt cag cgc gtt 720
 Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val
 225 230 235 240

cct gga ttc cgg gtg cag gct gtc gat acc att gct gcc gga gat acc 768
 Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr
 245 250 255

ttt aac ggt gcg tta atc acg gca ttg ctg gaa gaa aaa cca ttg cca 816
 Phe Asn Gly Ala Leu Ile Thr Ala Leu Leu Glu Glu Lys Pro Leu Pro
 260 265 270

gag gcg att cgt ttt gcc cat gct gcc gct gcg att gcc gta aca cgt 864
 Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ile Ala Val Thr Arg
 275 280 285

aaa ggc gca caa cct tcc gta ccg tgg cgt gaa gag atc gac gca ttt 912
 Lys Gly Ala Gln Pro Ser Val Pro Trp Arg Glu Glu Ile Asp Ala Phe
 290 295 300

tta gac agg cag agg tga 930
 Leu Asp Arg Gln Arg *
 305

<210> 287

<211> 38

<212> PRT

<213> Escherichia coli

<400> 287

Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
 1 5 10 15

Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
 20 25 30

His Lys Gln Arg Gln Gly
 35

<210> 288

<211> 443

<212> PRT

<213> Escherichia coli

<400> 288

Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
 1 5 10 15

Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
 20 25 30

Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
 35 40 45

<400> 289

Met	Arg	Leu	Asn	Thr	Leu	Ser	Pro	Ala	Glu	Gly	Ser	Lys	Lys	Ala	Gly
1			5						10					15	
Lys	Arg	Leu	Gly	Arg	Gly	Ile	Gly	Ser	Gly	Leu	Gly	Lys	Thr	Gly	Gly
		20					25						30		
Arg	Gly	His	Lys	Gly	Gln	Lys	Ser	Arg	Ser	Gly	Gly	Gly	Val	Arg	Arg
		35					40					45			
Gly	Phe	Glu	Gly	Gly	Gln	Met	Pro	Leu	Tyr	Arg	Arg	Leu	Pro	Lys	Phe
	50					55					60				
Gly	Phe	Thr	Ser	Arg	Lys	Ala	Ala	Ile	Thr	Ala	Glu	Ile	Arg	Leu	Ser
65					70					75					80
Asp	Leu	Ala	Lys	Val	Glu	Gly	Gly	Val	Val	Asp	Leu	Asn	Thr	Leu	Lys
				85					90					95	
Ala	Ala	Asn	Ile	Ile	Gly	Ile	Gln	Ile	Glu	Phe	Ala	Lys	Val	Ile	Leu
		100						105					110		
Ala	Gly	Glu	Val	Thr	Thr	Pro	Val	Thr	Val	Arg	Gly	Leu	Arg	Val	Thr
		115					120					125			
Lys	Gly	Ala	Arg	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Gly	Lys	Ile	Glu	Glu
	130					135						140			

<210> 290

<211> 59

<212> PRT

<213> Escherichia coli

<400> 290

Met	Ala	Lys	Thr	Ile	Lys	Ile	Thr	Gln	Thr	Arg	Ser	Ala	Ile	Gly	Arg
1				5					10					15	
Leu	Pro	Lys	His	Lys	Ala	Thr	Leu	Leu	Gly	Leu	Gly	Leu	Arg	Arg	Ile
		20						25					30		
Gly	His	Thr	Val	Glu	Arg	Glu	Asp	Thr	Pro	Ala	Ile	Arg	Gly	Met	Ile
		35					40					45			
Asn	Ala	Val	Ser	Phe	Met	Val	Lys	Val	Glu	Glu					
	50					55									

<210> 291

<211> 167

<212> PRT

<213> Escherichia coli

<400> 291

Met	Ala	His	Ile	Glu	Lys	Gln	Ala	Gly	Glu	Leu	Gln	Glu	Lys	Leu	Ile
1			5						10					15	
Ala	Val	Asn	Arg	Val	Ser	Lys	Thr	Val	Lys	Gly	Gly	Arg	Ile	Phe	Ser
		20						25					30		
Phe	Thr	Ala	Leu	Thr	Val	Val	Gly	Asp	Gly	Asn	Gly	Arg	Val	Gly	Phe
		35					40					45			
Gly	Tyr	Gly	Lys	Ala	Arg	Glu	Val	Pro	Ala	Ala	Ile	Gln	Lys	Ala	Met
	50					55					60				
Glu	Lys	Ala	Arg	Arg	Asn	Met	Ile	Asn	Val	Ala	Leu	Asn	Asn	Gly	Thr
65					70					75					80
Leu	Gln	His	Pro	Val	Lys	Gly	Val	His	Thr	Gly	Ser	Arg	Val	Phe	Met
			85						90					95	
Gln	Pro	Ala	Ser	Glu	Gly	Thr	Gly	Ile	Ile	Ala	Gly	Gly	Ala	Met	Arg
		100						105					110		

Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
 115 120 125
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
 130 135 140
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
 145 150 155 160
 Val Glu Glu Ile Leu Gly Lys
 165

<210> 292
 <211> 117
 <212> PRT
 <213> Escherichia coli

<400> 292
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1 5 10 15
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
 20 25 30
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu
 35 40 45
 Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr
 50 55 60
 Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu
 65 70 75 80
 Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly
 85 90 95
 Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu
 100 105 110
 Ala Gly Leu Gln Phe
 115

<210> 293
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 293
 Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp
 1 5 10 15
 Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu
 20 25 30
 Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn
 35 40 45
 Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln
 50 55 60
 Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr
 65 70 75 80
 Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala
 85 90 95
 Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro
 100 105 110
 Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln
 115 120 125
 Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val

130 135 140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys
145 150 155 160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys
165 170 175
Lys

<210> 294
<211> 130
<212> PRT
<213> Escherichia coli

<400> 294
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn
1 5 10 15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu
20 25 30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp
35 40 45
Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
50 55 60
Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
65 70 75 80
Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
85 90 95
Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
100 105 110
Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
115 120 125
Val Ala
130

<210> 295
<211> 101
<212> PRT
<213> Escherichia coli

<400> 295
Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
1 5 10 15
Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
20 25 30
Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
35 40 45
Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
50 55 60
Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
65 70 75 80
Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
85 90 95
Lys Lys Ala Ser Trp
100

<210> 296
 <211> 179
 <212> PRT
 <213> Escherichia coli

<400> 296
 Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
 1 5 10 15
 Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
 20 25 30
 Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
 35 40 45
 Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
 50 55 60
 Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
 65 70 75 80
 Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
 85 90 95
 Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
 100 105 110
 Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
 115 120 125
 Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
 130 135 140
 Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Thr Ala
 145 150 155 160
 Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
 165 170 175
 Phe Arg Lys

<210> 297
 <211> 104
 <212> PRT
 <213> Escherichia coli

<400> 297
 Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
 1 5 10 15
 Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
 20 25 30
 Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
 35 40 45
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
 50 55 60
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
 65 70 75 80
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
 85 90 95
 Lys Ser Asn Ser Glu Thr Ile Lys
 100

<210> 298
 <211> 123
 <212> PRT

[illegible]

Met	Ile	Gln	Glu	Gln	Thr	Met	Leu	Asn	Val	Ala	Asp	Asn	Ser	Gly	Ala
1				5					10					15	
Arg	Arg	Val	Met	Cys	Ile	Lys	Val	Leu	Gly	Gly	Ser	His	Arg	Arg	Tyr
			20					25					30		
Ala	Gly	Val	Gly	Asp	Ile	Ile	Lys	Ile	Thr	Ile	Lys	Glu	Ala	Ile	Pro
			35				40					45			
Arg	Gly	Lys	Val	Lys	Lys	Gly	Asp	Val	Leu	Lys	Ala	Val	Val	Val	Arg
			50			55					60				
Thr	Lys	Lys	Gly	Val	Arg	Arg	Pro	Asp	Gly	Ser	Val	Ile	Arg	Phe	Asp
65					70					75				80	
Gly	Asn	Ala	Cys	Val	Leu	Leu	Asn	Asn	Asn	Ser	Glu	Gln	Pro	Ile	Gly
				85					90					95	
Thr	Arg	Ile	Phe	Gly	Pro	Val	Thr	Arg	Glu	Leu	Arg	Ser	Glu	Lys	Phe
			100					105					110		
Met	Lys	Ile	Ile	Ser	Leu	Ala	Pro	Glu	Val	Leu					
			115				120								

<211> 485

<212> PRT

<213> Escherichia coli

Met 1	Gly	Ile	Tyr	Phe 5	Thr	Asn	Ser	Asp	Asp 10	Gln	Ile	Tyr	Phe	Lys 15	Arg
Ser	Glu	Gly	Met 20	Ser	Asp	Ile	Asn	His 25	Ala	Gly	Ser	Asp	Leu 30	Ile	Phe
Glu	Leu	Glu 35	Asp	Arg	Pro	Pro	Phe 40	His	Gln	Ala	Leu	Val 45	Gly	Ala	Ile
Thr	His 50	Leu	Leu	Ala	Ile	Phe 55	Val	Pro	Met	Val	Thr 60	Pro	Ala	Leu	Ile
Val 65	Gly	Ala	Ala	Leu	Gln 70	Leu	Ser	Ala	Glu	Thr 75	Thr	Ala	Tyr	Leu 80	Val
Ser	Met	Ala	Met	Ile 85	Ala	Ser	Gly	Ile	Gly 90	Thr	Trp	Leu	Gln 95	Val	Asn
Arg	Tyr	Gly	Ile 100	Val	Gly	Ser	Gly	Leu 105	Leu	Ser	Ile	Gln 110	Ser	Val	Asn
Phe	Ser	Phe 115	Val	Thr	Val	Met 120	Ile	Ala	Leu	Gly	Ser	Ser 125	Met	Lys	Ser
Asp	Gly 130	Phe	His	Glu	Glu	Leu 135	Ile	Met	Ser	Ser	Leu 140	Leu	Gly	Val	Ser
Phe 145	Val	Gly	Ala	Phe	Leu 150	Val	Val	Gly	Ser	Ser 155	Phe	Ile	Leu	Pro 160	Tyr
Leu	Arg	Arg	Val	Ile 165	Thr	Pro	Thr	Val	Ser 170	Gly	Ile	Val	Val	Leu 175	Met
Ile	Gly	Leu	Ser 180	Leu	Ile	Lys	Val	Gly 185	Ile	Ile	Asp	Phe	Gly 190	Gly	Gly
Phe	Ala	Ala 195	Lys	Ser	Ser	Gly	Thr 200	Phe	Gly	Asn	Tyr 205	Glu	His	Leu	Gly
Val	Gly 210	Leu	Leu	Val	Leu	Ile 215	Val	Val	Ile	Gly	Phe 220	Asn	Cys	Cys	Arg
Ser 225	Pro	Leu	Leu	Arg 230	Met	Gly	Gly	Ile	Ala 235	Ile	Gly	Leu	Cys	Val	Gly 240

His Pro Gln Ser Val Asp Ala Leu Phe Glu Ala Ser His Ile Asn
 145 Met Arg Met Ile Ala Gly Lys Val Met Met Asp Arg Asn Ala Pro Asp
 Tyr Leu Leu Asp Thr Ala Glu Ser Ser Tyr His Gln Ser Lys Asn Glu Leu
 Ile Glu Arg Trp His Lys Asn Gly Arg Leu Leu Tyr Ala Ile Thr Pro
 Arg Phe Ala Pro Thr Ser Ser Pro Glu Gln Met Ala Met Ala Gln Arg
 Leu Lys Glu Glu Tyr Pro Asp Thr Trp Val His Thr His Leu Cys Glu
 Asn Lys Asp Glu Ile Ala Trp Val Lys Ser Leu Tyr Pro Asp His Asp
 Gly Tyr Leu Asp Val Tyr His Gln Tyr Gly Leu Thr Gly Lys Asn Cys
 Val Phe Ala His Cys Val His Leu Glu Glu Lys Glu Trp Asp Arg Leu
 Ser Glu Thr Lys Ser Ser Ile Ala Phe Cys Pro Thr Ser Asn Leu Tyr
 Leu Gly Ser Gly Leu Phe Asn Leu Lys Lys Ala Trp Gln Lys Lys Val
 Lys Val Gly Met Gly Thr Asp Ile Gly Ala Gly Thr Thr Phe Asn Met
 Leu Gln Thr Leu Asn Glu Ala Tyr Lys Val Leu Gln Leu Gln Gly Tyr
 Arg Leu Ser Ala Tyr Glu Ala Phe Tyr Leu Ala Thr Leu Gly Gly Ala
 Lys Ser Leu Gly Leu Asp Asp Leu Ile Gly Asn Phe Leu Pro Gly Lys
 Glu Ala Asp Phe Val Val Met Glu Pro Thr Ala Thr Pro Leu Gln Gln
 Leu Arg Tyr Asp Asn Ser Val Ser Leu Val Asp Lys Leu Phe Val Met
 Met Thr Leu Gly Asp Asp Arg Ser Ile Tyr Arg Thr Tyr Val Asp Gly
 Arg Leu Val Tyr Glu Arg Asn

<210> 301
 <211> 189
 <212> PRT
 <213> Escherichia coli

<400> 301
 Met Ser Gly Asp Ile Leu Gln Thr Pro Asp Ala Pro Lys Pro Gln Gly
 1 5 10 15
 Ala Leu Asp Asn Tyr Phe Lys Ile Thr Ala Arg Gly Ser Thr Val Arg
 20 25 30
 Gln Glu Val Leu Ala Gly Leu Thr Thr Phe Leu Ala Met Val Tyr Ser
 35 40 45
 Val Ile Val Val Pro Gly Met Leu Gly Lys Ala Gly Phe Pro Pro Ala
 50 55 60
 Ala Val Phe Val Ala Thr Cys Leu Val Ala Gly Phe Gly Ser Leu Leu
 65 70 75 80

Met	Gly	Leu	Trp	Ala	Asn	Leu	Pro	Met	Ala	Ile	Gly	Cys	Ala	Ile	Ser
				85					90					95	
Leu	Thr	Ala	Phe	Thr	Ala	Phe	Ser	Leu	Val	Leu	Gly	Gln	Gln	Ile	Ser
			100					105					110		
Val	Pro	Val	Ala	Leu	Gly	Ala	Val	Phe	Leu	Met	Gly	Val	Ile	Phe	Thr
		115					120					125			
Ala	Ile	Ser	Val	Thr	Gly	Val	Arg	Thr	Trp	Ile	Leu	Arg	Asn	Leu	Pro
	130					135					140				
Met	Gly	Ile	Ala	His	Gly	Thr	Gly	Ile	Gly	Ile	Gly	Leu	Phe	Leu	Leu
145					150					155					160
Leu	Ile	Ala	Ala	Asn	Gly	Val	Gly	Met	Val	Ile	Lys	Asn	Pro	Ile	Glu
				165				170						175	
Gly	Leu	Gln	Trp	Arg	Ser	Val	Arg	Leu	Pro	Pro	Ser	Arg			
			180					185							

<210> 302
 <211> 276
 <212> PRT
 <213> Escherichia coli

<400> 302

Met	Ala	Leu	Gly	Ala	Phe	Thr	Ser	Phe	Pro	Val	Met	Met	Ser	Leu	Leu
1				5					10					15	
Gly	Leu	Ala	Val	Ile	Phe	Gly	Leu	Glu	Lys	Cys	Arg	Val	Pro	Gly	Gly
			20					25					30		
Ile	Leu	Leu	Val	Ile	Ile	Ala	Ile	Ser	Ile	Ile	Gly	Leu	Ile	Phe	Asp
		35					40					45			
Pro	Ala	Val	Lys	Tyr	His	Gly	Leu	Val	Ala	Met	Pro	Ser	Leu	Thr	Gly
	50					55				60					
Glu	Asp	Gly	Lys	Ser	Leu	Ile	Phe	Ser	Leu	Asp	Ile	Met	Gly	Ala	Leu
65					70					75					80
Gln	Pro	Thr	Val	Leu	Pro	Ser	Val	Leu	Ala	Leu	Val	Met	Thr	Ala	Val
				85					90					95	
Phe	Asp	Ala	Thr	Gly	Thr	Ile	Arg	Ala	Val	Ala	Gly	Gln	Ala	Asn	Leu
		100						105					110		
Leu	Asp	Lys	Asp	Asn	Gln	Ile	Ile	Asn	Gly	Gly	Lys	Ala	Leu	Thr	Ser
	115					120						125			
Asp	Ser	Val	Ser	Ser	Ile	Phe	Ser	Gly	Leu	Val	Gly	Ala	Ala	Pro	Ala
	130					135					140				
Ala	Val	Tyr	Ile	Glu	Ser	Ala	Ala	Gly	Thr	Ala	Ala	Gly	Gly	Lys	Thr
145					150					155					160
Gly	Leu	Thr	Ala	Thr	Val	Val	Gly	Ala	Leu	Phe	Leu	Leu	Ile	Leu	Phe
				165					170					175	
Leu	Ser	Pro	Leu	Ser	Phe	Leu	Ile	Pro	Gly	Tyr	Ala	Thr	Ala	Pro	Ala
		180						185					190		
Leu	Met	Tyr	Val	Gly	Leu	Leu	Met	Leu	Ser	Asn	Val	Ser	Lys	Leu	Asp
	195						200					205			
Phe	Asn	Asp	Phe	Ile	Asp	Ala	Met	Ala	Gly	Leu	Val	Cys	Ala	Val	Phe
	210					215					220				
Ile	Val	Leu	Thr	Cys	Asn	Ile	Val	Thr	Gly	Ile	Met	Leu	Gly	Phe	Val
225					230					235					240
Thr	Leu	Val	Val	Gly	Arg	Val	Phe	Ala	Arg	Glu	Trp	Gln	Lys	Leu	Asn
				245					250					255	
Ile	Gly	Thr	Val	Ile	Ile	Thr	Ala	Ala	Leu	Val	Ala	Phe	Tyr	Ala	Gly
			260					265					270		
Gly	Trp	Ala	Ile												

<210> 303
 <211> 466
 <212> PRT
 <213> Escherichia coli

<400> 303

Met	Asn	Ser	Glu	Gly	Gly	Lys	Pro	Gly	Asn	Val	Leu	Thr	Val	Asn	Gly
1				5					10					15	
Asn	Tyr	Thr	Gly	Asn	Asn	Gly	Leu	Met	Thr	Phe	Asn	Ala	Thr	Leu	Gly
			20					25					30		
Gly	Asp	Asn	Ser	Pro	Thr	Asp	Lys	Met	Asn	Val	Lys	Gly	Asp	Thr	Gln
		35					40					45			
Gly	Asn	Thr	Arg	Val	Arg	Val	Asp	Asn	Ile	Gly	Gly	Val	Gly	Ala	Gln
		50				55					60				
Thr	Val	Asn	Gly	Ile	Glu	Leu	Ile	Glu	Val	Gly	Gly	Asn	Ser	Ala	Gly
65				70					75					80	
Asn	Phe	Ala	Leu	Thr	Gly	Thr	Val	Glu	Ala	Gly	Ala	Tyr	Val	Tyr	
			85					90					95		
Thr	Leu	Ala	Lys	Gly	Lys	Gly	Asn	Asp	Glu	Lys	Asn	Trp	Tyr	Leu	Thr
			100					105					110		
Ser	Lys	Trp	Asp	Gly	Val	Thr	Pro	Ala	Asp	Thr	Pro	Asp	Pro	Ile	Asn
		115					120					125			
Asn	Pro	Pro	Val	Val	Asp	Pro	Glu	Gly	Pro	Ser	Val	Tyr	Arg	Pro	Glu
		130				135					140				
Ala	Gly	Ser	Tyr	Ile	Ser	Asn	Ile	Ala	Ala	Ala	Asn	Ser	Leu	Phe	Ser
145				150					155					160	
His	Arg	Leu	His	Asp	Arg	Leu	Gly	Glu	Pro	Gln	Tyr	Thr	Asp	Ser	Leu
			165					170					175		
His	Ser	Gln	Gly	Ser	Ala	Ser	Ser	Met	Trp	Met	Arg	His	Val	Gly	Gly
			180					185					190		
His	Glu	Arg	Ser	Arg	Ala	Gly	Asp	Gly	Gln	Leu	Asn	Thr	Gln	Ala	Asn
		195					200					205			
Arg	Tyr	Val	Leu	Gln	Leu	Gly	Gly	Asp	Leu	Ala	Gln	Trp	Ser	Ser	Asn
	210					215					220				
Ala	Gln	Asp	Arg	Trp	His	Leu	Gly	Val	Met	Ala	Gly	Tyr	Ala	Asn	Gln
225				230					235					240	
His	Ser	Asn	Thr	Gln	Ser	Asn	Arg	Val	Gly	Tyr	Lys	Ser	Asp	Gly	Arg
			245					250					255		
Ile	Ser	Gly	Tyr	Ser	Ala	Gly	Leu	Tyr	Ala	Thr	Trp	Tyr	Gln	Asn	Asp
		260						265					270		
Ala	Asn	Lys	Thr	Gly	Ala	Tyr	Val	Asp	Ser	Trp	Ala	Leu	Tyr	Asn	Trp
		275					280					285			
Phe	Asp	Asn	Ser	Val	Ser	Ser	Asp	Asn	Arg	Ser	Ala	Asp	Asp	Tyr	Asp
	290					295				300					
Ser	Arg	Gly	Val	Thr	Ala	Ser	Val	Glu	Gly	Gly	Tyr	Thr	Phe	Glu	Ala
305					310				315					320	
Gly	Thr	Phe	Ser	Gly	Ser	Glu	Gly	Thr	Leu	Asn	Thr	Trp	Tyr	Val	Gln
			325					330					335		
Pro	Gln	Ala	Gln	Ile	Thr	Trp	Met	Gly	Val	Lys	Asp	Ser	Asp	His	Thr
		340						345					350		
Arg	Lys	Asp	Gly	Thr	Arg	Ile	Glu	Thr	Glu	Gly	Asp	Gly	Asn	Val	Gln
		355				360						365			
Thr	Arg	Leu	Gly	Val	Lys	Thr	Tyr	Leu	Asn	Ser	His	His	Gln	Arg	Asp
	370					375					380				

Asp Gly Lys Gln Arg Glu Phe Gln Pro Tyr Ile Glu Ala Asn Trp Ile
 385 390 395 400
 Asn Asn Ser Lys Val Tyr Ala Val Lys Met Asn Gly Gln Thr Val Gly
 405 410 415
 Arg Glu Gly Ala Arg Asn Leu Gly Glu Val Arg Thr Gly Val Glu Ala
 420 425 430
 Lys Val Asn Asn Asn Leu Ser Leu Trp Gly Asn Val Gly Val Gln Leu
 435 440 445
 Gly Asp Lys Gly Tyr Ser Asp Thr Gln Gly Met Leu Gly Val Lys Tyr
 450 455 460
 Ser Trp
 465

<210> 304
 <211> 1325
 <212> PRT
 <213> Escherichia coli

<400> 304
 Met Asn Arg Ile Tyr Arg Val Ile Trp Asn Cys Thr Leu Gln Val Phe
 1 5 10 15
 Gln Ala Cys Ser Glu Leu Thr Arg Arg Ala Gly Lys Thr Ser Thr Val
 20 25 30
 Asn Leu Arg Lys Ser Ser Gly Leu Thr Thr Lys Phe Ser Arg Leu Thr
 35 40 45
 Leu Gly Val Leu Leu Ala Leu Ser Gly Ser Ala Ser Gly Ala Ser Leu
 50 55 60
 Glu Val Asp Asn Asp Gln Ile Thr Asn Ile Asp Thr Asp Val Ala Tyr
 65 70 75 80
 Asp Ala Tyr Leu Val Gly Trp Tyr Gly Thr Gly Val Leu Asn Ile Leu
 85 90 95
 Ala Gly Gly Asn Ala Ser Leu Thr Thr Ile Thr Thr Ser Val Ile Gly
 100 105 110
 Ala Asn Glu Asp Ser Glu Gly Thr Val Asn Val Leu Gly Gly Thr Trp
 115 120 125
 Arg Leu Tyr Asp Ser Gly Asn Asn Ala Arg Pro Leu Asn Val Gly Gln
 130 135 140
 Ser Gly Thr Gly Thr Leu Asn Ile Lys Gln Lys Gly His Val Asp Gly
 145 150 155 160
 Gly Tyr Leu Arg Leu Gly Ser Ser Thr Gly Gly Val Gly Thr Val Asn
 165 170 175
 Val Glu Gly Glu Asp Ser Val Leu Thr Thr Glu Leu Phe Glu Ile Gly
 180 185 190
 Ser Tyr Gly Thr Gly Ser Leu Asn Ile Thr Asp Lys Gly Tyr Val Thr
 195 200 205
 Ser Ser Ile Val Ala Ile Leu Gly Tyr Gln Ala Gly Ser Asn Gly Gln
 210 215 220
 Val Val Val Glu Lys Gly Gly Glu Trp Leu Ile Lys Asn Asn Asp Ser
 225 230 235 240
 Ser Ile Glu Phe Gln Ile Gly Asn Gln Gly Thr Gly Glu Ala Thr Ile
 245 250 255
 Arg Glu Gly Gly Leu Val Thr Ala Glu Asn Thr Ile Ile Gly Gly Asn
 260 265 270
 Ala Thr Gly Ile Gly Thr Leu Asn Val Gln Asp Gln Asp Ser Val Ile
 275 280 285
 Thr Val Arg Arg Leu Tyr Asn Gly Tyr Phe Gly Asn Gly Thr Val Asn

	1205		1210		1215
Asn Glu Gln Lys Asn Leu Gly Asp Ala Ser Val Ile Asn Asn Gly Leu					
	1220		1225		1230
Leu Thr Ile Ser Thr Glu Arg Ser Trp Ala Met Thr His Ser Ile Ser					
	1235		1240		1245
Gly Ser Gly Asp Val Thr Lys Leu Gly Thr Gly Ile Leu Thr Leu Asn					
	1250		1255		1260
Asn Asp Ser Ala Ala Tyr Gln Gly Thr Thr Asp Ile Val Gly Gly Glu					
1265	1270		1275		1280
Ile Ala Phe Gly Ser Asp Ser Ala Ile Asn Met Ala Ser Gln His Ile					
	1285		1290		1295
Asn Ile His Asn Ser Gly Val Met Ser Gly Asn Val Thr Thr Ala Gly					
	1300		1305		1310
Asp Met Asn Val Met Pro Gly Gly Gly Thr Ala Cys Arg					
	1315		1320		1325

<210> 305
 <211> 251
 <212> PRT
 <213> Escherichia coli

<400> 305

Met Thr Glu Ala Gln Arg His Gln Ile Leu Leu Glu Met Leu Ala Gln					
1	5		10		15
Leu Gly Phe Val Thr Val Glu Lys Val Val Glu Arg Leu Gly Ile Ser					
	20		25		30
Pro Ala Thr Ala Arg Arg Asp Ile Asn Lys Leu Asp Glu Ser Gly Lys					
	35		40		45
Leu Lys Lys Val Arg Asn Gly Ala Glu Ala Ile Thr Gln Gln Arg Pro					
	50		55		60
Arg Trp Thr Pro Met Asn Leu His Gln Ala Gln Asn His Asp Glu Lys					
65	70		75		80
Val Arg Ile Ala Lys Ala Ala Ser Gln Leu Val Asn Pro Gly Glu Ser					
	85		90		95
Val Val Ile Asn Cys Gly Ser Thr Ala Phe Leu Leu Gly Arg Glu Met					
	100		105		110
Cys Gly Lys Pro Val Gln Ile Ile Thr Asn Tyr Leu Pro Leu Ala Asn					
	115		120		125
Tyr Leu Ile Asp Gln Glu His Asp Ser Val Ile Ile Met Gly Gly Gln					
	130		135		140
Tyr Asn Lys Ser Gln Ser Ile Thr Leu Ser Pro Gln Gly Ser Glu Asn					
145	150		155		160
Ser Leu Tyr Ala Gly His Trp Met Phe Thr Ser Gly Lys Gly Leu Thr					
	165		170		175
Ala Glu Gly Leu Tyr Lys Thr Asp Met Leu Thr Ala Met Ala Glu Gln					
	180		185		190
Lys Met Leu Ser Val Val Gly Lys Leu Val Val Leu Val Asp Ser Ser					
	195		200		205
Lys Ile Gly Glu Arg Ala Gly Met Leu Phe Ser Arg Ala Asp Gln Ile					
	210		215		220
Asp Met Leu Ile Thr Gly Lys Asn Ala Asn Pro Glu Ile Leu Gln Gln					
225	230		235		240
Leu Glu Ala Gln Gly Val Ser Ile Leu Arg Val					
	245		250		

<210> 306
 <211> 274
 <212> PRT
 <213> Escherichia coli

<400> 306

Met Thr Glu Phe Thr Thr Leu Leu Gln Gln Gly Asn Ala Trp Phe Phe
 1 5 10 15
 Ile Pro Ser Ala Ile Leu Leu Gly Ala Leu His Gly Leu Glu Pro Gly
 20 25 30
 His Ser Lys Thr Met Met Ala Ala Phe Ile Ile Ala Ile Lys Gly Thr
 35 40 45
 Ile Lys Gln Ala Val Met Leu Gly Leu Ala Ala Thr Ile Ser His Thr
 50 55 60
 Ala Val Val Trp Leu Ile Ala Phe Gly Gly Met Val Ile Ser Lys Arg
 65 70 75 80
 Phe Thr Ala Gln Ser Ala Glu Pro Trp Leu Gln Leu Ile Ser Ala Val
 85 90 95
 Ile Ile Ile Ser Thr Ala Phe Trp Met Phe Trp Arg Thr Trp Arg Gly
 100 105 110
 Glu Arg Asn Trp Leu Glu Asn Met His Gly His Asp Tyr Glu His His
 115 120 125
 His His Asp His Glu His His His Asp His Gly His His His His
 130 135 140
 Glu His Gly Glu Tyr Gln Asp Ala His Ala Arg Ala His Ala Asn Asp
 145 150 155 160
 Ile Lys Arg Arg Phe Asp Gly Arg Glu Val Thr Asn Trp Gln Ile Leu
 165 170 175
 Leu Phe Gly Leu Thr Gly Gly Leu Ile Pro Cys Pro Ala Ala Ile Thr
 180 185 190
 Val Leu Leu Ile Cys Ile Gln Leu Lys Ala Leu Thr Leu Gly Ala Thr
 195 200 205
 Leu Val Val Ser Phe Ser Ile Gly Leu Ala Leu Thr Leu Val Thr Val
 210 215 220
 Gly Val Gly Ala Ala Ile Ser Val Gln Gln Val Ala Lys Arg Trp Ser
 225 230 235 240
 Gly Phe Asn Thr Leu Ala Lys Arg Ala Pro Tyr Phe Ser Ser Leu Leu
 245 250 255
 Ile Gly Leu Val Gly Val Tyr Met Gly Val His Gly Phe Met Gly Ile
 260 265 270
 Met Arg

<210> 307
 <211> 172
 <212> PRT
 <213> Escherichia coli

<400> 307

Met Ile Leu Lys Ser Ala Ile Ser Ala Asp Ser Leu Leu Ala Lys Asp
 1 5 10 15
 Ala Phe Arg Ala Ser Phe His Leu His Phe Leu Arg Asn His Gly Ile
 20 25 30
 Thr Asn Lys Ile Ser Leu Val Ser Tyr Ile Val Trp Gln Glu Arg Tyr
 35 40 45
 Ala Thr Asp Ile Thr Asp Pro Gln Ser Gly Glu Phe Met Thr Ile Lys

50		55		60
Asn Lys Met Leu Leu Gly Ala Leu Leu Leu Val Thr Ser Ala Ala Trp				
65		70		75
Ala Ala Pro Ala Thr Ala Gly Ser Thr Asn Thr Ser Gly Ile Ser Lys				80
	85		90	
Tyr Glu Leu Ser Ser Phe Ile Ala Asp Phe Lys His Phe Lys Pro Gly				95
	100		105	
Asp Thr Val Pro Glu Met Tyr Arg Thr Asp Glu Tyr Asn Ile Lys Gln				110
	115		120	
Trp Gln Leu Arg Asn Leu Pro Ala Pro Asp Ala Gly Thr His Trp Thr				125
	130		135	
Tyr Met Gly Gly Ala Tyr Val Leu Ile Ser Asp Thr Asp Gly Lys Ile				140
145		150		155
Ile Lys Ala Tyr Asp Gly Glu Ile Phe Tyr His Arg				160
	165		170	

<210> 308
 <211> 344
 <212> PRT
 <213> Escherichia coli

<400> 308
Met Glu Ile Arg Ile Met Leu Phe Ile Leu Met Met Met Val Met Pro
1 5 10 15
Val Ser Tyr Ala Cys Tyr Ser Glu Leu Ser Val Gln His Asn Leu
20 25 30
Val Val Gln Gly Asp Phe Ala Leu Thr Gln Thr Gln Met Ala Thr Tyr
35 40 45
Glu His Asn Phe Asn Asp Ser Ser Cys Val Ser Thr Asn Thr Ile Thr
50 55 60
Pro Met Ser Pro Ser Asp Ile Ile Val Gly Leu Tyr Asn Asp Thr Ile
65 70 75 80
Lys Leu Asn Leu His Phe Glu Trp Thr Asn Lys Asn Asn Ile Thr Leu
85 90 95
Ser Asn Asn Gln Thr Ser Phe Thr Ser Gly Tyr Ser Val Thr Val Thr
100 105 110
Pro Ala Ala Ser Asn Ala Lys Val Asn Val Ser Ala Gly Gly Gly Gly
115 120 125
Ser Val Met Ile Asn Gly Val Ala Thr Leu Ser Ser Ala Ser Ser Ser
130 135 140
Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
145 150 155 160
Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
165 170 175
Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
180 185 190
Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
195 200 205
Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
210 215 220
Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
225 230 235 240
Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
245 250 255
Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
260 265 270

Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
 275 280 285
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300
 Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335
 Ala Leu Ile Asn Val Lys Tyr Asp
 340

<210> 309
 <211> 826
 <212> PRT
 <213> Escherichia coli

<400> 309

Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
 1 5 10 15
 Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20 25 30
 Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35 40 45
 Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50 55 60
 Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65 70 75 80
 Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85 90 95
 Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
 100 105 110
 Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
 115 120 125
 Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
 130 135 140
 Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
 145 150 155 160
 Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
 165 170 175
 Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His
 180 185 190
 Ser Asp Ala Ser Phe Ser Lys Thr Asn Asn Asn Pro Gly Val Trp Lys
 195 200 205
 Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln Leu Leu Gly Thr
 210 215 220
 Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val
 225 230 235 240
 Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn
 245 250 255
 Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn
 260 265 270
 Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu
 275 280 285
 Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly
 290 295 300
 Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr

Val	Asn	Asp	Ile	His	Gly	His	Asn	Ile	Gly	Val	Val	Gly	Gln	Gly	Ser
770						775				780					
Gln	Leu	Phe	Ile	Arg	Thr	Asn	Glu	Val	Pro	Pro	Ser	Val	Asn	Val	Ala
785					790				795						800
Ile	Asp	Lys	Gln	Gln	Gly	Leu	Ser	Cys	Thr	Ile	Thr	Phe	Gly	Lys	Glu
			805						810					815	
Ile	Asp	Glu	Ser	Arg	Asn	Tyr	Ile	Cys	Gln						
		820						825							

<210> 310
 <211> 239
 <212> PRT
 <213> Escherichia coli

Met	Ala	Ala	Ile	Pro	Trp	Arg	Pro	Phe	Asn	Leu	Arg	Gly	Ile	Lys	Met
1				5					10					15	
Lys	Gly	Leu	Leu	Ser	Leu	Leu	Ile	Phe	Ser	Met	Val	Leu	Pro	Ala	His
		20						25					30		
Ala	Gly	Ile	Val	Ile	Tyr	Gly	Thr	Arg	Ile	Ile	Tyr	Pro	Ala	Glu	Asn
		35				40						45			
Lys	Glu	Val	Met	Val	Gln	Leu	Met	Asn	Gln	Gly	Asn	Arg	Ser	Ser	Leu
	50					55					60				
Leu	Gln	Ala	Trp	Ile	Asp	Asp	Gly	Asp	Thr	Ser	Leu	Pro	Pro	Glu	Lys
65					70					75					80
Ile	Gln	Val	Pro	Phe	Met	Leu	Thr	Pro	Pro	Val	Ala	Lys	Ile	Gly	Ala
				85					90					95	
Asn	Ser	Gly	Gln	Gln	Val	Lys	Ile	Lys	Ile	Met	Pro	Asn	Lys	Leu	Pro
			100					105					110		
Thr	Asn	Lys	Glu	Ser	Ile	Phe	Tyr	Leu	Asn	Val	Leu	Asp	Ile	Pro	Pro
		115					120					125			
Asn	Ser	Pro	Glu	Gln	Glu	Gly	Lys	Asn	Ala	Leu	Lys	Phe	Ala	Met	Gln
		130				135					140				
Asn	Arg	Ile	Lys	Leu	Phe	Tyr	Arg	Pro	Ala	Gly	Ile	Ala	Pro	Val	Asn
145					150					155					160
Lys	Ala	Thr	Phe	Lys	Lys	Leu	Leu	Val	Asn	Arg	Ser	Gly	Asn	Gly	Leu
			165					170						175	
Val	Ile	Lys	Asn	Asp	Ser	Ala	Asn	Trp	Val	Thr	Ile	Ser	Asp	Val	Lys
			180				185						190		
Ala	Asn	Asn	Val	Lys	Val	Asn	Tyr	Glu	Thr	Ile	Met	Ile	Ala	Pro	Leu
	195						200					205			
Glu	Ser	Gln	Ser	Val	Asn	Val	Lys	Ser	Asn	Asn	Ala	Asn	Asn	Trp	His
	210					215					220				
Leu	Thr	Ile	Ile	Asp	Asp	His	Gly	Asn	Tyr	Ile	Ser	Asp	Lys	Ile	
225					230					235					

<210> 311
 <211> 180
 <212> PRT
 <213> Escherichia coli

Met	Lys	Arg	Ser	Ile	Ile	Ala	Ala	Ala	Val	Phe	Ser	Ser	Phe	Phe	Met
1				5					10					15	
Ser	Ala	Gly	Val	Phe	Ala	Ala	Asp	Val	Asp	Thr	Gly	Thr	Leu	Thr	Ile

Phe Lys Leu Leu Gly Leu Tyr Asp Ile Glu Gln Cys Trp Val Cys Ala
65 70 75 80
Ala Ser Leu Arg Glu Arg Gly Leu Asp Pro Gln Thr Pro Phe Val Val
85 90 95
Glu Ala Thr Pro Leu Glu Ala Asp Ala Leu Arg Arg Glu Leu Ala Asn
100 105 110
Tyr Asp Val Ile Leu Arg Phe
115

<210> 314
<211> 128
<212> PRT
<213> Escherichia coli

<400> 314
Met Arg Phe Ala Ile Val Val Thr Gly Pro Ala Tyr Gly Thr Gln Gln
1 5 10 15
Ala Ser Ser Ala Phe Gln Phe Ala Gln Ala Leu Ile Ala Asp Gly His
20 25 30
Glu Leu Ser Ser Val Phe Phe Tyr Arg Glu Gly Val Tyr Asn Ala Asn
35 40 45
Gln Leu Thr Ser Pro Ala Ser Asp Glu Phe Asp Leu Val Arg Ala Trp
50 55 60
Gln Gln Leu Asn Ala Gln His Gly Val Ala Leu Asn Ile Cys Val Ala
65 70 75 80
Ala Ala Leu Arg Arg Gly Val Val Asp Glu Thr Glu Ala Gly Arg Leu
85 90 95
Gly Leu Ala Ser Ser Asn Leu Gln Gln Gly Phe Thr Leu Ser Gly Leu
100 105 110
Gly Ala Leu Ala Glu Ala Ser Leu Thr Cys Asp Arg Val Val Gln Phe
115 120 125

<210> 315
<211> 244
<212> PRT
<213> Escherichia coli

<400> 315
Met Phe Phe Phe Met Ser Arg Ser Leu Leu Thr Asn Glu Thr Ser Glu
1 5 10 15
Leu Asp Leu Leu Asp Gln Arg Pro Phe Asp Gln Thr Asp Phe Asp Ile
20 25 30
Leu Lys Ser Tyr Glu Ala Val Val Asp Gly Leu Ala Met Leu Ile Gly
35 40 45
Ser His Cys Glu Ile Val Leu His Ser Leu Gln Asp Leu Lys Cys Ser
50 55 60
Ala Ile Arg Ile Ala Asn Gly Glu His Thr Gly Arg Lys Ile Gly Ser
65 70 75 80
Pro Ile Thr Asp Leu Ala Leu Arg Met Leu His Asp Met Thr Gly Ala
85 90 95
Asp Ser Ser Val Ser Lys Cys Tyr Phe Thr Arg Ala Lys Ser Gly Val
100 105 110
Leu Met Lys Ser Leu Thr Ile Ala Ile Arg Asn Arg Glu Gln Arg Val
115 120 125
Ile Gly Leu Leu Cys Ile Asn Met Asn Leu Asp Val Pro Phe Ser Gln

130 135 140
 Ile Met Ser Thr Phe Val Pro Pro Glu Thr Pro Asp Val Gly Ser Ser
 145 150 155 160
 Val Asn Phe Ala Ser Ser Val Glu Asp Leu Val Thr Gln Thr Leu Glu
 165 170 175
 Phe Thr Ile Glu Val Asn Ala Asp Arg Asn Val Ser Asn Asn Ala
 180 185 190
 Lys Asn Arg Gln Ile Val Leu Asn Leu Tyr Glu Lys Gly Ile Phe Asp
 195 200 205
 Ile Lys Asp Ala Ile Asn Gln Val Ala Asp Arg Leu Asn Ile Ser Lys
 210 215 220
 His Thr Val Tyr Leu Tyr Ile Arg Gln Phe Lys Ser Gly Asp Phe Gln
 225 230 235 240
 Gly Gln Asp Lys

<210> 316
 <211> 84
 <212> PRT
 <213> Escherichia coli

<400> 316
 Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys
 1 5 10 15
 Met Glu Lys Ser Ile Val Val Ala Ile Glu Arg Phe Val Lys His Pro
 20 25 30
 Ile Tyr Gly Lys Phe Ile Lys Arg Thr Thr Lys Leu His Val His Asp
 35 40 45
 Glu Asn Asn Glu Cys Gly Ile Gly Asp Val Val Glu Ile Arg Glu Cys
 50 55 60
 Arg Pro Leu Ser Lys Thr Lys Ser Trp Thr Leu Val Arg Val Val Glu
 65 70 75 80
 Lys Ala Val Leu

<210> 317
 <211> 63
 <212> PRT
 <213> Escherichia coli

<400> 317
 Met Lys Ala Lys Glu Leu Arg Glu Lys Ser Val Glu Glu Leu Asn Thr
 1 5 10 15
 Glu Leu Leu Asn Leu Leu Arg Glu Gln Phe Asn Leu Arg Met Gln Ala
 20 25 30
 Ala Ser Gly Gln Leu Gln Gln Ser His Leu Leu Lys Gln Val Arg Arg
 35 40 45
 Asp Val Ala Arg Val Lys Thr Leu Leu Asn Glu Lys Ala Gly Ala
 50 55 60

<210> 318
 <211> 136
 <212> PRT
 <213> Escherichia coli

<400> 318
 Met Leu Gln Pro Lys Arg Thr Lys Phe Arg Lys Met His Lys Gly Arg
 1 5 10 15
 Asn Arg Gly Leu Ala Gln Gly Thr Asp Val Ser Phe Gly Ser Phe Gly
 20 25 30
 Leu Lys Ala Val Gly Arg Gly Arg Leu Thr Ala Arg Gln Ile Glu Ala
 35 40 45
 Ala Arg Arg Ala Met Thr Arg Ala Val Lys Arg Gln Gly Lys Ile Trp
 50 55 60
 Ile Arg Val Phe Pro Asp Lys Pro Ile Thr Glu Lys Pro Leu Ala Val
 65 70 75 80
 Arg Met Gly Lys Gly Lys Gly Asn Val Glu Tyr Trp Val Ala Leu Ile
 85 90 95
 Gln Pro Gly Lys Val Leu Tyr Glu Met Asp Gly Val Pro Glu Glu Leu
 100 105 110
 Ala Arg Glu Ala Phe Lys Leu Ala Ala Lys Leu Pro Ile Lys Thr
 115 120 125
 Thr Phe Val Thr Lys Thr Val Met
 130 135

<210> 319
 <211> 233
 <212> PRT
 <213> Escherichia coli

<400> 319
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
 85 90 95
 Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
 100 105 110
 Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
 115 120 125
 Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
 130 135 140
 Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
 145 150 155 160
 Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
 165 170 175
 Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
 180 185 190
 Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
 195 200 205
 Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
 210 215 220
 Lys Lys Gln Gln Arg Lys Gly Arg Lys

225

230

<210> 320

<211> 110

<212> PRT

<213> Escherichia coli

<400> 320

Met	Glu	Thr	Ile	Ala	Lys	His	Arg	His	Ala	Arg	Ser	Ser	Ala	Gln	Lys
1				5					10					15	
Val	Arg	Leu	Val	Ala	Asp	Leu	Ile	Arg	Gly	Lys	Lys	Val	Ser	Gln	Ala
			20					25					30		
Leu	Asp	Ile	Leu	Thr	Tyr	Thr	Asn	Lys	Lys	Ala	Ala	Val	Leu	Val	Lys
		35					40					45			
Lys	Val	Leu	Glu	Ser	Ala	Ile	Ala	Asn	Ala	Glu	His	Asn	Asp	Gly	Ala
		50				55					60				
Asp	Ile	Asp	Asp	Leu	Lys	Val	Thr	Lys	Ile	Phe	Val	Asp	Glu	Gly	Pro
65					70					75					80
Ser	Met	Lys	Arg	Ile	Met	Pro	Arg	Ala	Lys	Gly	Arg	Ala	Asp	Arg	Ile
				85					90					95	
Leu	Lys	Arg	Thr	Ser	His	Ile	Thr	Val	Val	Val	Ser	Asp	Arg		
			100					105					110		

<210> 321

<211> 92

<212> PRT

<213> Escherichia coli

<400> 321

Met	Pro	Arg	Ser	Leu	Lys	Lys	Gly	Pro	Phe	Ile	Asp	Leu	His	Leu	Leu
1				5					10					15	
Lys	Lys	Val	Glu	Lys	Ala	Val	Glu	Ser	Gly	Asp	Lys	Lys	Pro	Leu	Arg
			20					25					30		
Thr	Trp	Ser	Arg	Arg	Ser	Thr	Ile	Phe	Pro	Asn	Met	Ile	Gly	Leu	Thr
		35				40						45			
Ile	Ala	Val	His	Asn	Gly	Arg	Gln	His	Val	Pro	Val	Phe	Val	Thr	Asp
	50				55						60				
Glu	Met	Val	Gly	His	Lys	Leu	Gly	Glu	Phe	Ala	Pro	Thr	Arg	Thr	Tyr
65					70				75						80
Arg	Gly	His	Ala	Ala	Asp	Lys	Lys	Ala	Lys	Lys	Lys				
				85					90						

<210> 322

<211> 273

<212> PRT

<213> Escherichia coli

<400> 322

Met	Ala	Val	Val	Lys	Cys	Lys	Pro	Thr	Ser	Pro	Gly	Arg	Arg	His	Val
1				5					10					15	
Val	Lys	Val	Val	Asn	Pro	Glu	Leu	His	Lys	Gly	Lys	Pro	Phe	Ala	Pro
			20					25					30		
Leu	Leu	Glu	Lys	Asn	Ser	Lys	Ser	Gly	Gly	Arg	Asn	Asn	Asn	Gly	Arg
		35					40					45			

<213> Escherichia coli

<400> 324

Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
1 5 10 15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
20 25 30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
35 40 45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
50 55 60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65 70 75 80
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
85 90 95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
100 105 110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
115 120 125
Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
130 135 140
Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
145 150 155 160
Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
165 170 175
Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
180 185 190
Val Lys Gln Val Glu Glu Met Leu Ala
195 200

<210> 325

<211> 209

<212> PRT

<213> Escherichia coli

<400> 325

Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
1 5 10 15
Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
20 25 30
Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
35 40 45
Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
50 55 60
Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
65 70 75 80
Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
85 90 95
Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
100 105 110
Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
115 120 125
Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
130 135 140
Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
145 150 155 160

Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
165 170 175
Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
180 185 190
Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
195 200 205
Ala

<210> 326
<211> 103
<212> PRT
<213> Escherichia coli

<400> 326
Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg
1 5 10 15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr
20 25 30
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg
35 40 45
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln
50 55 60
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr
65 70 75 80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val
85 90 95
Asp Val Gln Ile Ser Leu Gly
100

<210> 327
<211> 104
<212> PRT
<213> Escherichia coli

<400> 327
Met Ile Arg Lys Ala Phe Val Met Gln Val Asn Pro Asp Ala His Glu
1 5 10 15
Glu Tyr Gln Arg Arg His Asn Pro Ile Trp Pro Glu Leu Glu Ala Val
20 25 30
Leu Lys Ser His Gly Ala His Asn Tyr Ala Ile Tyr Leu Asp Lys Ala
35 40 45
Arg Asn Leu Leu Phe Ala Met Val Glu Ile Glu Ser Glu Glu Arg Trp
50 55 60
Asn Ala Val Ala Ser Thr Asp Val Cys Gln Arg Trp Trp Lys Tyr Met
65 70 75 80
Thr Asp Val Met Pro Ala Asn Pro Asp Asn Ser Pro Val Ser Ser Glu
85 90 95
Leu Gln Glu Val Phe Tyr Leu Pro
100

<210> 328
<211> 287
<212> PRT

<213> Escherichia coli

<400> 328

Met Ile Arg Ser Met Thr Ala Tyr Ala Arg Arg Glu Ile Lys Gly Glu
1 5 10 15
Trp Gly Ser Ala Thr Trp Glu Met Arg Ser Val Asn Gln Arg Tyr Leu
20 25 30
Glu Thr Tyr Phe Arg Leu Pro Glu Gln Phe Arg Ser Leu Glu Pro Val
35 40 45
Val Arg Glu Arg Ile Arg Ser Arg Leu Thr Arg Gly Lys Val Glu Cys
50 55 60
Thr Leu Arg Tyr Glu Pro Asp Val Ser Ala Gln Gly Glu Leu Ile Leu
65 70 75 80
Asn Glu Lys Leu Ala Lys Gln Leu Val Thr Ala Ala Asn Trp Val Lys
85 90 95
Met Gln Ser Asp Glu Gly Glu Ile Asn Pro Val Asp Ile Leu Arg Trp
100 105 110
Pro Gly Val Met Ala Ala Gln Glu Gln Asp Leu Asp Ala Ile Ala Ala
115 120 125
Glu Ile Leu Ala Ala Leu Asp Gly Thr Leu Asp Asp Phe Ile Val Ala
130 135 140
Arg Glu Thr Glu Gly Gln Ala Leu Lys Ala Leu Ile Glu Gln Arg Leu
145 150 155 160
Glu Gly Val Thr Ala Glu Val Val Lys Val Arg Ser His Met Pro Glu
165 170 175
Ile Leu Gln Trp Gln Arg Glu Arg Leu Val Ala Lys Leu Glu Asp Ala
180 185 190
Gln Val Gln Leu Glu Asn Asn Arg Leu Glu Gln Glu Leu Val Leu Leu
195 200 205
Ala Gln Arg Ile Asp Val Ala Glu Glu Leu Asp Arg Leu Glu Ala His
210 215 220
Val Lys Glu Thr Tyr Asn Ile Leu Lys Lys Lys Glu Ala Val Gly Arg
225 230 235 240
Arg Leu Asp Phe Met Met Gln Glu Phe Asn Arg Glu Ser Asn Thr Leu
245 250 255
Ala Ser Lys Ser Ile Asn Ala Glu Val Thr Asn Ser Ala Ile Glu Leu
260 265 270
Lys Val Leu Ile Glu Gln Met Arg Glu Gln Ile Gln Asn Ile Glu
275 280 285

<210> 329

<211> 163

<212> PRT

<213> Escherichia coli

<400> 329

Met Ser Thr Glu Thr Ile Glu Ile Phe Asn Asn Ser Asp Glu Trp Ala
1 5 10 15
Asn Gln Leu Lys His Ala Leu Ser Lys Gly Glu Asn Leu Ala Leu Leu
20 25 30
His Gly Leu Thr Pro Asp Ile Leu Asp Arg Ile Tyr Ala Tyr Ala Phe
35 40 45
Asp Tyr His Glu Lys Gly Asn Ile Thr Asp Ala Glu Ile Tyr Tyr Lys
50 55 60
Phe Leu Cys Ile Tyr Ala Phe Glu Asn His Glu Tyr Leu Lys Asp Phe
65 70 75 80

Ala	Ser	Val	Cys	Gln	Pro	Lys	Lys	Lys	Tyr	Gln	Gln	Ala	Tyr	Asp	Leu
				85					90					95	
Tyr	Lys	Leu	Ser	Tyr	Asn	Tyr	Phe	Pro	Tyr	Asp	Asp	Tyr	Ser	Val	Ile
			100					105					110		
Tyr	Arg	Met	Gly	Gln	Cys	Gln	Ile	Gly	Ala	Lys	Asn	Ile	Asp	Asn	Ala
		115					120					125			
Met	Gln	Cys	Phe	Tyr	His	Ile	Asn	Asn	Cys	Glu	Asp	Asp	Ser	Val	
		130				135				140					
Lys	Ser	Lys	Ala	Gln	Ala	Tyr	Ile	Glu	Leu	Leu	Asn	Asp	Asn	Ser	Glu
145					150					155					160
Asp	Asn	Gly													

<210> 330
 <211> 648
 <212> PRT
 <213> Escherichia coli

<400> 330

Met	Asn	Ile	Leu	Gly	Phe	Phe	Gln	Arg	Leu	Gly	Arg	Ala	Leu	Gln	Leu
1				5					10					15	
Pro	Ile	Ala	Val	Leu	Pro	Val	Ala	Ala	Leu	Leu	Leu	Arg	Phe	Gly	Gln
			20					25					30		
Pro	Asp	Leu	Leu	Asn	Val	Ala	Phe	Ile	Ala	Gln	Ala	Gly	Gly	Ala	Ile
		35					40					45			
Phe	Asp	Asn	Leu	Ala	Leu	Ile	Phe	Ala	Ile	Gly	Val	Ala	Ser	Ser	Trp
		50				55					60				
Ser	Lys	Asp	Ser	Ala	Gly	Ala	Ala	Ala	Leu	Ala	Gly	Ala	Val	Gly	Tyr
65					70				75						80
Phe	Val	Leu	Thr	Lys	Ala	Met	Val	Thr	Ile	Asn	Pro	Glu	Ile	Asn	Met
				85					90					95	
Gly	Val	Leu	Ala	Gly	Ile	Ile	Thr	Gly	Leu	Val	Gly	Gly	Ala	Ala	Tyr
			100					105					110		
Asn	Arg	Trp	Ser	Asp	Ile	Lys	Leu	Pro	Asp	Phe	Leu	Ser	Phe	Phe	Gly
		115				120						125			
Gly	Lys	Arg	Phe	Val	Pro	Ile	Ala	Thr	Gly	Phe	Phe	Cys	Leu	Val	Leu
	130					135					140				
Ala	Ala	Ile	Phe	Gly	Tyr	Val	Trp	Pro	Pro	Val	Gln	His	Ala	Ile	His
145					150					155					160
Ala	Gly	Gly	Glu	Trp	Ile	Val	Ser	Ala	Gly	Ala	Leu	Gly	Ser	Gly	Ile
			165						170					175	
Phe	Gly	Phe	Ile	Asn	Arg	Leu	Leu	Ile	Pro	Thr	Gly	Leu	His	Gln	Val
			180					185					190		
Leu	Asn	Thr	Ile	Ala	Trp	Phe	Gln	Ile	Gly	Glu	Phe	Thr	Asn	Ala	Ala
		195					200					205			
Gly	Thr	Val	Phe	His	Gly	Asp	Ile	Asn	Arg	Phe	Tyr	Ala	Gly	Asp	Gly
	210					215					220				
Thr	Ala	Gly	Met	Phe	Met	Ser	Gly	Phe	Phe	Pro	Ile	Met	Met	Phe	Gly
225					230					235					240
Leu	Pro	Gly	Ala	Ala	Leu	Ala	Met	Tyr	Phe	Ala	Ala	Pro	Lys	Glu	Arg
				245					250					255	
Arg	Pro	Met	Val	Gly	Gly	Met	Leu	Leu	Ser	Val	Ala	Val	Thr	Ala	Phe
			260					265					270		
Leu	Thr	Gly	Val	Thr	Glu	Pro	Leu	Glu	Phe	Leu	Phe	Met	Phe	Leu	Ala
		275					280					285			
Pro	Leu	Leu	Tyr	Leu	Leu	His	Ala	Leu	Leu	Thr	Gly	Ile	Ser	Leu	Phe

Gly	Val	Asp	Asn	Tyr	Arg	Gly	Pro	Ser	Thr	Ala	Ala	Gln	Met	Thr	Phe	
	35						40					45				
Asn	Tyr	Thr	Ser	Thr	Ala	Ser	Asn	Leu	Val	Phe	Tyr	Lys	Pro	Thr	Gln	
	50					55				60						
Leu	Gly	Pro	Thr	Gly	Val	Lys	Met	Tyr	Trp	Ser	Tyr	Leu	Asp	Thr	Gly	
65					70					75					80	
Thr	Gly	Gly	Gly	Ile	Leu	Tyr	Cys	Asn	Thr	Ser	Gly	Arg	Ala	Asn	Pro	
				85					90					95		
Gly	Pro	Ile	Thr	Ile	Glu	Asn	Ala	Met	Val	Tyr	Ser	Gly	Lys	Asp	Tyr	
			100					105					110			
Gly	Gly	His	Lys	Leu	Phe	Asn	Thr	Ser	Val	Pro	Gly	Leu	Tyr	Tyr	Thr	
		115					120					125				
Met	Leu	Ile	Ser	Arg	Val	Trp	Ser	Ala	Tyr	Asp	Thr	Ile	Thr	Asp	Ile	
	130					135					140					
Gln	Ser	Pro	Gly	Ile	Tyr	Ile	Gly	Asp	Pro	Ser	Asn	Gln	Glu	Phe	Phe	
145					150					155					160	
Phe	Ser	Val	Thr	Asp	Ser	Asp	Leu	Gln	Thr	Lys	Gly	Cys	Asn	Lys	Ala	
				165					170					175		
Asp	Asp	Tyr	Asp	Lys	Phe	Trp	Ala	Ile	Gly	Gly	Ile	Val	His	Asn	Ile	
		180					185						190			
Thr	Val	Glu	Phe	Tyr	Thr	Asp	Thr	Asn	Phe	Asp	Pro	Thr	Leu	Asn	Gln	
		195					200					205				
Gln	Val	Gln	Leu	Ser	Ser	Ser	Ser	Asn	Tyr	Leu	Tyr	Ser	Phe	Lys	Ala	
	210					215					220					
Tyr	Ser	Pro	Gly	Thr	Lys	Val	Val	Asp	His	Ser	Asn	His	Ile	Tyr	Val	
225					230					235					240	
Asn	Phe	Thr	Leu	Asn	Val	Lys	Leu	Thr	Leu	Pro	Thr	Cys	Phe	Thr		
			245					250					255			
Ser	Ile	Leu	Thr	Gly	Pro	Ser	Val	Asn	Gly	Ser	Thr	Val	Arg	Met	Gly	
		260						265					270			
Glu	Tyr	Ser	Ser	Gly	Thr	Ile	Lys	Asn	Gly	Ala	Ser	Pro	Val	Pro	Phe	
		275					280					285				
Asp	Ile	Ser	Leu	Gln	Asn	Cys	Ile	Arg	Val	Arg	Asn	Ile	Glu	Thr	Lys	
	290					295					300					
Leu	Val	Thr	Gly	Lys	Val	Gly	Thr	Gln	Asn	Thr	Gln	Leu	Leu	Gly	Asn	
305					310					315					320	
Thr	Leu	Thr	Gly	Ser	Thr	Ala	Ala	Lys	Gly	Val	Gly	Val	Leu	Ile	Glu	
				325					330					335		
Gly	Leu	Ala	Thr	Ser	Lys	Asn	Pro	Leu	Met	Thr	Leu	Lys	Pro	Asn	Asp	
		340						345					350			
Thr	Asn	Ser	Val	Tyr	Ile	Asp	Tyr	Glu	Thr	Glu	Asp	Asp	Thr	Ser	Asp	
		355					360					365				
Gly	Val	Tyr	Pro	Asn	Gln	Gly	Asn	Gly	Thr	Ser	Gln	Pro	Leu	His	Phe	
	370					375					380					
Gln	Ala	Thr	Leu	Lys	Gln	Asp	Gly	Asn	Ile	Ala	Ile	Glu	Pro	Gly	Glu	
385					390					395					400	
Phe	Lys	Ala	Thr	Ser	Thr	Phe	Gln	Val	Thr	Tyr	Pro					
			405						410							

<210> 332

<211> 198

<212> PRT

<213> Escherichia coli

<400> 332

Met His Pro Thr Gln Arg Lys Leu Met Lys Arg Ile Ile Leu Phe Leu

Pro Ala Thr Phe Thr Val Thr Tyr Asn
 195 200

<210> 334
 <211> 203
 <212> PRT
 <213> Escherichia coli

<400> 334
 Met Glu Phe Gly Val Arg Phe Ser Asn Tyr Lys Gly Arg Gln Met Ile
 1 5 10 15
 Lys Thr Thr Pro His Lys Ile Val Ile Leu Met Gly Ile Leu Leu Ser
 20 25 30
 Pro Ser Val Phe Ala Thr Asp Ile Asn Val Glu Phe Thr Ala Thr Val
 35 40 45
 Lys Ala Thr Thr Cys Asn Ile Thr Leu Thr Gly Asn Asn Val Thr Asn
 50 55 60
 Asp Gly Asn Asn Asn Tyr Thr Leu Arg Ile Pro Lys Met Gly Leu Asp
 65 70 75 80
 Lys Ile Ala Asn Lys Thr Thr Glu Ser Gln Ala Asp Phe Lys Leu Val
 85 90 95
 Ala Ser Gly Cys Ser Ser Gly Ile Ser Trp Ile Asp Thr Thr Leu Thr
 100 105 110
 Gly Asn Ala Ser Ser Ser Ser Pro Lys Leu Ile Ile Pro Gln Ser Gly
 115 120 125
 Asp Ser Ser Ser Thr Thr Ser Asn Ile Gly Met Gly Phe Lys Lys Arg
 130 135 140
 Thr Thr Asp Asp Ala Thr Phe Leu Lys Pro Asn Ser Ala Glu Lys Ile
 145 150 155 160
 Arg Trp Ser Thr Asp Glu Met Gln Pro Asp Lys Gly Leu Glu Met Thr
 165 170 175
 Val Ala Leu Arg Glu Thr Asp Ala Gly Gln Gly Val Pro Gly Asn Phe
 180 185 190
 Arg Ala Leu Ala Thr Phe Asn Phe Ile Tyr Gln
 195 200

<210> 335
 <211> 139
 <212> PRT
 <213> Escherichia coli

<400> 335
 Met Ala Met Thr Tyr His Leu Asp Val Val Ser Ala Glu Gln Gln Met
 1 5 10 15
 Phe Ser Gly Leu Val Glu Lys Ile Gln Val Thr Gly Ser Glu Gly Glu
 20 25 30
 Leu Gly Ile Tyr Pro Gly His Ala Pro Leu Leu Thr Ala Ile Lys Pro
 35 40 45
 Gly Met Ile Arg Ile Val Lys Gln His Gly His Glu Glu Phe Ile Tyr
 50 55 60
 Leu Ser Gly Gly Ile Leu Glu Val Gln Pro Gly Asn Val Thr Val Leu
 65 70 75 80
 Ala Asp Thr Ala Ile Arg Gly Gln Asp Leu Asp Glu Ala Arg Ala Met
 85 90 95
 Glu Ala Lys Arg Lys Ala Glu Glu His Ile Ser Ser Ser His Gly Asp

	100		105		110
Val	Asp	Tyr	Ala	Gln	Ala
	115		120		125
Leu	Arg	Val	Ile	Glu	Leu
	130		135		

<210> 336
 <211> 460
 <212> PRT
 <213> Escherichia coli

<400> 336

Met	Ala	Thr	Gly	Lys	Ile	Val	Gln	Val	Ile	Gly	Ala	Val	Val	Asp	Val
1				5				10						15	
Glu	Phe	Pro	Gln	Asp	Ala	Val	Pro	Arg	Val	Tyr	Asp	Ala	Leu	Glu	Val
			20					25					30		
Gln	Asn	Gly	Asn	Glu	Arg	Leu	Val	Leu	Glu	Val	Gln	Gln	Gln	Leu	Gly
		35					40					45			
Gly	Gly	Ile	Val	Arg	Thr	Ile	Ala	Met	Gly	Ser	Ser	Asp	Gly	Leu	Arg
	50				55					60					
Arg	Gly	Leu	Asp	Val	Lys	Asp	Leu	Glu	His	Pro	Ile	Glu	Val	Pro	Val
65					70					75				80	
Gly	Lys	Ala	Thr	Leu	Gly	Arg	Ile	Met	Asn	Val	Leu	Gly	Glu	Pro	Val
				85					90					95	
Asp	Met	Lys	Gly	Glu	Ile	Gly	Glu	Glu	Arg	Trp	Ala	Ile	His	Arg	
			100					105					110		
Ala	Ala	Pro	Ser	Tyr	Glu	Glu	Leu	Ser	Asn	Ser	Gln	Glu	Leu	Leu	Glu
		115					120					125			
Thr	Gly	Ile	Lys	Val	Ile	Asp	Leu	Met	Cys	Pro	Phe	Ala	Lys	Gly	Gly
	130					135					140				
Lys	Val	Gly	Leu	Phe	Gly	Gly	Ala	Gly	Val	Gly	Lys	Thr	Val	Asn	Met
145					150					155				160	
Met	Glu	Leu	Ile	Arg	Asn	Ile	Ala	Ile	Glu	His	Ser	Gly	Tyr	Ser	Val
				165					170					175	
Phe	Ala	Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly	Asn	Asp	Phe	Tyr	His
			180					185					190		
Glu	Met	Thr	Asp	Ser	Asn	Val	Ile	Asp	Lys	Val	Ser	Leu	Val	Tyr	Gly
		195					200					205			
Gln	Met	Asn	Glu	Pro	Pro	Gly	Asn	Arg	Leu	Arg	Val	Ala	Leu	Thr	Gly
	210					215					220				
Leu	Thr	Met	Ala	Glu	Lys	Phe	Arg	Asp	Glu	Gly	Arg	Asp	Val	Leu	Leu
225					230					235				240	
Phe	Val	Asp	Asn	Ile	Tyr	Arg	Tyr	Thr	Leu	Ala	Gly	Thr	Glu	Val	Ser
			245						250					255	
Ala	Leu	Leu	Gly	Arg	Met	Pro	Ser	Ala	Val	Gly	Tyr	Gln	Pro	Thr	Leu
			260					265					270		
Ala	Glu	Glu	Met	Gly	Val	Leu	Gln	Glu	Arg	Ile	Thr	Ser	Thr	Lys	Thr
		275					280					285			
Gly	Ser	Ile	Thr	Ser	Val	Gln	Ala	Val	Tyr	Val	Pro	Ala	Asp	Asp	Leu
	290					295					300				
Thr	Asp	Pro	Ser	Pro	Ala	Thr	Thr	Phe	Ala	His	Leu	Asp	Ala	Thr	Val
305					310					315				320	
Val	Leu	Ser	Arg	Gln	Ile	Ala	Ser	Leu	Gly	Ile	Tyr	Pro	Ala	Val	Asp
			325						330					335	
Pro	Leu	Asp	Ser	Thr	Ser	Arg	Gln	Leu	Asp	Pro	Leu	Val	Val	Gly	Gln
			340					345					350		

Glu His Tyr Asp Thr Ala Arg Gly Val Gln Ser Ile Leu Gln Arg Tyr
 355 360 365
 Gln Glu Leu Lys Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser
 370 375 380
 Glu Glu Asp Lys Leu Val Val Ala Arg Ala Arg Lys Ile Gln Arg Phe
 385 390 395 400
 Leu Ser Gln Pro Phe Val Ala Glu Val Phe Thr Gly Ser Pro Gly
 405 410 415
 Lys Tyr Val Ser Leu Lys Asp Thr Ile Arg Gly Phe Lys Gly Ile Met
 420 425 430
 Glu Gly Glu Tyr Asp His Leu Pro Glu Gln Ala Phe Tyr Met Val Gly
 435 440 445
 Ser Ile Glu Glu Ala Val Glu Lys Ala Lys Lys Leu
 450 455 460

<210> 337
 <211> 287
 <212> PRT
 <213> Escherichia coli

<400> 337
 Met Ala Gly Ala Lys Glu Ile Arg Ser Lys Ile Ala Ser Val Gln Asn
 1 5 10 15
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
 20 25 30
 Arg Lys Ser Gln Asp Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Thr
 35 40 45
 Met Arg Lys Val Ile Gly His Leu Ala His Gly Asn Leu Glu Tyr Lys
 50 55 60
 His Pro Tyr Leu Glu Asp Arg Asp Val Lys Arg Val Gly Tyr Leu Val
 65 70 75 80
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
 85 90 95
 Lys Lys Leu Leu Ala Glu Met Lys Thr Trp Thr Asp Lys Gly Val Gln
 100 105 110
 Cys Asp Leu Ala Met Ile Gly Ser Lys Gly Val Ser Phe Phe Asn Ser
 115 120 125
 Val Gly Gly Asn Val Val Ala Gln Val Thr Gly Met Gly Asp Asn Pro
 130 135 140
 Ser Leu Ser Glu Leu Ile Gly Pro Val Lys Val Met Leu Gln Ala Tyr
 145 150 155 160
 Asp Glu Gly Arg Leu Asp Lys Leu Tyr Ile Val Ser Asn Lys Phe Ile
 165 170 175
 Asn Thr Met Ser Gln Val Pro Thr Ile Ser Gln Leu Leu Pro Leu Pro
 180 185 190
 Ala Ser Asp Asp Asp Asp Leu Lys His Lys Ser Trp Asp Tyr Leu Tyr
 195 200 205
 Glu Pro Asp Pro Lys Ala Leu Leu Asp Thr Leu Leu Arg Arg Tyr Val
 210 215 220
 Glu Ser Gln Val Tyr Gln Gly Val Val Glu Asn Leu Ala Ser Glu Gln
 225 230 235 240
 Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Gly Gly Ser
 245 250 255
 Leu Ile Lys Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala Ser
 260 265 270
 Ile Thr Gln Glu Leu Thr Glu Ile Val Ser Gly Ala Ala Ala Val

<210> 338
 <211> 513
 <212> PRT
 <213> Escherichia coli

<400> 338

Met	Gln	Leu	Asn	Ser	Thr	Glu	Ile	Ser	Glu	Leu	Ile	Lys	Gln	Arg	Ile
1				5					10					15	
Ala	Gln	Phe	Asn	Val	Val	Ser	Glu	Ala	His	Asn	Glu	Gly	Thr	Ile	Val
			20					25					30		
Ser	Val	Ser	Asp	Gly	Val	Ile	Arg	Ile	His	Gly	Leu	Ala	Asp	Cys	Met
		35					40					45			
Gln	Gly	Glu	Met	Ile	Ser	Leu	Pro	Gly	Asn	Arg	Tyr	Ala	Ile	Ala	Leu
	50					55					60				
Asn	Leu	Glu	Arg	Asp	Ser	Val	Gly	Ala	Val	Val	Met	Gly	Pro	Tyr	Ala
65					70					75					80
Asp	Leu	Ala	Glu	Gly	Met	Lys	Val	Lys	Cys	Thr	Gly	Arg	Ile	Leu	Glu
			85					90						95	
Val	Pro	Val	Gly	Arg	Gly	Leu	Leu	Gly	Arg	Val	Val	Asn	Thr	Leu	Gly
			100					105					110		
Ala	Pro	Ile	Asp	Gly	Lys	Gly	Pro	Leu	Asp	His	Asp	Gly	Phe	Ser	Ala
		115					120					125			
Val	Glu	Ala	Ile	Ala	Pro	Gly	Val	Ile	Glu	Arg	Gln	Ser	Val	Asp	Gln
	130					135					140				
Pro	Val	Gln	Thr	Gly	Tyr	Lys	Ala	Val	Asp	Ser	Met	Ile	Pro	Ile	Gly
145					150					155					160
Arg	Gly	Gln	Arg	Glu	Leu	Ile	Ile	Gly	Asp	Arg	Gln	Thr	Gly	Lys	Thr
				165					170					175	
Ala	Leu	Ala	Ile	Asp	Ala	Ile	Ile	Asn	Gln	Arg	Asp	Ser	Gly	Ile	Lys
			180					185					190		
Cys	Ile	Tyr	Val	Ala	Ile	Gly	Gln	Lys	Ala	Ser	Thr	Ile	Ser	Asn	Val
	195						200					205			
Val	Arg	Lys	Leu	Glu	Glu	His	Gly	Ala	Leu	Ala	Asn	Thr	Ile	Val	Val
	210					215					220				
Val	Ala	Thr	Ala	Ser	Glu	Ser	Ala	Ala	Leu	Gln	Tyr	Leu	Ala	Pro	Tyr
225					230					235				240	
Ala	Gly	Cys	Ala	Met	Gly	Glu	Tyr	Phe	Arg	Asp	Arg	Gly	Glu	Asp	Ala
			245						250					255	
Leu	Ile	Ile	Tyr	Asp	Asp	Leu	Ser	Lys	Gln	Ala	Val	Ala	Tyr	Arg	Gln
			260					265					270		
Ile	Ser	Leu	Leu	Leu	Arg	Arg	Pro	Pro	Gly	Arg	Glu	Ala	Phe	Pro	Gly
	275						280					285			
Asp	Val	Phe	Tyr	Leu	His	Ser	Arg	Leu	Leu	Glu	Arg	Ala	Ala	Arg	Val
	290					295					300				
Asn	Ala	Glu	Tyr	Val	Glu	Ala	Phe	Thr	Lys	Gly	Glu	Val	Lys	Gly	Lys
305					310					315					320
Thr	Gly	Ser	Leu	Thr	Ala	Leu	Pro	Ile	Ile	Glu	Thr	Gln	Ala	Gly	Asp
				325					330					335	
Val	Ser	Ala	Phe	Val	Pro	Thr	Asn	Val	Ile	Ser	Ile	Thr	Asp	Gly	Gln
			340				345						350		
Ile	Phe	Leu	Glu	Thr	Asn	Leu	Phe	Asn	Ala	Gly	Ile	Arg	Pro	Ala	Val
	355					360						365			
Asn	Pro	Gly	Ile	Ser	Val	Ser	Arg	Val	Gly	Gly	Ala	Ala	Gln	Thr	Lys
	370					375					380				

Ile Met Lys Lys Leu Ser Gly Gly Ile Arg Thr Ala Leu Ala Gln Tyr
 385 390 395 400
 Arg Glu Leu Ala Ala Phe Ser Gln Phe Ala Ser Asp Leu Asp Asp Ala
 405 410 415
 Thr Arg Lys Gln Leu Asp His Gly Gln Lys Val Thr Glu Leu Leu Lys
 420 425 430
 Gln Lys Gln Tyr Ala Pro Met Ser Val Ala Gln Gln Ser Leu Val Leu
 435 440 445
 Phe Ala Ala Glu Arg Gly Tyr Leu Ala Asp Val Glu Leu Ser Lys Ile
 450 455 460
 Gly Ser Phe Glu Ala Ala Leu Leu Ala Tyr Val Asp Arg Asp His Ala
 465 470 475 480
 Pro Leu Met Gln Glu Ile Asn Gln Thr Gly Gly Tyr Asn Asp Glu Ile
 485 490 495
 Glu Gly Lys Leu Lys Gly Ile Leu Asp Ser Phe Lys Ala Thr Gln Ser
 500 505 510
 Trp

<210> 339
 <211> 177
 <212> PRT
 <213> Escherichia coli

<400> 339
 Met Ser Glu Phe Ile Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15
 Asp Phe Ala Val Glu His Gln Ser Val Glu Arg Trp Gln Asp Met Leu
 20 25 30
 Ala Phe Ala Ala Glu Val Thr Lys Asn Glu Gln Met Ala Glu Leu Leu
 35 40 45
 Ser Gly Ala Leu Ala Pro Glu Thr Leu Ala Glu Ser Phe Ile Ala Val
 50 55 60
 Cys Gly Glu Gln Leu Asp Glu Asn Gly Gln Asn Leu Ile Arg Val Met
 65 70 75 80
 Ala Glu Asn Gly Arg Leu Asn Ala Leu Pro Asp Val Leu Glu Gln Phe
 85 90 95
 Ile His Leu Arg Ala Val Ser Glu Ala Thr Ala Glu Val Asp Val Ile
 100 105 110
 Ser Ala Ala Ala Leu Ser Glu Gln Leu Ala Lys Ile Ser Ala Ala
 115 120 125
 Met Glu Lys Arg Leu Ser Arg Lys Val Lys Leu Asn Cys Lys Ile Asp
 130 135 140
 Lys Ser Val Met Ala Gly Val Ile Ile Arg Ala Gly Asp Met Val Ile
 145 150 155 160
 Asp Gly Ser Val Arg Gly Arg Leu Glu Arg Leu Ala Asp Val Leu Gln
 165 170 175
 Ser

<210> 340
 <211> 156
 <212> PRT
 <213> Escherichia coli

<400> 340

Met Asn Leu Asn Ala Thr Ile Leu Gly Gln Ala Ile Ala Phe Val Leu
1 5 10 15
Phe Val Leu Phe Cys Met Lys Tyr Val Trp Pro Pro Leu Met Ala Ala
20 25 30
Ile Glu Lys Arg Gln Lys Glu Ile Ala Asp Gly Leu Ala Ser Ala Glu
35 40 45
Arg Ala His Lys Asp Leu Asp Leu Ala Lys Ala Ser Ala Thr Asp Gln
50 55 60
Leu Lys Lys Ala Lys Ala Glu Ala Gln Val Ile Ile Glu Gln Ala Asn
65 70 75 80
Lys Arg Arg Ser Gln Ile Leu Asp Glu Ala Lys Ala Glu Ala Glu Gln
85 90 95
Glu Arg Thr Lys Ile Val Ala Gln Ala Gln Ala Glu Ile Glu Ala Glu
100 105 110
Arg Lys Arg Ala Arg Glu Glu Leu Arg Lys Gln Val Ala Ile Leu Ala
115 120 125
Val Ala Gly Ala Glu Lys Ile Ile Glu Arg Ser Val Asp Glu Ala Ala
130 135 140
Asn Ser Asp Ile Val Asp Lys Leu Val Ala Glu Leu
145 150 155

<210> 341

<211> 79

<212> PRT

<213> Escherichia coli

<400> 341

Met Glu Asn Leu Asn Met Asp Leu Leu Tyr Met Ala Ala Ala Val Met
1 5 10 15
Met Gly Leu Ala Ala Ile Gly Ala Ala Ile Gly Ile Gly Ile Leu Gly
20 25 30
Gly Lys Phe Leu Glu Gly Ala Ala Arg Gln Pro Asp Leu Ile Pro Leu
35 40 45
Leu Arg Thr Gln Phe Phe Ile Val Met Gly Leu Val Asp Ala Ile Pro
50 55 60
Met Ile Ala Val Gly Leu Gly Leu Tyr Val Met Phe Ala Val Ala
65 70 75

<210> 342

<211> 271

<212> PRT

<213> Escherichia coli

<400> 342

Met Ala Ser Glu Asn Met Thr Pro Gln Asp Tyr Ile Gly His His Leu
1 5 10 15
Asn Asn Leu Gln Leu Asp Leu Arg Thr Phe Ser Leu Val Asp Pro Gln
20 25 30
Asn Pro Pro Ala Thr Phe Trp Thr Ile Asn Ile Asp Ser Met Phe Phe
35 40 45
Ser Val Val Leu Gly Leu Leu Phe Leu Val Leu Phe Arg Ser Val Ala
50 55 60
Lys Lys Ala Thr Ser Gly Val Pro Gly Lys Phe Gln Thr Ala Ile Glu
65 70 75 80

Leu Val Ile Gly Phe Val Asn Gly Ser Val Lys Asp Met Tyr His Gly
 85 90 95
 Lys Ser Lys Leu Ile Ala Pro Leu Ala Leu Thr Ile Phe Val Trp Val
 100 105 110
 Phe Leu Met Asn Leu Met Asp Leu Leu Pro Ile Asp Leu Leu Pro Tyr
 115 120 125
 Ile Ala Glu His Val Leu Gly Leu Pro Ala Leu Arg Val Val Pro Ser
 130 135 140
 Ala Asp Val Asn Val Thr Leu Ser Met Ala Leu Gly Val Phe Ile Leu
 145 150 155 160
 Ile Leu Phe Tyr Ser Ile Lys Met Lys Gly Ile Gly Gly Phe Thr Lys
 165 170 175
 Glu Leu Thr Leu Gln Pro Phe Asn His Trp Ala Phe Ile Pro Val Asn
 180 185 190
 Leu Ile Leu Glu Gly Val Ser Leu Leu Ser Lys Pro Val Ser Leu Gly
 195 200 205
 Leu Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile Leu
 210 215 220
 Ile Ala Gly Leu Leu Pro Trp Trp Ser Gln Trp Ile Leu Asn Val Pro
 225 230 235 240
 Trp Ala Ile Phe His Ile Leu Ile Ile Thr Leu Gln Ala Phe Ile Phe
 245 250 255
 Met Val Leu Thr Ile Val Tyr Leu Ser Met Ala Ser Glu Glu His
 260 265 270

<210> 343
 <211> 130
 <212> PRT
 <213> Escherichia coli

<400> 343
 Met Lys Asn Val Met Ser Val Ser Leu Val Ser Arg Asn Val Ala Arg
 1 5 10 15
 Lys Leu Leu Leu Val Gln Leu Leu Val Val Ile Ala Ser Gly Leu Leu
 20 25 30
 Phe Ser Leu Lys Asp Pro Phe Trp Gly Val Ser Ala Ile Ser Gly Gly
 35 40 45
 Leu Ala Val Phe Leu Pro Asn Val Leu Phe Met Ile Phe Ala Trp Arg
 50 55 60
 His Gln Ala His Thr Pro Ala Lys Gly Arg Val Ala Trp Thr Phe Ala
 65 70 75 80
 Phe Gly Glu Ala Phe Lys Val Leu Ala Met Leu Val Leu Leu Val Val
 85 90 95
 Ala Leu Ala Val Leu Lys Ala Val Phe Leu Pro Leu Ile Val Thr Trp
 100 105 110
 Val Leu Val Leu Val Val Gln Ile Leu Ala Pro Ala Val Ile Asn Asn
 115 120 125
 Lys Gly
 130

<210> 344
 <211> 413
 <212> PRT
 <213> Escherichia coli

<212> PRT
 <213> Escherichia coli

<400> 345

Met	Ser	Ser	Ile	Ser	Leu	Ile	Gln	Pro	Asp	Arg	Asp	Leu	Phe	Ser	Trp
1				5					10					15	
Pro	Gln	Tyr	Trp	Ala	Ala	Cys	Phe	Gly	Pro	Ala	Pro	Phe	Leu	Pro	Met
			20					25					30		
Ser	Arg	Glu	Glu	Met	Asp	Gln	Leu	Gly	Trp	Asp	Ser	Cys	Asp	Ile	Ile
		35					40					45			
Leu	Val	Thr	Gly	Asp	Ala	Tyr	Val	Asp	His	Pro	Ser	Phe	Gly	Met	Ala
	50					55					60				
Ile	Cys	Gly	Arg	Met	Leu	Glu	Ala	Gln	Gly	Phe	Arg	Val	Gly	Ile	Ile
65					70					75					80
Ala	Gln	Pro	Asp	Trp	Ser	Ser	Lys	Asp	Asp	Phe	Met	Arg	Leu	Gly	Lys
			85						90					95	
Pro	Asn	Leu	Phe	Phe	Gly	Val	Thr	Ala	Gly	Asn	Met	Asp	Ser	Met	Ile
			100						105					110	
Asn	Arg	Tyr	Thr	Ala	Asp	Arg	Arg	Leu	Arg	His	Asp	Asp	Ala	Tyr	Thr
		115					120					125			
Pro	Asp	Asn	Val	Ala	Gly	Lys	Arg	Pro	Asp	Arg	Ala	Thr	Leu	Val	Tyr
	130					135					140				
Thr	Gln	Arg	Cys	Lys	Glu	Ala	Trp	Lys	Asp	Val	Pro	Val	Ile	Leu	Gly
145					150					155					160
Gly	Ile	Glu	Ala	Ser	Leu	Arg	Arg	Thr	Ala	His	Tyr	Asp	Tyr	Trp	Ser
				165					170					175	
Asp	Thr	Val	Arg	Arg	Ser	Val	Leu	Val	Asp	Ser	Lys	Ala	Asp	Met	Leu
			180					185					190		
Met	Phe	Gly	Asn	Gly	Glu	Arg	Pro	Leu	Val	Glu	Val	Ala	His	Arg	Leu
		195					200					205			
Ala	Met	Gly	Glu	Pro	Ile	Ser	Glu	Ile	Arg	Asp	Val	Arg	Asn	Thr	Ala
	210					215					220				
Ile	Ile	Val	Lys	Glu	Ala	Leu	Pro	Gly	Trp	Ser	Gly	Val	Asp	Ser	Thr
225					230					235					240
Arg	Leu	Asp	Thr	Pro	Gly	Lys	Ile	Asp	Pro	Ile	Pro	His	Pro	Tyr	Gly
			245					250						255	
Glu	Asp	Leu	Pro	Cys	Ala	Asp	Asn	Lys	Pro	Val	Ala	Pro	Lys	Lys	Gln
		260					265						270		
Glu	Ala	Lys	Ala	Val	Thr	Val	Gln	Pro	Pro	Arg	Pro	Lys	Pro	Trp	Glu
	275						280					285			
Lys	Thr	Tyr	Val	Leu	Leu	Pro	Ser	Phe	Glu	Lys	Val	Lys	Gly	Asp	Lys
	290					295					300				
Val	Leu	Tyr	Ala	His	Ala	Ser	Arg	Ile	Leu	His	His	Glu	Thr	Asn	Pro
305					310					315					320
Ala	Val	Pro	Ala	His											
				325											

<210> 346
 <211> 226
 <212> PRT
 <213> Escherichia coli

<400> 346

Met	Ile	Gln	Tyr	Leu	Asn	Val	Phe	Phe	Tyr	Asp	Ile	Tyr	Pro	Tyr	Ile
1				5					10					15	
Cys	Ala	Thr	Val	Phe	Phe	Leu	Gly	Ser	Trp	Leu	Arg	Tyr	Asp	Tyr	Gly

Asp	Asp	Thr	Arg	Gln	Ala	Leu	Asp	Ala	Val	Trp	Glu	Glu	Glu	Gln	Val
			180					185					190		
Lys	Phe	Ile	Glu	Asp	Asn	Ala	Thr	Ala	Cys	Asp	Ser	Ser	Pro	Leu	Asn
		195					200					205			
Gln	Tyr	Gln	Arg	Arg	Phe	Ser	Gln	Asp	Val	Ala	Pro	Gln	Tyr	Val	Asp
	210					215					220				
Ile	Ser	Ala	Gly	Gly	Gly	Lys									
225					230										

<210> 348
 <211> 514
 <212> PRT
 <213> Escherichia coli

<400> 348															
Met	Lys	Ile	Arg	Ser	Gln	Val	Gly	Met	Val	Leu	Asn	Leu	Asp	Lys	Cys
1				5					10					15	
Ile	Gly	Cys	His	Thr	Cys	Ser	Val	Thr	Cys	Lys	Asn	Val	Trp	Thr	Gly
			20					25					30		
Arg	Glu	Gly	Met	Glu	Tyr	Ala	Trp	Phe	Asn	Asn	Val	Glu	Thr	Lys	Pro
		35					40					45			
Gly	Ile	Gly	Tyr	Pro	Lys	Asn	Trp	Glu	Asp	Gln	Glu	Glu	Trp	Gln	Gly
	50					55					60				
Gly	Trp	Val	Arg	Asp	Val	Asn	Gly	Lys	Ile	Arg	Pro	Arg	Leu	Gly	Asn
65					70				75						80
Lys	Met	Gly	Val	Ile	Thr	Lys	Ile	Phe	Ala	Asn	Pro	Val	Val	Pro	Gln
				85				90						95	
Ile	Asp	Asp	Tyr	Tyr	Glu	Pro	Phe	Thr	Phe	Asp	Tyr	Glu	His	Leu	His
			100				105						110		
Ser	Ala	Pro	Glu	Gly	Lys	His	Ile	Pro	Thr	Ala	Arg	Pro	Arg	Ser	Leu
		115					120					125			
Ile	Asp	Gly	Lys	Arg	Met	Asp	Lys	Val	Ile	Trp	Gly	Pro	Asn	Trp	Glu
	130					135					140				
Glu	Leu	Leu	Gly	Gly	Glu	Phe	Glu	Lys	Arg	Ala	Arg	Asp	Arg	Asn	Phe
145					150					155					160
Glu	Ala	Met	Gln	Lys	Glu	Met	Tyr	Gly	Gln	Phe	Glu	Asn	Thr	Phe	Met
				165				170						175	
Met	Tyr	Leu	Pro	Arg	Leu	Cys	Glu	His	Cys	Leu	Asn	Pro	Ser	Cys	Val
			180				185						190		
Ala	Thr	Cys	Pro	Ser	Gly	Ala	Ile	Tyr	Lys	Arg	Glu	Glu	Asp	Gly	Ile
		195					200					205			
Val	Leu	Ile	Asp	Gln	Asp	Lys	Cys	Arg	Gly	Trp	Arg	Leu	Cys	Ile	Ser
	210					215					220				
Gly	Cys	Pro	Tyr	Lys	Lys	Ile	Tyr	Phe	Asn	Trp	Lys	Ser	Gly	Lys	Ser
225					230				235						240
Glu	Lys	Cys	Ile	Phe	Cys	Tyr	Pro	Arg	Ile	Glu	Ser	Gly	Gln	Pro	Thr
				245					250					255	
Val	Cys	Ser	Glu	Thr	Cys	Val	Gly	Arg	Ile	Arg	Tyr	Leu	Gly	Val	Leu
			260				265						270		
Leu	Tyr	Asp	Ala	Asp	Arg	Ile	Glu	Glu	Ala	Ala	Ser	Thr	Glu	Arg	Glu
		275					280					285			
Val	Asp	Leu	Tyr	Glu	Arg	Gln	Cys	Glu	Val	Phe	Leu	Asp	Pro	His	Asp
	290					295				300					
Pro	Ser	Val	Ile	Glu	Glu	Ala	Leu	Lys	Gln	Gly	Ile	Pro	Gln	Asn	Val
305					310				315						320
Ile	Asp	Ala	Ala	Gln	Arg	Ser	Pro	Val	Tyr	Lys	Met	Ala	Met	Asp	Trp

Leu Leu Met Leu Thr Leu Ser Arg Gly Gly Pro Ile Val Trp Ile Ser
 1105 1110 1115 1120
 Glu Thr Asp Ala Arg Glu Leu Thr Ile Val Asp Asn Asp Trp Val Glu
 1125 1130 1135
 Val Phe Asn Ala Asn Gly Ala Leu Thr Ala Arg Ala Val Val Ser Gln
 1140 1145 1150
 Arg Val Pro Pro Gly Met Thr Met Met Tyr His Ala Gln Glu Arg Ile
 1155 1160 1165
 Met Asn Ile Pro Gly Ser Glu Val Thr Gly Met Arg Gly Gly Ile His
 1170 1175 1180
 Asn Ser Val Thr Arg Val Cys Pro Lys Pro Thr His Met Ile Gly Gly
 1185 1190 1195 1200
 Tyr Ala Gln Leu Ala Trp Gly Phe Asn Tyr Tyr Gly Thr Val Gly Ser
 1205 1210 1215
 Asn Arg Asp Glu Phe Ile Met Ile Arg Lys Met Lys Asn Val Asn Trp
 1220 1225 1230
 Leu Asp Asp Glu Gly Arg Asp Gln Val Gln Glu Ala Lys Lys
 1235 1240 1245

<210> 350
 <211> 165
 <212> PRT
 <213> Escherichia coli

<400> 350
 Met Asp Leu Ser Gln Leu Thr Pro Arg Arg Pro Tyr Leu Leu Arg Ala
 1 5 10 15
 Phe Tyr Glu Trp Leu Leu Asp Asn Gln Leu Thr Pro His Leu Val Val
 20 25 30
 Asp Val Thr Leu Pro Gly Val Gln Val Pro Met Glu Tyr Ala Arg Asp
 35 40 45
 Gly Gln Ile Val Leu Asn Ile Ala Pro Arg Ala Val Gly Asn Leu Glu
 50 55 60
 Leu Ala Asn Asp Glu Val Arg Phe Asn Ala Arg Phe Gly Gly Ile Pro
 65 70 75 80
 Arg Gln Val Ser Val Pro Leu Ala Ala Val Leu Ala Ile Tyr Ala Arg
 85 90 95
 Glu Asn Gly Ala Gly Thr Met Phe Glu Pro Glu Ala Ala Tyr Asp Glu
 100 105 110
 Asp Thr Ser Ile Met Asn Asp Glu Ala Ser Ala Asp Asn Glu Thr
 115 120 125
 Val Met Ser Val Ile Asp Gly Asp Lys Pro Asp His Asp Asp Asp Thr
 130 135 140
 His Pro Asp Asp Glu Pro Pro Gln Pro Pro Arg Gly Gly Arg Pro Ala
 145 150 155 160
 Leu Arg Val Val Lys
 165

<210> 351
 <211> 212
 <212> PRT
 <213> Escherichia coli

<400> 351
 Met Ala Val Ala Ala Asn Lys Arg Ser Val Met Thr Leu Phe Ser Gly

1	5	10	15
Pro Thr Asp Ile Tyr Ser His Gln Val Arg Ile Val Leu Ala Glu Lys			
	20	25	30
Gly Val Ser Phe Glu Ile Glu His Val Glu Lys Asp Asn Pro Pro Gln			
	35	40	45
Asp Leu Ile Asp Leu Asn Pro Asn Gln Ser Val Pro Thr Leu Val Asp			
	50	55	60
Arg Glu Leu Thr Leu Trp Glu Ser Arg Ile Ile Met Glu Tyr Leu Asp			
65	70	75	80
Glu Arg Phe Pro His Pro Pro Leu Met Pro Val Tyr Pro Val Ala Arg			
	85	90	95
Gly Glu Ser Arg Leu Tyr Met His Arg Ile Glu Lys Asp Trp Tyr Thr			
	100	105	110
Leu Met Asn Thr Ile Ile Asn Gly Ser Ala Ser Glu Ala Asp Ala Ala			
	115	120	125
Arg Lys Gln Leu Arg Glu Glu Leu Leu Ala Ile Ala Pro Val Phe Gly			
	130	135	140
Gln Lys Pro Tyr Phe Leu Ser Asp Glu Phe Ser Leu Val Asp Cys Tyr			
145	150	155	160
Leu Ala Pro Leu Leu Trp Arg Leu Pro Gln Leu Gly Ile Glu Phe Ser			
	165	170	175
Gly Pro Gly Ala Lys Glu Leu Lys Gly Tyr Met Thr Arg Val Phe Glu			
	180	185	190
Arg Asp Ser Phe Leu Ala Ser Leu Thr Glu Ala Glu Arg Glu Met Arg			
	195	200	205
Leu Gly Arg Ser			
210			

<210> 352
 <211> 505
 <212> PRT
 <213> Escherichia coli

<400> 352
Met Ser Glu Gln His Ala Gln Gly Ala Asp Ala Val Val Asp Leu Asn
1 5 10 15
Asn Glu Leu Lys Thr Arg Arg Glu Lys Leu Ala Asn Leu Arg Glu Gln
20 25 30
Gly Ile Ala Phe Pro Asn Asp Phe Arg Arg Asp His Thr Ser Asp Gln
35 40 45
Leu His Ala Glu Phe Asp Gly Lys Glu Asn Glu Glu Leu Glu Ala Leu
50 55 60
Asn Ile Glu Val Ala Val Ala Gly Arg Met Met Thr Arg Arg Ile Met
65 70 75 80
Gly Lys Ala Ser Phe Val Thr Leu Gln Asp Val Gly Gly Arg Ile Gln
85 90 95
Leu Tyr Val Ala Arg Asp Asp Leu Pro Glu Gly Val Tyr Asn Glu Gln
100 105 110
Phe Lys Lys Trp Asp Leu Gly Asp Ile Leu Gly Ala Lys Gly Lys Leu
115 120 125
Phe Lys Thr Lys Thr Gly Glu Leu Ser Ile His Cys Thr Glu Leu Arg
130 135 140
Leu Leu Thr Lys Ala Leu Arg Pro Leu Pro Asp Lys Phe His Gly Leu
145 150 155 160
Gln Asp Gln Glu Ala Arg Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Ser
165 170 175

530 535 540
 Asn Gly Val Arg Glu Val Gln Leu Ala Tyr Lys Leu Asp Ile Asn Glu
 545 550 555 560
 Phe Arg Gly Asn Arg Ser Leu Gln Ile Ile Ile Asp Asn Ile Trp Pro
 565 570 575
 Ile

<210> 355
 <211> 236
 <212> PRT
 <213> Escherichia coli

<400> 355
 Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
 1 5 10 15
 Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
 20 25 30
 Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
 35 40 45
 Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
 50 55 60
 His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
 65 70 75 80
 Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 85 90 95
 Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 100 105 110
 Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 115 120 125
 Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 130 135 140
 Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 145 150 155 160
 Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 165 170 175
 Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 180 185 190
 Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 195 200 205
 Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 210 215 220
 Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 225 230 235

<210> 356
 <211> 298
 <212> PRT
 <213> Escherichia coli

<400> 356
 Met Lys Gln Asp Leu Ala Arg Ile Glu Gln Phe Leu Asp Ala Leu Trp
 1 5 10 15
 Leu Glu Lys Asn Leu Ala Glu Asn Thr Leu Asn Ala Tyr Arg Arg Asp
 20 25 30

115	120	125
Ile Val Pro Val Ile Asn Glu Asn Asp Ala Val Ala Thr Ala Glu Ile		
130	135	140
Lys Val Gly Asp Asn Asp Asn Leu Ser Ala Leu Ala Ala Ile Leu Ala		
145	150	155
Gly Ala Asp Lys Leu Leu Leu Thr Asp Gln Lys Gly Leu Tyr Thr		
165	170	175
Ala Asp Pro Arg Ser Asn Pro Gln Ala Glu Leu Ile Lys Asp Val Tyr		
180	185	190
Gly Ile Asp Asp Ala Leu Arg Ala Ile Ala Gly Asp Ser Val Ser Gly		
195	200	205
Leu Gly Thr Gly Gly Met Ser Thr Lys Leu Gln Ala Ala Asp Val Ala		
210	215	220
Cys Arg Ala Gly Ile Asp Thr Ile Ile Ala Ala Gly Ser Lys Pro Gly		
225	230	235
Val Ile Gly Asp Val Met Glu Gly Ile Ser Val Gly Thr Leu Phe His		
245	250	255
Ala Gln Ala Thr Pro Leu Glu Asn Arg Lys Arg Trp Ile Phe Gly Ala		
260	265	270
Pro Pro Ala Gly Glu Ile Thr Val Asp Glu Gly Ala Thr Ala Ala Ile		
275	280	285
Leu Glu Arg Gly Ser Ser Leu Leu Pro Lys Gly Ile Lys Ser Val Thr		
290	295	300
Gly Asn Phe Ser Arg Gly Glu Val Ile Arg Ile Cys Asn Leu Glu Gly		
305	310	315
Arg Asp Ile Ala His Gly Val Ser Arg Tyr Asn Ser Asp Ala Leu Arg		
325	330	335
Arg Ile Ala Gly His His Ser Gln Glu Ile Asp Ala Ile Leu Gly Tyr		
340	345	350
Glu Tyr Gly Pro Val Ala Val His Arg Asp Asp Met Ile Thr Arg		
355	360	365

<210> 358
 <211> 417
 <212> PRT
 <213> Escherichia coli

<400> 358

Met Leu Glu Gln Met Gly Ile Ala Ala Lys Gln Ala Ser Tyr Lys Leu	
1 5 10 15	
Ala Gln Leu Ser Ser Arg Glu Lys Asn Arg Val Leu Glu Lys Ile Ala	
20 25 30	
Asp Glu Leu Glu Ala Gln Ser Glu Ile Ile Leu Asn Ala Asn Ala Gln	
35 40 45	
Asp Val Ala Asp Ala Arg Ala Asn Gly Leu Ser Glu Ala Met Leu Asp	
50 55 60	
Arg Leu Ala Leu Thr Pro Ala Arg Leu Lys Gly Ile Ala Asp Asp Val	
65 70 75 80	
Arg Gln Val Cys Asn Leu Ala Asp Pro Val Gly Gln Val Ile Asp Gly	
85 90 95	
Gly Val Leu Asp Ser Gly Leu Arg Leu Glu Arg Arg Arg Val Pro Leu	
100 105 110	
Gly Val Ile Gly Val Ile Tyr Glu Ala Arg Pro Asn Val Thr Val Asp	
115 120 125	
Val Ala Ser Leu Cys Leu Lys Thr Gly Asn Ala Val Ile Leu Arg Gly	
130 135 140	

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Gly	Lys	Glu	Thr	Cys	Arg	Thr	Asn	Ala	Ala	Thr	Val	Ala	Val	Ile	Gln
145					150					155					160
Asp	Ala	Leu	Lys	Ser	Cys	Gly	Leu	Pro	Ala	Gly	Ala	Val	Gln	Ala	Ile
				165					170						175
Asp	Asn	Pro	Asp	Arg	Ala	Leu	Val	Ser	Glu	Met	Leu	Arg	Met	Asp	Lys
			180					185					190		
Tyr	Ile	Asp	Met	Leu	Ile	Pro	Arg	Gly	Gly	Ala	Gly	Leu	His	Lys	Leu
	195					200						205			
Cys	Arg	Glu	Gln	Ser	Thr	Ile	Pro	Val	Ile	Thr	Gly	Gly	Ile	Gly	Val
	210					215					220				
Cys	His	Ile	Tyr	Val	Asp	Glu	Ser	Val	Glu	Ile	Ala	Glu	Ala	Leu	Lys
225					230					235					240
Val	Ile	Val	Asn	Ala	Lys	Thr	Gln	Arg	Pro	Ser	Thr	Cys	Asn	Thr	Val
			245						250						255
Glu	Thr	Leu	Leu	Val	Asn	Lys	Asn	Ile	Ala	Asp	Ser	Phe	Leu	Pro	Ala
		260					265						270		
Leu	Ser	Lys	Gln	Met	Ala	Glu	Ser	Gly	Val	Thr	Leu	His	Ala	Asp	Ala
	275						280					285			
Ala	Ala	Leu	Ala	Gln	Leu	Gln	Ala	Gly	Pro	Ala	Lys	Val	Val	Ala	Val
	290					295					300				
Lys	Ala	Glu	Glu	Tyr	Asp	Asp	Glu	Phe	Leu	Ser	Leu	Asp	Leu	Asn	Val
305					310					315					320
Lys	Ile	Val	Ser	Asp	Leu	Asp	Asp	Ala	Ile	Ala	His	Ile	Arg	Glu	His
			325						330					335	
Gly	Thr	Gln	His	Ser	Asp	Ala	Ile	Leu	Thr	Arg	Asp	Met	Arg	Asn	Ala
		340						345					350		
Gln	Arg	Phe	Val	Asn	Glu	Val	Asp	Ser	Ser	Ala	Val	Tyr	Val	Asn	Ala
		355					360					365			
Ser	Thr	Arg	Phe	Thr	Asp	Gly	Gly	Gln	Phe	Gly	Leu	Gly	Ala	Glu	Val
	370					375					380				
Ala	Val	Ser	Thr	Gln	Lys	Leu	His	Ala	Arg	Gly	Pro	Met	Gly	Leu	Glu
385					390					395					400
Ala	Leu	Thr	Thr	Tyr	Lys	Trp	Ile	Gly	Ile	Gly	Asp	Tyr	Thr	Ile	Arg
				405					410					415	
Ala															

<210> 359
 <211> 186
 <212> PRT
 <213> Escherichia coli

<400> 359

Met	Met	Thr	Arg	Gln	Ala	Ser	Met	Lys	Gly	Phe	Pro	Ile	Ala	His	Ile
1				5					10					15	
Phe	His	Pro	Ser	Ile	Pro	Pro	Met	His	Ala	Val	Val	Asn	Asn	His	Asn
		20					25						30		
Arg	Asn	Ile	Asp	Tyr	Trp	Thr	Val	Lys	Arg	Lys	Phe	Ala	Glu	Ile	Val
	35					40						45			
Ser	Thr	Asn	Asp	Val	Asn	Lys	Ile	Tyr	Ser	Ile	Ser	Asn	Glu	Leu	Arg
	50					55					60				
Arg	Val	Leu	Ser	Ala	Ile	Thr	Ala	Leu	Asn	Phe	Tyr	His	Gly	Asp	Val
65					70					75					80
Pro	Ser	Val	Met	Ile	Arg	Ile	Gln	Pro	Glu	Asn	Met	Ser	Pro	Phe	Ile
			85						90					95	
Ile	Asp	Ile	Ser	Thr	Gly	Glu	His	Asp	Asp	Tyr	Ile	Ile	Gln	Thr	Leu

[illegible]

<400>	360														
Met	Phe	Pro	Val	Ser	Ser	Ile	Gly	Asn	Asp	Ile	Ser	Ser	Asp	Leu	Val
1				5					10					15	
Arg	Arg	Lys	Met	Asn	Asp	Leu	Pro	Glu	Ser	Pro	Thr	Gly	Asn	Asn	Leu
			20					25					30		
Glu	Ala	Leu	Ala	Pro	Gly	Ile	Glu	Lys	Leu	Lys	Gln	Thr	Ser	Ile	Glu
		35					40					45			
Met	Val	Thr	Leu	Leu	Asn	Thr	Leu	Gln	Pro	Gly	Gly	Lys	Cys	Ile	Ile
	50					55					60				
Thr	Gly	Asp	Phe	Gln	Lys	Glu	Leu	Ala	Tyr	Leu	Gln	Asn	Val	Ile	Leu
65					70					75				80	
Tyr	Asn	Val	Ser	Ser	Leu	Arg	Leu	Asp	Phe	Leu	Gly	Tyr	Asn	Ala	Gln
				85					90					95	
Ile	Ile	Gln	Arg	Ser	Asp	Asn	Thr	Cys	Glu	Leu	Thr	Ile	Asn	Glu	Pro
			100					105					110		
Leu	Lys	Asn	Gln	Glu	Ile	Ser	Thr	Gly	Asn	Ile	Asn	Ile	Asn	Cys	Pro
		115					120					125			
Leu	Lys	Asp	Ile	Tyr	Asn	Glu	Ile	Arg	Arg	Leu	Asn	Val	Ile	Phe	Ser
	130					135					140				
Cys	Gly	Thr	Gly	Asp	Ile	Val	Asp	Leu	Ser	Ser	Leu	Asp	Leu	Arg	Asn
145					150					155				160	
Val	Asp	Leu	Asp	Tyr	Tyr	Asp	Phe	Thr	Asp	Lys	His	Met	Ala	Asn	Thr
				165					170					175	
Ile	Leu	Asn	Pro	Phe	Lys	Leu	Asn	Ser	Thr	Asn	Phe	Thr	Asn	Ala	Asn
			180					185					190		
Met	Phe	Gln	Val	Asn	Phe	Val	Ser	Ser	Thr	Gln	Asn	Ala	Thr	Ile	Ser
		195				200						205			
Trp	Asp	Tyr	Leu	Leu	Lys	Ile	Thr	Pro	Val	Leu	Ile	Ser	Ile	Ser	Asp
	210					215					220				
Met	Tyr	Ser	Glu	Glu	Lys	Ile	Lys	Phe	Val	Glu	Ser	Cys	Leu	Asn	Glu
225					230					235				240	
Pro	Gly	Asp	Ile	Thr	Glu	Glu	Gln	Leu	Lys	Ile	Met	Arg	Phe	Ala	Ile
				245					250					255	
Ile	Lys	Ser	Ile	Pro	Arg	Ala	Thr	Leu	Thr	Asp	Lys	Leu	Glu	Asn	Glu
			260					265					270		
Leu	Thr	Lys	Glu	Ile	Tyr	Lys	Ser	Ser	Ser	Lys	Ile	Ile	Asn	Cys	Leu
		275				280						285			
Asn	Arg	Ile	Lys	Leu	Thr	Glu	Met	Lys	Glu	Phe	Ser	Ser	Glu	Lys	Ile
	290					295					300				

Tyr Asp Tyr Ile Asp Ile Ile Ile Glu Asp Tyr Glu Asn Thr Lys Glu
 305 310 315 320
 Asn Ala Tyr Leu Val Val Pro Gln Ile Asn Tyr Thr Met Asp Leu Asn
 325 330 335
 Ile Glu Asp Ser Ser Ser Glu Glu Leu Leu Ser Asp Asn Thr Leu Glu
 340 345 350
 Lys Asp Glu Asn Ser Pro Asp Asn Gly Phe Glu Val Gly Glu Tyr Asn
 355 360 365
 Thr Tyr Glu Ala Tyr Asn Ser Glu Lys Gln Tyr Phe Thr Arg Glu Asp
 370 375 380
 Tyr Thr Tyr Asp Tyr Asp Leu Leu Asn Ala Ile
 385 390 395

<210> 361
 <211> 315
 <212> PRT
 <213> Escherichia coli

<400> 361
 Met Cys His Arg Ala Phe Arg Leu His Leu Cys Lys Asp Trp Val Phe
 1 5 10 15
 Met Phe Ser Gly Leu Leu Ile Ile Leu Val Pro Leu Ile Val Gly Tyr
 20 25 30
 Leu Ile Pro Leu Arg Gln Gln Ala Leu Lys Val Ile Asn Gln Leu
 35 40 45
 Leu Ser Trp Met Val Tyr Leu Ile Leu Phe Phe Met Gly Ile Ser Leu
 50 55 60
 Ala Phe Leu Asp Asn Leu Ala Ser Asn Leu Leu Ala Ile Leu His Tyr
 65 70 75 80
 Ser Ala Val Ser Ile Thr Val Ile Leu Leu Cys Asn Ile Ala Ala Leu
 85 90 95
 Met Trp Leu Glu Arg Gly Leu Pro Trp Arg Asn His His Gln Gln Glu
 100 105 110
 Lys Leu Pro Ser Arg Ile Ala Met Ala Leu Glu Ser Leu Lys Leu Cys
 115 120 125
 Gly Val Val Val Ile Gly Phe Ala Ile Gly Leu Ser Gly Leu Ala Phe
 130 135 140
 Leu Gln His Ala Thr Glu Ala Ser Glu Tyr Thr Leu Ile Leu Leu Leu
 145 150 155 160
 Phe Leu Val Gly Ile Gln Leu Arg Asn Asn Gly Met Thr Leu Lys Gln
 165 170 175
 Ile Val Leu Asn Arg Arg Gly Met Ile Val Ala Val Val Val Val
 180 185 190
 Ser Ser Leu Ile Gly Gly Leu Ile Asn Ala Phe Ile Leu Asp Leu Pro
 195 200 205
 Ile Asn Thr Ala Leu Ala Met Ala Ser Gly Phe Gly Trp Tyr Ser Leu
 210 215 220
 Ser Gly Ile Leu Leu Thr Glu Ser Phe Gly Pro Val Ile Gly Ser Ala
 225 230 235 240
 Ala Phe Phe Asn Asp Leu Ala Arg Glu Leu Ile Ala Ile Met Leu Ile
 245 250 255
 Pro Gly Leu Ile Arg Arg Ser Arg Ser Thr Ala Leu Gly Leu Cys Gly
 260 265 270
 Ala Thr Ser Met Asp Phe Thr Leu Pro Val Leu Gln Arg Thr Gly Gly
 275 280 285
 Leu Asp Met Val Pro Ala Ala Ile Val His Gly Phe Ile Leu Ser Leu

290 295 300
 Leu Val Pro Ile Leu Ile Ala Phe Phe Ser Ala
 305 310 315

<210> 362
 <211> 96
 <212> PRT
 <213> Escherichia coli

<400> 362
 Met Gln Asn Thr Thr His Asp Asn Val Ile Leu Glu Leu Thr Val Arg
 1 5 10 15
 Asn His Pro Gly Val Met Thr His Val Cys Gly Leu Phe Ala Arg Arg
 20 25 30
 Ala Phe Asn Val Glu Gly Ile Leu Cys Leu Pro Ile Gln Asp Ser Asp
 35 40 45
 Lys Ser His Ile Trp Leu Leu Val Asn Asp Asp Gln Arg Leu Glu Gln
 50 55 60
 Met Ile Ser Gln Ile Asp Lys Leu Glu Asp Val Val Lys Val Gln Arg
 65 70 75 80
 Asn Gln Ser Asp Pro Thr Met Phe Asn Lys Ile Ala Val Phe Phe Gln
 85 90 95

<210> 363
 <211> 562
 <212> PRT
 <213> Escherichia coli

<400> 363
 Met Ala Ser Ser Gly Thr Thr Ser Thr Arg Lys Arg Phe Thr Gly Ala
 1 5 10 15
 Glu Phe Ile Val His Phe Leu Glu Gln Gln Gly Ile Lys Ile Val Thr
 20 25 30
 Gly Ile Pro Gly Gly Ser Ile Leu Pro Val Tyr Asp Ala Leu Ser Gln
 35 40 45
 Ser Thr Gln Ile Arg His Ile Leu Ala Arg His Glu Gln Gly Ala Gly
 50 55 60
 Phe Ile Ala Gln Gly Met Ala Arg Thr Asp Gly Lys Pro Ala Val Cys
 65 70 75 80
 Met Ala Cys Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Ala Ile Ala
 85 90 95
 Asp Ala Arg Leu Asp Ser Ile Pro Leu Ile Cys Ile Thr Gly Gln Val
 100 105 110
 Pro Ala Ser Met Ile Gly Thr Asp Ala Phe Gln Glu Val Asp Thr Tyr
 115 120 125
 Gly Ile Ser Ile Pro Ile Thr Lys His Asn Tyr Leu Val Arg His Ile
 130 135 140
 Glu Glu Leu Pro Gln Val Met Ser Asp Ala Phe Arg Ile Ala Gln Ser
 145 150 155 160
 Gly Arg Pro Gly Pro Val Trp Ile Asp Ile Pro Lys Asp Val Gln Thr
 165 170 175
 Ala Val Phe Glu Ile Glu Thr Gln Pro Ala Met Ala Glu Lys Ala Ala
 180 185 190
 Ala Pro Ala Phe Ser Glu Glu Ser Ile Arg Asp Ala Ala Ala Met Ile
 195 200 205

20

25

30

<210> 365

<211> 338

<212> PRT

<213> Escherichia coli

<400> 365

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Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1           5           10           15
Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
      20           25           30
Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
      35           40           45
Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50           55           60
Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
65           70           75           80
Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
      85           90           95
Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
      100          105          110
Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
      115          120          125
Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
      130          135          140
Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
145          150          155          160
Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
      165          170          175
His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
      180          185          190
Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
      195          200          205
Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
      210          215          220
Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
225          230          235          240
Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
      245          250          255
Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
      260          265          270
Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
      275          280          285
His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
      290          295          300
Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
305          310          315          320
Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
      325          330          335
Ser His

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<210> 366

<211> 157

<212> PRT
 <213> Escherichia coli

<400> 366

Met	Val	Tyr	Ile	Ile	Ile	Val	Ser	His	Gly	His	Glu	Asp	Tyr	Ile	Lys
1				5					10					15	
Lys	Leu	Leu	Glu	Asn	Leu	Asn	Ala	Asp	Asp	Glu	His	Tyr	Lys	Ile	Ile
			20					25					30		
Val	Arg	Asp	Asn	Lys	Asp	Ser	Leu	Leu	Leu	Lys	Gln	Ile	Cys	Gln	His
		35					40					45			
Tyr	Ala	Gly	Leu	Asp	Tyr	Ile	Ser	Gly	Gly	Val	Tyr	Gly	Phe	Gly	His
	50					55					60				
Asn	Asn	Asn	Ile	Ala	Val	Ala	Tyr	Val	Lys	Glu	Lys	Tyr	Arg	Pro	Ala
65					70					75					80
Asp	Asp	Asp	Tyr	Ile	Leu	Phe	Leu	Asn	Pro	Asp	Ile	Ile	Met	Lys	His
				85					90					95	
Asp	Asp	Leu	Leu	Thr	Tyr	Ile	Lys	Tyr	Val	Glu	Ser	Lys	Arg	Tyr	Ala
			100					105					110		
Phe	Ser	Thr	Leu	Cys	Leu	Phe	Arg	Asp	Glu	Ala	Lys	Ser	Leu	His	Asp
		115					120					125			
Tyr	Ser	Val	Arg	Lys	Phe	Pro	Val	Leu	Ser	Asp	Phe	Ile	Val	Ser	Phe
	130					135					140				
Met	Leu	Gly	Ile	Lys	Glu	Gly	Ala	Asn	Lys	Ser	Leu	Ile			
145					150					155					

<210> 367
 <211> 372
 <212> PRT
 <213> Escherichia coli

<400> 367

Met	Gly	Lys	Ser	Ile	Val	Val	Val	Ser	Ala	Val	Asn	Phe	Thr	Thr	Gly
1				5					10					15	
Gly	Pro	Phe	Thr	Ile	Leu	Lys	Lys	Phe	Leu	Ala	Ala	Thr	Asn	Asn	Lys
			20					25					30		
Glu	Asn	Val	Ser	Phe	Ile	Ala	Leu	Val	His	Ser	Ala	Lys	Glu	Leu	Lys
		35					40					45			
Glu	Ser	Tyr	Pro	Trp	Val	Lys	Phe	Ile	Glu	Phe	Pro	Glu	Val	Lys	Gly
	50					55					60				
Ser	Trp	Leu	Lys	Arg	Leu	His	Phe	Glu	Tyr	Val	Val	Cys	Lys	Lys	Leu
65					70					75					80
Ser	Lys	Glu	Leu	Asn	Ala	Thr	His	Trp	Ile	Cys	Leu	His	Asp	Ile	Thr
				85					90					95	
Ala	Asn	Val	Val	Thr	Lys	Lys	Arg	Tyr	Val	Tyr	Cys	His	Asn	Pro	Ala
			100					105					110		
Pro	Phe	Tyr	Lys	Gly	Ile	Leu	Phe	Arg	Glu	Ile	Leu	Met	Glu	Pro	Ser
		115					120					125			
Phe	Phe	Leu	Phe	Lys	Met	Leu	Tyr	Gly	Leu	Ile	Tyr	Lys	Ile	Asn	Ile
	130					135					140				
Lys	Lys	Asn	Thr	Ala	Val	Phe	Val	Gln	Gln	Phe	Trp	Met	Lys	Glu	Lys
145					150					155				160	
Phe	Ile	Lys	Lys	Tyr	Ser	Ile	Asn	Asn	Ile	Ile	Val	Ser	Arg	Pro	Glu
			165						170					175	
Ile	Lys	Leu	Ser	Asp	Lys	Ser	Gln	Leu	Thr	Asp	Asp	Asp	Ser	Gln	Phe
		180						185					190		
Lys	Asn	Asn	Pro	Ser	Glu	Leu	Thr	Ile	Phe	Tyr	Pro	Ala	Val	Pro	Arg

<210> 369
 <211> 330
 <212> PRT
 <213> Escherichia coli

<400> 369

Met	Tyr	Phe	Leu	Asn	Asp	Leu	Asn	Phe	Ser	Arg	Arg	Asp	Ala	Gly	Phe
1				5					10					15	
Lys	Ala	Arg	Lys	Asp	Ala	Leu	Asp	Ile	Ala	Ser	Asp	Tyr	Glu	Asn	Ile
			20					25					30		
Ser	Val	Val	Asn	Ile	Pro	Leu	Trp	Gly	Gly	Val	Val	Gln	Arg	Ile	Ile
		35					40					45			
Ser	Ser	Val	Lys	Leu	Ser	Thr	Phe	Leu	Cys	Gly	Leu	Glu	Asn	Lys	Asp
	50					55					60				
Val	Leu	Ile	Phe	Asn	Phe	Pro	Met	Ala	Lys	Pro	Phe	Trp	His	Ile	Leu
65				70					75						80
Ser	Phe	Phe	His	Arg	Leu	Leu	Lys	Phe	Arg	Ile	Val	Pro	Leu	Ile	His
			85					90						95	
Asp	Ile	Asp	Glu	Leu	Arg	Gly	Gly	Gly	Gly	Ser	Asp	Ser	Val	Arg	Leu
		100					105						110		
Ala	Thr	Cys	Asp	Met	Val	Ile	Ser	His	Asn	Pro	Gln	Met	Thr	Lys	Tyr
		115					120					125			
Leu	Ser	Lys	Tyr	Met	Ser	Gln	Asp	Lys	Ile	Lys	Asp	Ile	Lys	Ile	Phe
	130					135					140				
Asp	Tyr	Leu	Val	Ser	Ser	Asp	Val	Glu	His	Arg	Asp	Val	Thr	Asp	Lys
145				150					155						160
Gln	Arg	Gly	Val	Ile	Tyr	Ala	Gly	Asn	Leu	Ser	Arg	His	Lys	Cys	Ser
			165					170						175	
Phe	Ile	Tyr	Thr	Glu	Gly	Cys	Asp	Phe	Thr	Leu	Phe	Gly	Val	Asn	Tyr
		180					185					190			
Glu	Asn	Lys	Asp	Asn	Pro	Lys	Tyr	Leu	Gly	Ser	Phe	Asp	Ala	Gln	Ser
		195				200						205			
Pro	Glu	Lys	Ile	Asn	Leu	Pro	Gly	Met	Gln	Phe	Gly	Leu	Ile	Trp	Asp
	210				215						220				
Gly	Asp	Ser	Val	Glu	Thr	Cys	Ser	Gly	Ala	Phe	Gly	Asp	Tyr	Leu	Lys
225				230					235						240
Phe	Asn	Asn	Pro	His	Lys	Thr	Ser	Leu	Tyr	Leu	Ser	Met	Glu	Leu	Pro
			245					250						255	
Val	Phe	Ile	Trp	Asp	Lys	Ala	Ala	Leu	Ala	Asp	Phe	Ile	Val	Asp	Asn
		260					265						270		
Arg	Ile	Gly	Tyr	Ala	Val	Gly	Ser	Ile	Lys	Glu	Met	Gln	Glu	Ile	Val
	275					280						285			
Asp	Ser	Met	Thr	Ile	Glu	Thr	Tyr	Lys	Gln	Ile	Ser	Glu	Asn	Thr	Lys
	290				295						300				
Ile	Ile	Ser	Gln	Lys	Ile	Arg	Thr	Gly	Ser	Tyr	Phe	Arg	Asp	Val	Leu
305				310					315						320
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg						
			325						330						

<210> 370
 <211> 388
 <212> PRT
 <213> Escherichia coli

145		150		155		160									
Cys	Gln	Leu	Tyr	Gln	Arg	Ser	Cys	Asp	Val	Phe	Leu	Gly	Leu	Pro	Phe
		165		170		175									
Asn	Ile	Ala	Ser	Tyr	Ala	Leu	Leu	Val	His	Met	Met	Ala	Gln	Gln	Cys
		180		185		190									
Asp	Leu	Glu	Val	Gly	Asp	Phe	Val	Trp	Thr	Gly	Gly	Asp	Thr	His	Leu
	195			200		205									
Tyr	Ser	Asn	His	Met	Asp	Gln	Thr	His	Leu	Gln	Leu	Ser	Arg	Glu	Pro
	210			215		220									
Arg	Pro	Leu	Pro	Lys	Leu	Ile	Ile	Lys	Arg	Lys	Pro	Glu	Ser	Ile	Phe
225				230		235									240
Asp	Tyr	Arg	Phe	Glu	Asp	Phe	Glu	Ile	Glu	Gly	Tyr	Asp	Pro	His	Pro
		245		250		255									
Gly	Ile	Lys	Ala	Pro	Val	Ala	Ile								
	260														

<210> 375
 <211> 291
 <212> PRT
 <213> Escherichia coli

<400> 375
Met Thr Ser Ser Tyr Leu His Phe Pro Glu Phe Asp Pro Val Ile Phe
1 5 10 15
Ser Ile Gly Pro Val Ala Leu His Trp Tyr Gly Leu Met Tyr Leu Val
20 25 30
Gly Phe Ile Phe Ala Met Trp Leu Ala Thr Arg Arg Ala Asn Arg Pro
35 40 45
Gly Ser Gly Trp Thr Lys Asn Glu Val Glu Asn Leu Leu Tyr Ala Gly
50 55 60
Phe Leu Gly Val Phe Leu Gly Gly Arg Ile Gly Tyr Val Leu Phe Tyr
65 70 75 80
Asn Phe Pro Gln Phe Met Ala Asp Pro Leu Tyr Leu Phe Arg Val Trp
85 90 95
Asp Gly Gly Met Ser Phe His Gly Gly Leu Ile Gly Val Ile Val Val
100 105 110
Met Ile Ile Phe Ala Arg Arg Thr Lys Arg Ser Phe Phe Gln Val Ser
115 120 125
Asp Phe Ile Ala Pro Leu Ile Pro Phe Gly Leu Gly Ala Gly Arg Leu
130 135 140
Gly Asn Phe Ile Asn Gly Glu Leu Trp Gly Arg Val Asp Pro Asn Phe
145 150 155 160
Pro Phe Ala Met Leu Phe Pro Gly Ser Arg Thr Glu Asp Ile Leu Leu
165 170 175
Leu Gln Thr Asn Pro Gln Trp Gln Ser Ile Phe Asp Thr Tyr Gly Val
180 185 190
Leu Pro Arg His Pro Ser Gln Leu Tyr Glu Leu Leu Leu Glu Gly Val
195 200 205
Val Leu Phe Ile Ile Leu Asn Leu Tyr Ile Arg Lys Pro Arg Pro Met
210 215 220
Gly Ala Val Ser Gly Leu Phe Leu Ile Gly Tyr Gly Ala Phe Arg Ile
225 230 235 240
Ile Val Glu Phe Phe Arg Gln Pro Asp Ala Gln Phe Thr Gly Ala Trp
245 250 255
Val Gln Tyr Ile Ser Met Gly Gln Ile Leu Ser Ile Pro Met Ile Val
260 265 270

Ala Gly Val Ile Met Met Val Trp Ala Tyr Arg Arg Ser Pro Gln Gln
 275 280 285
 His Val Ser
 290

<210> 376
 <211> 241
 <212> PRT
 <213> Escherichia coli

<400> 376
 Met Asp Ser Leu Asn Leu Asn Lys His Ile Ser Gly Gln Phe Asn Ala
 1 5 10 15
 Glu Leu Glu Ser Ile Arg Thr Gln Val Met Thr Met Gly Gly Met Val
 20 25 30
 Glu Gln Gln Leu Ser Asp Ala Ile Thr Ala Met His Asn Gln Asp Ser
 35 40 45
 Asp Leu Ala Lys Arg Val Ile Glu Gly Asp Lys Asn Val Asn Met Met
 50 55 60
 Glu Val Ala Ile Asp Glu Ala Cys Val Arg Ile Ile Ala Lys Arg Gln
 65 70 75 80
 Pro Thr Ala Ser Asp Leu Arg Leu Val Met Val Ile Ser Lys Thr Ile
 85 90 95
 Ala Glu Leu Glu Arg Ile Gly Asp Val Ala Asp Lys Ile Cys Arg Thr
 100 105 110
 Ala Leu Glu Lys Phe Ser Gln Gln His Gln Pro Leu Leu Val Ser Leu
 115 120 125
 Glu Ser Leu Gly Arg His Thr Ile Gln Met Leu His Asp Val Leu Asp
 130 135 140
 Ala Phe Ala Arg Met Asp Ile Asp Glu Ala Val Arg Ile Tyr Arg Glu
 145 150 155 160
 Asp Lys Lys Val Asp Gln Glu Tyr Glu Gly Ile Val Arg Gln Leu Met
 165 170 175
 Thr Tyr Met Met Glu Asp Ser Arg Thr Ile Pro Ser Val Leu Thr Ala
 180 185 190
 Leu Phe Cys Ala Arg Ser Ile Glu Arg Ile Gly Asp Arg Cys Gln Asn
 195 200 205
 Ile Cys Glu Phe Ile Phe Tyr Tyr Val Lys Gly Gln Asp Phe Arg His
 210 215 220
 Val Gly Gly Asp Glu Leu Asp Lys Leu Leu Ala Gly Lys Asp Ser Asp
 225 230 235 240
 Lys

<210> 377
 <211> 257
 <212> PRT
 <213> Escherichia coli

<400> 377
 Met Ser Met Val Glu Thr Ala Pro Ser Lys Ile Gln Val Arg Asn Leu
 1 5 10 15
 Asn Phe Tyr Tyr Gly Lys Phe His Ala Leu Lys Asn Ile Asn Leu Asp
 20 25 30
 Ile Ala Lys Asn Gln Val Thr Ala Phe Ile Gly Pro Ser Gly Cys Gly

Ala	Leu	Leu	Gln	Val	Pro	Ile	Val	Ile	Arg	Thr	Thr	Glu	Asn	Met	Leu
			165						170					175	
Lys	Leu	Val	Pro	Tyr	Ser	Leu	Arg	Glu	Ala	Ala	Tyr	Ala	Leu	Gly	Thr
			180					185					190		
Pro	Lys	Trp	Lys	Met	Ile	Ser	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Val	Ser
		195					200					205			
Gly	Ile	Met	Thr	Gly	Ile	Leu	Leu	Ala	Ile	Ala	Arg	Ile	Ala	Gly	Glu
	210					215					220				
Thr	Ala	Pro	Leu	Leu	Phe	Thr	Ala	Leu	Ser	Asn	Gln	Phe	Trp	Ser	Thr
225					230					235					240
Asp	Met	Met	Gln	Pro	Ile	Ala	Asn	Leu	Pro	Val	Thr	Ile	Phe	Lys	Phe
			245						250					255	
Ala	Met	Ser	Pro	Phe	Ala	Glu	Trp	Gln	Gln	Leu	Ala	Trp	Ala	Gly	Val
			260					265					270		
Leu	Ile	Ile	Thr	Leu	Cys	Val	Leu	Leu	Leu	Asn	Ile	Leu	Ala	Arg	Val
		275					280					285			
Val	Phe	Ala	Lys	Asn	Lys	His	Gly								
	290					295									

<210> 379
 <211> 319
 <212> PRT
 <213> Escherichia coli

<400> 379

Met	Ala	Ala	Thr	Lys	Pro	Ala	Phe	Asn	Pro	Pro	Gly	Lys	Lys	Gly	Asp
1				5					10					15	
Ile	Ile	Phe	Ser	Val	Leu	Val	Lys	Leu	Ala	Ala	Leu	Ile	Val	Leu	Leu
			20					25					30		
Met	Leu	Gly	Gly	Ile	Ile	Val	Ser	Leu	Ile	Ile	Ser	Ser	Trp	Pro	Ser
		35					40					45			
Ile	Gln	Lys	Phe	Gly	Leu	Ala	Phe	Leu	Trp	Thr	Lys	Glu	Trp	Asp	Ala
	50					55					60				
Pro	Asn	Asp	Ile	Tyr	Gly	Ala	Leu	Val	Pro	Ile	Tyr	Gly	Thr	Leu	Val
65					70					75					80
Thr	Ser	Phe	Ile	Ala	Leu	Leu	Ile	Ala	Val	Pro	Val	Ser	Phe	Gly	Ile
			85						90					95	
Ala	Leu	Phe	Leu	Thr	Glu	Leu	Ala	Pro	Gly	Trp	Leu	Lys	Arg	Pro	Leu
			100					105					110		
Gly	Ile	Ala	Ile	Glu	Leu	Leu	Ala	Ala	Ile	Pro	Ser	Ile	Val	Tyr	Gly
		115					120					125			
Met	Trp	Gly	Leu	Phe	Ile	Phe	Ala	Pro	Leu	Phe	Ala	Val	Tyr	Phe	Gln
	130					135					140				
Glu	Pro	Val	Gly	Asn	Ile	Met	Ser	Asn	Ile	Pro	Ile	Val	Gly	Ala	Leu
145					150					155					160
Phe	Ser	Gly	Pro	Ala	Phe	Gly	Ile	Gly	Ile	Leu	Ala	Ala	Gly	Val	Ile
				165					170					175	
Leu	Ala	Ile	Met	Ile	Ile	Pro	Tyr	Ile	Ala	Ala	Val	Met	Arg	Asp	Val
			180					185					190		
Phe	Glu	Gln	Thr	Pro	Val	Met	Met	Lys	Glu	Ser	Ala	Tyr	Gly	Ile	Gly
		195					200					205			
Cys	Thr	Thr	Trp	Glu	Val	Ile	Trp	Arg	Ile	Val	Leu	Pro	Phe	Thr	Lys
	210					215					220				
Asn	Gly	Val	Ile	Gly	Gly	Ile	Met	Leu	Gly	Leu	Gly	Arg	Ala	Leu	Gly
225					230					235					240
Glu	Thr	Met	Ala	Val	Thr	Phe	Ile	Ile	Gly	Asn	Thr	Tyr	Gln	Leu	Asp

Leu Pro Asp Ser Val Val Glu Gln Val Arg Ala Ala Trp Lys Thr Asn
 325 330 335
 Ile Lys Asp Ser Ser Gly Lys Pro Leu Tyr
 340 345

<210> 381
 <211> 236
 <212> PRT
 <213> Escherichia coli

<400> 381
 Met Gly Ser Gly Leu Val Asn Gly Gly Asp Tyr Phe Tyr Asn Asn Leu
 1 5 10 15
 Ser Phe Thr Val Thr Arg Tyr Asn Gly Ile Met Ala Thr Asp Ser Thr
 20 25 30
 Gln Cys Val Lys Lys Ser Arg Gly Arg Pro Lys Val Phe Asp Arg Asp
 35 40 45
 Ala Ala Leu Asp Lys Ala Met Lys Leu Phe Trp Gln His Gly Tyr Glu
 50 55 60
 Ala Thr Ser Leu Ala Asp Leu Val Glu Ala Thr Gly Ala Lys Ala Pro
 65 70 75 80
 Thr Leu Tyr Ala Glu Phe Thr Asn Lys Glu Gly Leu Phe Arg Ala Val
 85 90 95
 Leu Asp Arg Tyr Ile Asp Arg Phe Ala Lys His Glu Ala Gln Leu
 100 105 110
 Phe Cys Glu Glu Lys Ser Val Glu Ser Ala Leu Ala Asp Tyr Phe Ala
 115 120 125
 Ala Ile Ala Asn Cys Phe Thr Ser Lys Asp Thr Pro Ala Gly Cys Phe
 130 135 140
 Met Ile Asn Asn Cys Thr Thr Leu Ser Pro Asp Ser Gly Asp Ile Ala
 145 150 155 160
 Asn Thr Leu Lys Ser Arg His Ala Met Gln Glu Arg Thr Leu Gln Gln
 165 170 175
 Phe Leu Cys Gln Arg Gln Ala Arg Gly Glu Ile Pro Pro His Cys Asp
 180 185 190
 Val Thr His Leu Ala Glu Phe Leu Asn Cys Ile Ile Gln Gly Met Ser
 195 200 205
 Ile Ser Ala Arg Glu Gly Ala Ser Leu Glu Lys Leu Met Gln Ile Ala
 210 215 220
 Gly Thr Thr Leu Arg Leu Trp Pro Glu Leu Val Lys
 225 230 235

<210> 382
 <211> 181
 <212> PRT
 <213> Escherichia coli

<400> 382
 Met Gln Ala Lys Ile Ala Ala Ser Asn Thr Gly Glu Leu Asp Ala Leu
 1 5 10 15
 Gln Gln Leu Gly Phe Ser Leu Val Glu Gly Glu Val Asp Leu Ala Leu
 20 25 30
 Pro Val Asn Asn Ala Ser Asp Ser Gly Ala Val Val Ala Gln Glu Thr
 35 40 45
 Asp Ile Pro Ala Leu Arg Gln Leu Ala Ser Ala Ala Phe Ala Gln Ser

50		55		60	
Arg Phe Arg Ala Pro Trp Tyr Ala Pro Asp Ala Ser Ser Arg Phe Tyr					
65		70		75	80
Ala Gln Trp Ile Glu Asn Ala Val Arg Gly Thr Phe Asp His Gln Cys					
	85		90		95
Leu Ile Leu Arg Ala Ala Ser Gly Asp Ile Arg Gly Tyr Val Ser Leu					
	100		105		110
Arg Glu Leu Asn Ala Thr Asp Ala Arg Ile Gly Leu Leu Ala Gly Arg					
	115		120		125
Gly Ala Gly Ala Glu Leu Met Gln Thr Ala Leu Asn Trp Ala Tyr Arg					
	130		135		140
Arg Gly Lys Thr Thr Leu Arg Val Ala Thr Gln Met Gly Asn Thr Ala					
145		150		155	160
Ala Leu Lys Arg Tyr Ile Gln Ser Gly Ala Asn Val Glu Ser Thr Ala					
	165		170		175
Tyr Trp Leu Tyr Arg					
	180				

<210> 383
 <211> 376
 <212> PRT
 <213> Escherichia coli

<400> 383	
Met Ile Pro Phe Asn Ala Pro Pro Val Val Gly Thr Glu Leu Asp Tyr	
1	5
Met Gln Ser Ala Met Gly Ser Gly Lys Leu Cys Gly Asp Gly Gly Phe	
	20
Thr Arg Arg Cys Gln Gln Trp Leu Glu Gln Arg Phe Gly Ser Ala Lys	
	35
Val Leu Leu Thr Pro Ser Cys Thr Ala Ser Leu Glu Met Ala Ala Leu	
	50
Leu Leu Asp Ile Gln Pro Gly Asp Glu Val Ile Met Pro Ser Tyr Thr	
65	70
Phe Val Ser Thr Ala Asn Ala Phe Val Leu Arg Gly Ala Lys Ile Val	
	85
Phe Val Asp Val Arg Pro Asp Thr Met Asn Ile Asp Glu Thr Leu Ile	
	100
Glu Ala Ala Ile Thr Asp Lys Thr Arg Val Ile Val Pro Val His Tyr	
	115
Ala Gly Val Ala Cys Glu Met Asp Thr Ile Met Ala Leu Ala Lys Lys	
	130
His Asn Leu Phe Val Val Glu Asp Ala Ala Gln Gly Val Met Ser Thr	
145	150
Tyr Lys Gly Arg Ala Leu Gly Thr Ile Gly His Ile Gly Cys Phe Ser	
	165
Phe His Glu Thr Lys Asn Tyr Thr Ala Gly Gly Glu Gly Gly Ala Thr	
	180
Leu Ile Asn Asp Lys Ala Leu Ile Glu Arg Ala Glu Ile Ile Arg Glu	
	195
Lys Gly Thr Asn Arg Ser Gln Phe Phe Arg Gly Gln Val Asp Lys Tyr	
	210
Thr Trp Arg Asp Ile Gly Ser Ser Tyr Leu Met Ser Asp Leu Gln Ala	
225	230
Ala Tyr Leu Trp Ala Gln Leu Glu Ala Ala Asp Arg Ile Asn Gln Gln	
	245
	250
	255

Arg Leu Ala Leu Trp Gln Asn Tyr Tyr Asp Ala Leu Ala Pro Leu Ala
 260 265 270
 Lys Ala Gly Arg Ile Glu Leu Pro Ser Ile Pro Asp Gly Cys Val Gln
 275 280 285
 Asn Ala His Met Phe Tyr Ile Lys Leu Arg Asp Ile Asp Asp Arg Ser
 290 295 300
 Ala Leu Ile Asn Phe Leu Lys Glu Ala Glu Ile Met Ala Val Phe His
 305 310 315 320
 Tyr Ile Pro Leu His Gly Cys Pro Ala Gly Glu His Phe Gly Glu Phe
 325 330 335
 His Gly Glu Asp Arg Tyr Thr Thr Lys Glu Ser Glu Arg Leu Leu Arg
 340 345 350
 Leu Pro Leu Phe Tyr Asn Leu Ser Pro Val Asn Gln Arg Thr Val Ile
 355 360 365
 Ala Thr Leu Leu Asn Tyr Phe Ser
 370 375

<210> 384
 <211> 416
 <212> PRT
 <213> Escherichia coli

<400> 384
 Met Ser Leu Ala Lys Ala Ser Leu Trp Thr Ala Ala Ser Thr Leu Val
 1 5 10 15
 Lys Ile Gly Ala Gly Leu Leu Val Gly Lys Leu Leu Ala Val Ser Phe
 20 25 30
 Gly Pro Ala Gly Leu Gly Leu Ala Ala Asn Phe Arg Gln Leu Ile Thr
 35 40 45
 Val Leu Gly Val Leu Ala Gly Ala Gly Ile Phe Asn Gly Val Thr Lys
 50 55 60
 Tyr Val Ala Gln Tyr His Asp Asn Pro Gln Gln Leu Arg Arg Val Val
 65 70 75 80
 Gly Thr Ser Ser Ala Met Val Leu Gly Phe Ser Thr Leu Met Ala Leu
 85 90 95
 Val Phe Val Leu Ala Ala Ala Pro Ile Ser Gln Gly Leu Phe Gly Asn
 100 105 110
 Thr Asp Tyr Gln Gly Leu Val Arg Leu Val Ala Leu Val Gln Met Gly
 115 120 125
 Ile Ala Trp Gly Asn Leu Leu Ala Leu Met Lys Gly Phe Arg Asp
 130 135 140
 Ala Ala Gly Asn Ala Leu Ser Leu Ile Val Gly Ser Leu Ile Gly Val
 145 150 155 160
 Leu Ala Tyr Tyr Val Ser Tyr Arg Leu Gly Gly Tyr Glu Gly Ala Leu
 165 170 175
 Leu Gly Leu Ala Leu Ile Pro Ala Leu Val Val Ile Pro Ala Ala Ile
 180 185 190
 Met Leu Ile Lys Arg Gly Val Ile Pro Leu Ser Tyr Leu Lys Pro Ser
 195 200 205
 Trp Asp Asn Gly Leu Ala Gly Gln Leu Ser Lys Phe Thr Leu Met Ala
 210 215 220
 Leu Ile Thr Ser Val Thr Leu Pro Val Ala Tyr Ile Met Met Arg Lys
 225 230 235 240
 Leu Leu Ala Ala Gln Tyr Ser Trp Asp Glu Val Gly Ile Trp Gln Gly
 245 250 255
 Val Ser Ser Ile Ser Asp Ala Tyr Leu Gln Phe Ile Thr Ala Ser Phe

				165					170				175				
Met	Arg	Asp	Cys	Arg	Leu	Val	His	Pro	Asp	Ala	Leu	Tyr	Met	Gly	Val		
			180					185					190				
Gly	Gly	Thr	Tyr	Asp	Val	Phe	Thr	Gly	His	Val	Lys	Arg	Ala	Pro	Lys		
		195					200					205					
Ile	Trp	Gln	Thr	Leu	Gly	Leu	Glu	Trp	Leu	Tyr	Arg	Leu	Leu	Ser	Gln		
	210					215					220						
Pro	Ser	Arg	Ile	Lys	Arg	Gln	Leu	Arg	Leu	Leu	Arg	Tyr	Leu	Arg	Trp		
225					230					235					240		
His	Tyr	Thr	Gly	Asn	Leu												
				245													

<210> 387
 <211> 74
 <212> PRT
 <213> Escherichia coli

Met	Thr	Val	Leu	Ile	His	Val	Leu	Gly	Ser	Asp	Ile	Pro	His	His	Asn		
1				5					10					15			
Arg	Thr	Val	Leu	Arg	Phe	Phe	Asn	Asp	Ala	Leu	Ala	Ala	Thr	Ser	Glu		
		20					25					30					
His	Ala	Arg	Glu	Phe	Met	Val	Val	Gly	Lys	Asp	Asp	Gly	Leu	Ser	Asp		
	35					40					45						
Ser	Cys	Pro	Ala	Leu	Ser	Val	Gln	Phe	Phe	Pro	Trp	Glu	Lys	Ile	Ala		
	50				55						60						
Gly	Gly	Ser	Gly	His	Arg	Glu	Ser	Lys	Ser								
65					70												

<210> 388
 <211> 204
 <212> PRT
 <213> Escherichia coli

Met	Arg	Gly	Glu	Leu	Phe	Phe	Pro	Thr	Arg	Met	Asp	Pro	Ser	Leu			
1				5				10					15				
Asn	Thr	Met	Ala	Asn	Asp	Arg	Gln	Arg	Glu	Gly	Lys	Met	Thr	Ile	Leu		
		20					25					30					
Val	Gly	Asn	Ser	Gly	Asp	Arg	Ser	Asn	Glu	His	Ile	Ala	Ala	Leu	Arg		
		35				40					45						
Ala	Val	His	Gln	Gln	Phe	Gly	Asp	Thr	Val	Lys	Val	Val	Val	Pro	Met		
	50				55						60						
Gly	Tyr	Pro	Pro	Asn	Asn	Glu	Ala	Tyr	Ile	Glu	Glu	Val	Arg	Gln	Ala		
65				70				75						80			
Gly	Leu	Glu	Leu	Phe	Ser	Glu	Glu	Asn	Leu	Gln	Ile	Leu	Ser	Glu	Lys		
			85					90					95				
Leu	Glu	Phe	Asp	Ala	Tyr	Leu	Ala	Leu	Leu	Arg	Gln	Cys	Asp	Leu	Gly		
		100					105				110						
Tyr	Phe	Ile	Phe	Ala	Arg	Gln	Gln	Gly	Ile	Gly	Thr	Leu	Cys	Leu	Leu		
	115					120					125						
Ile	Gln	Ala	Gly	Ile	Pro	Cys	Val	Leu	Asn	Arg	Glu	Asn	Pro	Phe	Trp		
	130				135						140						
Gln	Asp	Met	Thr	Glu	Gln	His	Leu	Pro	Val	Leu	Phe	Thr	Thr	Asp	Asp		
145					150					155					160		

Leu Asn Glu Asp Ile Val Arg Glu Ala Gln Arg Gln Leu Ala Ser Val
165 170 175
Asp Lys Asn Thr Ile Ala Phe Phe Ser Pro Asn Tyr Leu Gln Gly Trp
180 185 190
Gln Arg Ala Leu Ala Ile Ala Ala Arg Glu Val Ala
195 200

<210> 389
<211> 182
<212> PRT
<213> Escherichia coli

<400> 389
Met Ile Arg Gln Arg Arg Arg Ala Leu Thr Pro Glu Gln Gln Gln Glu
1 5 10 15
Met Gly Gln Gln Ala Ala Thr Arg Met Met Thr Tyr Pro Pro Val Val
20 25 30
Met Ala His Thr Val Ala Val Phe Leu Ser Phe Asp Gly Glu Leu Asp
35 40 45
Thr Gln Pro Leu Ile Glu Gln Leu Trp Arg Ala Gly Lys Arg Val Tyr
50 55 60
Leu Pro Val Leu His Pro Phe Ser Ala Gly Asn Leu Leu Phe Leu Asn
65 70 75 80
Tyr His Pro Gln Ser Glu Leu Val Met Asn Arg Leu Lys Ile His Glu
85 90 95
Pro Lys Leu Asp Val Arg Asp Val Leu Pro Leu Ser Arg Leu Asp Val
100 105 110
Leu Ile Thr Pro Leu Val Ala Phe Asp Glu Tyr Gly Gln Arg Leu Gly
115 120 125
Met Gly Gly Gly Phe Tyr Asp Arg Thr Leu Gln Asn Trp Gln His Tyr
130 135 140
Lys Thr Gln Pro Val Gly Tyr Ala His Asp Cys Gln Leu Val Glu Lys
145 150 155 160
Leu Pro Val Glu Glu Trp Asp Ile Pro Leu Pro Ala Val Val Thr Pro
165 170 175
Ser Lys Val Trp Glu Trp
180

<210> 390
<211> 91
<212> PRT
<213> Escherichia coli

<400> 390
Met Ala Arg Val Thr Val Gln Asp Ala Val Glu Lys Ile Gly Asn Arg
1 5 10 15
Phe Asp Leu Val Leu Val Ala Ala Arg Arg Ala Arg Gln Met Gln Val
20 25 30
Gly Gly Lys Asp Pro Leu Val Pro Glu Glu Asn Asp Lys Thr Thr Val
35 40 45
Ile Ala Leu Arg Glu Ile Glu Glu Gly Leu Ile Asn Asn Gln Ile Leu
50 55 60
Asp Val Arg Glu Arg Gln Glu Gln Gln Glu Glu Ala Ala Glu Leu
65 70 75 80
Gln Ala Val Thr Ala Ile Ala Glu Gly Arg Arg

<210> 391
 <211> 702
 <212> PRT
 <213> Escherichia coli

<400> 391

Met	Tyr	Leu	Phe	Glu	Ser	Leu	Asn	Gln	Leu	Ile	Gln	Thr	Tyr	Leu	Pro
1				5					10					15	
Glu	Asp	Gln	Ile	Lys	Arg	Leu	Arg	Gln	Ala	Tyr	Leu	Val	Ala	Arg	Asp
			20					25					30		
Ala	His	Glu	Gly	Gln	Thr	Arg	Ser	Ser	Gly	Glu	Pro	Tyr	Ile	Thr	His
		35				40						45			
Pro	Val	Ala	Val	Ala	Cys	Ile	Leu	Ala	Glu	Met	Lys	Leu	Asp	Tyr	Glu
	50					55					60				
Thr	Leu	Met	Ala	Ala	Leu	Leu	His	Asp	Val	Ile	Glu	Asp	Thr	Pro	Ala
65					70					75					80
Thr	Tyr	Gln	Asp	Met	Glu	Gln	Leu	Phe	Gly	Lys	Ser	Val	Ala	Glu	Leu
			85						90					95	
Val	Glu	Gly	Val	Ser	Lys	Leu	Asp	Lys	Leu	Lys	Phe	Arg	Asp	Lys	Lys
			100					105					110		
Glu	Ala	Gln	Ala	Glu	Asn	Phe	Arg	Lys	Met	Ile	Met	Ala	Met	Val	Gln
		115					120					125			
Asp	Ile	Arg	Val	Ile	Leu	Ile	Lys	Leu	Ala	Asp	Arg	Thr	His	Asn	Met
	130					135					140				
Arg	Thr	Leu	Gly	Ser	Leu	Arg	Pro	Asp	Lys	Arg	Arg	Arg	Ile	Ala	Arg
145					150					155					160
Glu	Thr	Leu	Glu	Ile	Tyr	Ser	Pro	Leu	Ala	His	Arg	Leu	Gly	Ile	His
			165						170					175	
His	Ile	Lys	Thr	Glu	Leu	Glu	Glu	Leu	Gly	Phe	Glu	Ala	Leu	Tyr	Pro
			180					185					190		
Asn	Arg	Tyr	Arg	Val	Ile	Lys	Glu	Val	Val	Lys	Ala	Ala	Arg	Gly	Asn
		195					200					205			
Arg	Lys	Glu	Met	Ile	Gln	Lys	Ile	Leu	Ser	Glu	Ile	Glu	Gly	Arg	Leu
	210					215					220				
Gln	Glu	Ala	Gly	Ile	Pro	Cys	Arg	Val	Ser	Gly	Arg	Glu	Lys	His	Leu
225					230					235					240
Tyr	Ser	Ile	Tyr	Cys	Lys	Met	Val	Leu	Lys	Glu	Gln	Arg	Phe	His	Ser
			245						250					255	
Ile	Met	Asp	Ile	Tyr	Ala	Phe	Arg	Val	Ile	Val	Asn	Asp	Ser	Asp	Thr
		260						265					270		
Cys	Tyr	Arg	Val	Leu	Gly	Gln	Met	His	Ser	Leu	Tyr	Lys	Pro	Arg	Pro
		275					280					285			
Gly	Arg	Val	Lys	Asp	Tyr	Ile	Ala	Ile	Pro	Lys	Ala	Asn	Gly	Tyr	Gln
	290					295					300				
Ser	Leu	His	Thr	Ser	Met	Ile	Gly	Pro	His	Gly	Val	Pro	Val	Glu	Val
305					310					315					320
Gln	Ile	Arg	Thr	Glu	Asp	Met	Asp	Gln	Met	Ala	Glu	Met	Gly	Val	Ala
			325						330					335	
Ala	His	Trp	Ala	Tyr	Lys	Glu	His	Gly	Glu	Thr	Ser	Thr	Thr	Ala	Gln
			340					345					350		
Ile	Arg	Ala	Gln	Arg	Trp	Met	Gln	Ser	Leu	Leu	Glu	Leu	Gln	Gln	Ser
		355					360					365			
Ala	Gly	Ser	Ser	Phe	Glu	Phe	Ile	Glu	Ser	Val	Lys	Ser	Asp	Leu	Phe
	370					375						380			

65		70		75		80									
Asp	Ala	Val	Ala	His	Leu	Lys	Gly	Gln	Gly	Met	Gln	Ile	Leu	Ala	Thr
			85						90					95	
His	Leu	Ser	Asp	Asn	Ala	Val	Asp	Phe	Arg	Glu	Ile	Asp	Tyr	Thr	Arg
			100					105					110		
Pro	Thr	Cys	Ile	Leu	Met	Gly	Gln	Glu	Lys	Thr	Gly	Ile	Thr	Gln	Glu
		115					120					125			
Ala	Leu	Ala	Leu	Ala	Asp	Gln	Asp	Ile	Ile	Ile	Pro	Met	Ile	Gly	Met
	130					135					140				
Val	Gln	Ser	Leu	Asn	Val	Ser	Val	Ala	Ser	Ala	Leu	Ile	Leu	Tyr	Glu
145				150						155					160
Ala	Gln	Arg	Gln	Arg	Gln	Asn	Ala	Gly	Met	Tyr	Leu	Arg	Glu	Asn	Ser
				165					170					175	
Met	Leu	Pro	Glu	Ala	Glu	Gln	Gln	Arg	Leu	Leu	Phe	Glu	Gly	Gly	Tyr
			180					185					190		
Pro	Val	Leu	Ala	Lys	Val	Ala	Lys	Arg	Lys	Gly	Leu	Pro	Tyr	Pro	His
		195					200					205			
Val	Asn	Gln	Gln	Gly	Glu	Ile	Glu	Ala	Asp	Ala	Asp	Trp	Trp	Ala	Thr
	210					215					220				
Met	Gln	Ala	Ala	Gly											
225															

<210> 393
 <211> 693
 <212> PRT
 <213> Escherichia coli

<400> 393

Met	Lys	Gly	Arg	Leu	Leu	Asp	Ala	Val	Pro	Leu	Ser	Ser	Leu	Thr	Gly
1				5					10				15		
Val	Gly	Ala	Ala	Leu	Ser	Asn	Lys	Leu	Ala	Lys	Ile	Asn	Leu	His	Thr
		20						25				30			
Val	Gln	Asp	Leu	Leu	Leu	His	Leu	Pro	Leu	Arg	Tyr	Glu	Asp	Arg	Thr
		35				40						45			
His	Leu	Tyr	Pro	Ile	Gly	Glu	Leu	Leu	Pro	Gly	Val	Tyr	Ala	Thr	Val
	50				55					60					
Glu	Gly	Glu	Val	Leu	Asn	Cys	Asn	Ile	Ser	Phe	Gly	Gly	Arg	Arg	Met
65				70					75						80
Met	Thr	Cys	Gln	Ile	Ser	Asp	Gly	Ser	Gly	Ile	Leu	Thr	Met	Arg	Phe
			85					90					95		
Phe	Asn	Phe	Ser	Ala	Ala	Met	Lys	Asn	Ser	Leu	Ala	Ala	Gly	Arg	Arg
		100					105						110		
Val	Leu	Ala	Tyr	Gly	Glu	Ala	Lys	Arg	Gly	Lys	Tyr	Gly	Ala	Glu	Met
	115						120					125			
Ile	His	Pro	Glu	Tyr	Arg	Val	Gln	Gly	Asp	Leu	Ser	Thr	Pro	Glu	Leu
	130					135					140				
Gln	Glu	Thr	Leu	Thr	Pro	Val	Tyr	Pro	Thr	Thr	Glu	Gly	Val	Lys	Gln
145					150					155					160
Ala	Thr	Leu	Arg	Lys	Leu	Thr	Asp	Gln	Ala	Leu	Asp	Leu	Leu	Asp	Thr
				165				170						175	
Cys	Ala	Ile	Glu	Glu	Leu	Leu	Pro	Pro	Glu	Leu	Ser	Gln	Gly	Met	Met
		180					185					190			
Thr	Leu	Pro	Glu	Ala	Leu	Arg	Thr	Leu	His	Arg	Pro	Pro	Pro	Thr	Leu
	195						200				205				
Gln	Leu	Ser	Asp	Leu	Glu	Thr	Gly	Gln	His	Pro	Ala	Gln	Arg	Arg	Leu
	210					215					220				

675
Arg Tyr Ser Asn Ala
690

680

685

<210> 394
<211> 428
<212> PRT
<213> Escherichia coli

<400> 394

Met	Lys	Thr	Ser	Leu	Phe	Lys	Ser	Leu	Tyr	Phe	Gln	Val	Leu	Thr	Ala
1				5					10					15	
Ile	Ala	Ile	Gly	Ile	Leu	Leu	Gly	His	Phe	Tyr	Pro	Glu	Ile	Gly	Glu
			20					25					30		
Gln	Met	Lys	Pro	Leu	Gly	Asp	Gly	Phe	Val	Lys	Leu	Ile	Lys	Met	Ile
		35					40					45			
Ile	Ala	Pro	Val	Ile	Phe	Cys	Thr	Val	Val	Thr	Gly	Ile	Ala	Gly	Met
	50					55					60				
Glu	Ser	Met	Lys	Ala	Val	Gly	Arg	Thr	Gly	Ala	Val	Ala	Leu	Leu	Tyr
65					70					75					80
Phe	Glu	Ile	Val	Ser	Thr	Ile	Ala	Leu	Ile	Ile	Gly	Leu	Ile	Ile	Val
			85						90					95	
Asn	Val	Val	Gln	Pro	Gly	Ala	Gly	Met	Asn	Val	Asp	Pro	Ala	Thr	Leu
			100					105					110		
Asp	Ala	Lys	Ala	Val	Ala	Val	Tyr	Ala	Asp	Gln	Ala	Lys	Asp	Gln	Gly
		115					120					125			
Ile	Val	Ala	Phe	Ile	Met	Asp	Val	Ile	Pro	Ala	Ser	Val	Ile	Gly	Ala
	130					135					140				
Phe	Ala	Ser	Gly	Asn	Ile	Leu	Gln	Val	Leu	Leu	Phe	Ala	Val	Leu	Phe
145					150					155					160
Gly	Phe	Ala	Leu	His	Arg	Leu	Gly	Ser	Lys	Gly	Gln	Leu	Ile	Phe	Asn
				165				170						175	
Val	Ile	Glu	Ser	Phe	Ser	Gln	Val	Ile	Phe	Gly	Ile	Ile	Asn	Met	Ile
			180					185					190		
Met	Arg	Leu	Ala	Pro	Ile	Gly	Ala	Phe	Gly	Ala	Met	Ala	Phe	Thr	Ile
		195				200					205				
Gly	Lys	Tyr	Gly	Val	Gly	Thr	Leu	Val	Gln	Leu	Gly	Gln	Leu	Ile	Ile
	210					215					220				
Cys	Phe	Tyr	Ile	Thr	Cys	Ile	Leu	Phe	Val	Val	Leu	Val	Leu	Gly	Ser
225					230					235					240
Ile	Ala	Lys	Ala	Thr	Gly	Phe	Ser	Ile	Phe	Lys	Phe	Ile	Arg	Tyr	Ile
				245					250					255	
Arg	Glu	Glu	Leu	Leu	Ile	Val	Leu	Gly	Thr	Ser	Ser	Ser	Glu	Ser	Ala
			260					265					270		
Leu	Pro	Arg	Met	Leu	Asp	Lys	Met	Glu	Lys	Leu	Gly	Cys	Arg	Lys	Ser
		275					280					285			
Val	Val	Gly	Leu	Val	Ile	Pro	Thr	Gly	Tyr	Ser	Phe	Asn	Leu	Asp	Gly
	290					295					300				
Thr	Ser	Ile	Tyr	Leu	Thr	Met	Ala	Ala	Val	Phe	Ile	Ala	Gln	Ala	Thr
305					310					315					320
Asn	Ser	Gln	Met	Asp	Ile	Val	His	Gln	Ile	Thr	Leu	Leu	Ile	Val	Leu
				325					330					335	
Leu	Leu	Ser	Ser	Lys	Gly	Ala	Ala	Gly	Val	Thr	Gly	Ser	Gly	Phe	Ile
			340					345					350		
Val	Leu	Ala	Ala	Thr	Leu	Ser	Ala	Val	Gly	His	Leu	Pro	Val	Ala	Gly
		355					360					365			

Leu Ala Leu Ile Leu Gly Ile Asp Arg Phe Met Ser Glu Ala Arg Ala
 370 375 380
 Leu Thr Asn Leu Val Gly Asn Gly Val Ala Thr Ile Val Val Ala Lys
 385 390 395 400
 Trp Val Lys Glu Leu Asp His Lys Lys Leu Asp Asp Val Leu Asn Asn
 405 410 415
 Arg Ala Pro Asp Gly Lys Thr His Glu Leu Ser Ser
 420 425

<210> 395
 <211> 396
 <212> PRT
 <213> Escherichia coli

<400> 395
 Met Thr Thr Arg Gln His Ser Ser Phe Ala Ile Val Phe Ile Leu Gly
 1 5 10 15
 Leu Leu Ala Met Leu Met Pro Leu Ser Ile Asp Met Tyr Leu Pro Ala
 20 25 30
 Leu Pro Val Ile Ser Ala Gln Phe Gly Val Pro Ala Gly Ser Thr Gln
 35 40 45
 Met Thr Leu Ser Thr Tyr Ile Leu Gly Phe Ala Leu Gly Gln Leu Ile
 50 55 60
 Tyr Gly Pro Met Ala Asp Ser Phe Gly Arg Lys Pro Val Val Leu Gly
 65 70 75 80
 Gly Thr Leu Val Phe Ala Ala Ala Val Ala Cys Ala Leu Ala Asn
 85 90 95
 Thr Ile Asp Gln Leu Ile Val Met Arg Phe Phe His Gly Leu Ala Ala
 100 105 110
 Ala Ala Ala Ser Val Val Ile Asn Ala Leu Met Arg Asp Ile Tyr Pro
 115 120 125
 Lys Glu Glu Phe Ser Arg Met Met Ser Phe Val Met Leu Val Thr Thr
 130 135 140
 Ile Ala Pro Leu Met Ala Pro Ile Val Gly Gly Trp Val Leu Val Trp
 145 150 155 160
 Leu Ser Trp His Tyr Ile Phe Trp Ile Leu Ala Leu Ala Ala Ile Leu
 165 170 175
 Ala Ser Ala Met Ile Phe Phe Leu Ile Lys Glu Thr Leu Pro Pro Glu
 180 185 190
 Arg Arg Gln Pro Phe His Ile Arg Thr Thr Ile Gly Asn Phe Ala Ala
 195 200 205
 Leu Phe Arg His Lys Arg Val Leu Ser Tyr Met Leu Ala Ser Gly Phe
 210 215 220
 Ser Phe Ala Gly Met Phe Ser Phe Leu Ser Ala Gly Pro Phe Val Tyr
 225 230 235 240
 Ile Glu Ile Asn His Val Ala Pro Glu Asn Phe Gly Tyr Tyr Phe Ala
 245 250 255
 Leu Asn Ile Val Phe Leu Phe Val Met Thr Ile Phe Asn Ser Arg Phe
 260 265 270
 Val Arg Arg Ile Gly Ala Leu Asn Met Phe Arg Ser Gly Leu Trp Ile
 275 280 285
 Gln Phe Ile Met Ala Ala Trp Met Val Ile Ser Ala Leu Leu Gly Leu
 290 295 300
 Gly Phe Trp Ser Leu Val Val Gly Val Ala Ala Phe Val Gly Cys Val
 305 310 315 320
 Ser Met Val Ser Ser Asn Ala Met Ala Val Ile Leu Asp Glu Phe Pro

<211> 238
 <212> PRT
 <213> Escherichia coli

<400> 398

Met	Gly	Arg	Lys	Trp	Ala	Asn	Ile	Val	Ala	Lys	Lys	Thr	Ala	Lys	Asp
1				5					10					15	
Gly	Ala	Thr	Ser	Lys	Ile	Tyr	Ala	Lys	Phe	Gly	Val	Glu	Ile	Tyr	Ala
			20					25					30		
Ala	Ala	Lys	Gln	Gly	Glu	Pro	Asp	Pro	Glu	Leu	Asn	Thr	Ser	Leu	Lys
		35					40					45			
Phe	Val	Ile	Glu	Arg	Ala	Lys	Gln	Ala	Gln	Val	Pro	Lys	His	Val	Ile
	50					55					60				
Asp	Lys	Ala	Ile	Asp	Lys	Ala	Lys	Gly	Gly	Gly	Asp	Glu	Thr	Phe	Val
65					70					75					80
Gln	Gly	Arg	Tyr	Glu	Gly	Phe	Gly	Pro	Asn	Gly	Ser	Met	Ile	Ile	Ala
			85						90					95	
Glu	Thr	Leu	Thr	Ser	Asn	Val	Asn	Arg	Thr	Ile	Ala	Asn	Val	Arg	Thr
			100					105					110		
Ile	Phe	Asn	Lys	Lys	Gly	Gly	Asn	Ile	Gly	Ala	Ala	Gly	Ser	Val	Ser
		115					120					125			
Tyr	Met	Phe	Asp	Asn	Thr	Gly	Val	Ile	Val	Phe	Lys	Gly	Thr	Asp	Pro
	130					135					140				
Asp	His	Ile	Phe	Glu	Ile	Leu	Leu	Glu	Ala	Glu	Val	Asp	Val	Arg	Asp
145					150					155					160
Val	Thr	Glu	Glu	Glu	Gly	Asn	Ile	Val	Ile	Tyr	Thr	Glu	Pro	Thr	Asp
			165						170					175	
Leu	His	Lys	Gly	Ile	Ala	Ala	Leu	Lys	Ala	Ala	Gly	Ile	Thr	Glu	Phe
			180					185					190		
Ser	Thr	Thr	Glu	Leu	Glu	Met	Ile	Ala	Gln	Ser	Glu	Val	Glu	Leu	Ser
		195					200					205			
Pro	Glu	Asp	Leu	Glu	Ile	Phe	Glu	Gly	Leu	Val	Asp	Ala	Leu	Glu	Asp
	210					215					220				
Asp	Asp	Asp	Val	Gln	Lys	Val	Tyr	His	Asn	Val	Ala	Asn	Leu		
225					230					235					

<210> 399
 <211> 261
 <212> PRT
 <213> Escherichia coli

<400> 399

Met	Val	Leu	Met	Ser	Glu	Thr	Lys	Asn	Glu	Leu	Glu	Asp	Leu	Leu	Glu
1				5					10					15	
Lys	Ala	Ala	Thr	Glu	Pro	Ala	His	Arg	Pro	Ala	Phe	Phe	Arg	Thr	Leu
			20					25					30		
Leu	Glu	Ser	Thr	Val	Trp	Val	Pro	Gly	Thr	Ala	Ala	Gln	Gly	Glu	Ala
		35					40					45			
Val	Val	Glu	Asp	Ser	Ala	Leu	Asp	Leu	Gln	His	Trp	Glu	Lys	Glu	Asp
	50					55					60				
Gly	Thr	Ser	Val	Ile	Pro	Phe	Phe	Thr	Ser	Leu	Glu	Ala	Leu	Gln	Gln
65					70					75					80
Ala	Val	Glu	Asp	Glu	Gln	Ala	Phe	Val	Val	Met	Pro	Val	Arg	Thr	Leu
			85						90					95	
Phe	Glu	Met	Thr	Leu	Gly	Glu	Thr	Leu	Phe	Leu	Asn	Ala	Lys	Leu	Pro
			100					105					110		

Thr Gly Lys Glu Phe Met Pro Arg Glu Ile Ser Leu Leu Ile Gly Glu
 115 120 125
 Glu Gly Asn Pro Leu Ser Ser Gln Glu Ile Leu Glu Gly Gly Glu Ser
 130 135 140
 Leu Ile Leu Ser Glu Val Ala Glu Pro Pro Ala Gln Met Ile Asp Ser
 145 150 155 160
 Leu Thr Thr Leu Phe Lys Thr Ile Lys Pro Val Lys Arg Ala Phe Ile
 165 170 175
 Cys Ser Ile Lys Glu Asn Glu Glu Ala Gln Pro Asn Leu Leu Ile Gly
 180 185 190
 Ile Glu Ala Asp Gly Asp Ile Glu Glu Ile Ile Gln Ala Thr Gly Ser
 195 200 205
 Val Ala Thr Asp Thr Leu Pro Gly Asp Glu Pro Ile Asp Ile Cys Gln
 210 215 220
 Val Lys Lys Gly Glu Lys Gly Ile Ser His Phe Ile Thr Glu His Ile
 225 230 235 240
 Ala Pro Phe Tyr Glu Arg Arg Trp Gly Gly Phe Leu Arg Asp Phe Lys
 245 250 255
 Gln Asn Arg Ile Ile
 260

<210> 400
 <211> 421
 <212> PRT
 <213> Escherichia coli

<400> 400
 Met Leu Thr Lys Lys Lys Trp Ala Leu Phe Ser Leu Leu Thr Leu Cys
 1 5 10 15
 Gly Gly Thr Ile Tyr Lys Leu Pro Ser Leu Lys Asp Ala Phe Tyr Ile
 20 25 30
 Pro Met Gln Glu Tyr Phe His Leu Thr Asn Gly Gln Ile Gly Asn Ala
 35 40 45
 Met Ser Val Asn Ser Phe Val Thr Thr Val Gly Phe Phe Leu Ser Ile
 50 55 60
 Tyr Phe Ala Asp Lys Leu Pro Arg Arg Tyr Thr Met Ser Phe Ser Leu
 65 70 75 80
 Ile Ala Thr Gly Leu Leu Gly Val Tyr Leu Thr Thr Met Pro Gly Tyr
 85 90 95
 Trp Gly Ile Leu Phe Val Trp Ala Leu Phe Gly Val Thr Cys Asp Met
 100 105 110
 Met Asn Trp Pro Val Leu Leu Lys Ser Val Ser Arg Leu Gly Asn Ser
 115 120 125
 Glu Gln Gln Gly Arg Leu Phe Gly Phe Phe Glu Thr Gly Arg Gly Ile
 130 135 140
 Val Asp Thr Val Val Ala Phe Ser Ala Leu Ala Val Phe Thr Trp Phe
 145 150 155 160
 Gly Ser Gly Leu Leu Gly Phe Lys Ala Gly Ile Trp Phe Tyr Ser Leu
 165 170 175
 Ile Val Ile Ala Val Gly Ile Ile Ile Phe Phe Val Leu Asn Asp Lys
 180 185 190
 Glu Glu Ala Pro Ser Val Glu Val Lys Lys Glu Asp Gly Ala Ser Lys
 195 200 205
 Asn Thr Ser Met Thr Ser Val Leu Lys Asp Lys Thr Ile Trp Leu Ile
 210 215 220
 Ala Phe Asn Val Phe Phe Val Tyr Ala Val Tyr Cys Gly Leu Thr Phe

				645						650						655			
Pro	Leu	Pro	Leu	Glu	Pro	Trp	Leu	Pro	Ala	Ser	Glu	Arg	Arg	Ala	Val				
			660					665						670					
Arg	Leu	Pro	Pro	Ala	Ser	Thr	Ser	Cys	Pro	Pro	Tyr	Gly	His	Asp	Ala				
		675					680					685							
Gln	Leu	Pro	Leu	Gln	Leu	Thr	Gly	Val	Arg	Asp	Gly	Ala	Ile	Ile	Lys				
	690					695					700								
Arg	Leu	Pro	Gly	Ala	Ala	Glu	Ala	Thr	Leu	Pro	Leu	Gln	Ser	Ser	Gly				
705					710					715					720				
Gly	Ala	Gly	Glu	Arg	Trp	Trp	Phe	Leu	Asn	Gly	Glu	Pro	Leu	Thr	Glu				
				725					730					735					
Arg	Gly	Arg	Asn	Val	Thr	Leu	His	Leu	Thr	Asp	Lys	Gly	Asp	Tyr	Gln				
			740					745					750						
Leu	Leu	Val	Met	Asp	Asp	Val	Gly	Gln	Ile	Ala	Thr	Val	Lys	Phe	Val				
		755					760					765							
Met	Gln																		
	770																		

<210> 402

<211> 1653

<212> PRT

<213> Escherichia coli

<400> 402

Met	Lys	Lys	Leu	Arg	Val	Ala	Ala	Cys	Met	Leu	Met	Leu	Ala	Leu	Ala				
1				5					10					15					
Gly	Cys	Asp	Asn	Asn	Asp	Asn	Ala	Pro	Thr	Ala	Val	Lys	Lys	Asp	Ala				
			20					25					30						
Pro	Ser	Glu	Val	Thr	Lys	Ala	Ala	Ser	Ser	Glu	Asn	Ala	Ser	Ser	Ala				
		35					40					45							
Lys	Leu	Ser	Val	Pro	Glu	Arg	Gln	Lys	Leu	Ala	Gln	Gln	Ser	Ala	Gly				
	50					55					60								
Lys	Val	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Glu	Val	Gln	Leu	Asp	Gly	Ala				
65					70					75				80					
Ala	Thr	Leu	Val	Leu	Thr	Phe	Ser	Ile	Pro	Leu	Asp	Pro	Asp	Gln	Asp				
				85					90					95					
Phe	Ser	Arg	Val	Ile	His	Val	Val	Asp	Lys	Lys	Ser	Gly	Lys	Val	Asp				
		100						105					110						
Gly	Ala	Trp	Glu	Leu	Ser	Asp	Asn	Leu	Lys	Glu	Leu	Arg	Leu	Arg	His				
		115					120						125						
Leu	Glu	Pro	Lys	Arg	Asp	Leu	Ile	Val	Thr	Ile	Gly	Lys	Glu	Val	Lys				
	130					135					140								
Ala	Leu	Asn	Asn	Ala	Thr	Phe	Ser	Lys	Asp	Tyr	Glu	Lys	Thr	Ile	Thr				
145					150					155					160				
Thr	Arg	Asp	Ile	Gln	Pro	Ser	Val	Gly	Phe	Ala	Ser	Arg	Gly	Ser	Leu				
			165						170					175					
Leu	Pro	Gly	Lys	Val	Val	Glu	Gly	Leu	Pro	Val	Met	Ala	Leu	Asn	Val				
			180					185					190						
Asn	Asn	Val	Asp	Val	Asn	Phe	Phe	Arg	Val	Lys	Pro	Glu	Ser	Leu	Pro				
		195					200					205							
Ala	Phe	Ile	Ser	Gln	Trp	Glu	Tyr	Arg	Asn	Ser	Leu	Ala	Asn	Trp	Gln				
		210				215						220							
Ser	Asp	Lys	Leu	Leu	Gln	Met	Ala	Asp	Leu	Val	Tyr	Thr	Gly	Arg	Phe				
225					230					235					240				
Asp	Leu	Asn	Pro	Ala	Arg	Asn	Thr	Arg	Glu	Lys	Leu	Leu	Leu	Pro	Leu				
			245						250					255					

1620 1625 1630
 Ser Met Tyr Val Pro Gln Trp Arg Ala Thr Gly Ala Ala Glu Asp Leu
 1635 1640 1645
 Leu Ile Val Arg Pro
 1650

<210> 403
 <211> 264
 <212> PRT
 <213> Escherichia coli

<400> 403
 Met Asp Leu Leu Tyr Arg Val Lys Thr Leu Trp Ala Ala Leu Arg Gly
 1 5 10 15
 Asn His Tyr Thr Trp Pro Ala Ile Asp Ile Thr Leu Pro Gly Asn Arg
 20 25 30
 His Phe His Leu Ile Gly Ser Ile His Met Gly Ser His Asp Met Ala
 35 40 45
 Pro Leu Pro Thr Arg Leu Leu Lys Lys Leu Lys Asn Ala Asp Ala Leu
 50 55 60
 Ile Val Glu Ala Asp Val Ser Thr Ser Asp Thr Pro Phe Ala Asn Leu
 65 70 75 80
 Pro Ala Cys Glu Ala Leu Glu Glu Arg Ile Ser Glu Glu Gln Leu Gln
 85 90 95
 Asn Leu Gln His Ile Ser Gln Glu Met Gly Ile Ser Pro Ser Leu Phe
 100 105 110
 Ser Thr Gln Pro Leu Trp Gln Ile Ala Met Val Leu Gln Ala Thr Gln
 115 120 125
 Ala Gln Lys Leu Gly Leu Arg Ala Glu Tyr Gly Ile Asp Tyr Gln Leu
 130 135 140
 Leu Gln Ala Ala Lys Gln Gln His Lys Pro Val Ile Glu Leu Glu Gly
 145 150 155 160
 Ala Glu Asn Gln Ile Ala Met Leu Leu Gln Leu Pro Asp Lys Gly Leu
 165 170 175
 Ala Leu Leu Asp Asp Thr Leu Thr His Trp His Thr Asn Ala Arg Leu
 180 185 190
 Leu Gln Gln Met Met Ser Trp Trp Leu Asn Ala Pro Pro Gln Asn Asn
 195 200 205
 Asp Ile Thr Leu Pro Asn Thr Phe Ser Gln Ser Leu Tyr Asp Val Leu
 210 215 220
 Met His Gln Arg Asn Leu Ala Trp Arg Asp Lys Leu Arg Ala Met Pro
 225 230 235 240
 Pro Gly Arg Tyr Val Val Ala Val Gly Ala Leu His Leu Tyr Gly Glu
 245 250 255
 Gly Asn Leu Pro Gln Met Leu Arg
 260

<210> 404
 <211> 322
 <212> PRT
 <213> Escherichia coli

<400> 404
 Met Asp Asn Phe Leu Ala Leu Thr Leu Thr Gly Lys Lys Pro Val Ile
 1 5 10 15

Arg	Val	Lys	Arg	Asn	Pro	Val	Ser	Gly	Glu	Val	Leu	Trp	Gln	Gly	Asn	
		20						25					30			
Asp	Ala	Asp	Ala	Ala	Gln	Val	Glu	Gln	Ala	Cys	Arg	Ala	Ala	Arg	Ala	
		35					40					45				
Ala	Phe	Pro	Arg	Trp	Ala	Arg	Leu	Ser	Phe	Ala	Glu	Arg	His	Ala	Val	
		50				55					60					
Val	Glu	Arg	Phe	Ala	Ala	Leu	Leu	Glu	Ser	Asn	Lys	Ala	Glu	Leu	Thr	
		65			70					75					80	
Ala	Ile	Ile	Ala	Arg	Glu	Thr	Gly	Lys	Pro	Arg	Trp	Glu	Ala	Ala	Thr	
				85					90					95		
Glu	Val	Thr	Ala	Met	Ile	Asn	Lys	Ile	Ala	Ile	Ser	Ile	Lys	Ala	Tyr	
			100					105					110			
His	Val	Arg	Thr	Gly	Glu	Gln	Arg	Ser	Glu	Met	Pro	Asp	Gly	Ala	Ala	
		115					120					125				
Ser	Leu	Arg	His	Arg	Pro	His	Gly	Val	Leu	Ala	Val	Phe	Gly	Pro	Tyr	
		130				135					140					
Asn	Phe	Pro	Gly	His	Leu	Pro	Asn	Gly	His	Ile	Val	Pro	Ala	Leu	Leu	
					150					155					160	
Ala	Gly	Asn	Thr	Ile	Ile	Phe	Lys	Pro	Ser	Glu	Leu	Thr	Pro	Trp	Ser	
				165				170						175		
Gly	Glu	Ala	Val	Met	Arg	Leu	Trp	Gln	Gln	Ala	Gly	Leu	Pro	Pro	Gly	
			180					185					190			
Val	Leu	Asn	Leu	Val	Gln	Gly	Gly	Arg	Glu	Thr	Gly	Gln	Ala	Leu	Ser	
		195				200						205				
Ala	Leu	Glu	Asp	Leu	Asp	Gly	Leu	Leu	Phe	Thr	Gly	Ser	Ala	Asn	Thr	
		210				215					220					
Gly	Tyr	Gln	Leu	His	Arg	Gln	Leu	Ser	Gly	Gln	Pro	Glu	Lys	Ile	Leu	
		225			230					235				240		
Ala	Leu	Glu	Met	Gly	Gly	Asn	Asn	Pro	Leu	Ile	Ile	Asp	Glu	Val	Ala	
				245					250					255		
Asp	Ile	Asp	Ala	Ala	Val	His	Leu	Thr	Ile	Gln	Ser	Ala	Phe	Val	Thr	
			260					265					270			
Ala	Gly	Gln	Arg	Cys	Thr	Cys	Ala	Arg	Arg	Leu	Leu	Leu	Lys	Ser	Gly	
		275					280					285				
Ala	Gln	Gly	Asp	Ala	Phe	Leu	Ala	Arg	Leu	Val	Ala	Val	Ser	Gln	Arg	
		290				295					300					
Leu	Thr	Pro	Gly	Asn	Trp	Asp	Asp	Glu	Pro	Gln	Pro	Phe	Ile	Gly	Gly	
		305			310					315				320		
Leu	Ile	Ser	Glu	Gln	Ala	Ala	Gln	Gln	Val	Val	Thr	Ala	Trp	Gln	Gln	
				325					330					335		
Leu	Glu	Ala	Met	Gly	Gly	Arg	Pro	Leu	Leu	Ala	Pro	Arg	Leu	Leu	Gln	
		340						345					350			
Ala	Gly	Thr	Ser	Leu	Leu	Thr	Pro	Gly	Ile	Ile	Glu	Met	Thr	Gly	Val	
		355					360					365				
Ala	Gly	Val	Pro	Asp	Glu	Glu	Val	Phe	Gly	Pro	Leu	Leu	Arg	Val	Trp	
		370				375					380					
Arg	Tyr	Asp	Thr	Phe	Asp	Glu	Ala	Ile	Arg	Met	Ala	Asn	Asn	Thr	Arg	
		385			390					395				400		
Phe	Gly	Leu	Ser	Cys	Gly	Leu	Val	Ser	Pro	Glu	Arg	Glu	Lys	Phe	Asp	
				405					410					415		
Gln	Leu	Leu	Leu	Glu	Ala	Arg	Ala	Gly	Ile	Val	Asn	Trp	Asn	Lys	Pro	
				420				425					430			
Leu	Thr	Gly	Ala	Ala	Ser	Thr	Ala	Pro	Phe	Gly	Gly	Ile	Gly	Ala	Ser	
		435					440					445				
Gly	Asn	His	Arg	Pro	Ser	Ala	Trp	Tyr	Ala	Ala	Asp	Tyr	Cys	Ala	Trp	
		450				455					460					
Pro	Met	Ala	Ser	Leu	Glu	Ser	Asp	Ser	Leu	Thr	Leu	Pro	Ala	Thr	Leu	

465 470 475 480
 Asn Pro Gly Leu Asp Phe Ser Asp Glu Val Val Arg
 485 490

<210> 407
 <211> 344
 <212> PRT
 <213> Escherichia coli

<400> 407
 Met Met Val Ile Arg Pro Val Glu Arg Ser Asp Val Ser Ala Leu Met
 1 5 10 15
 Gln Leu Ala Ser Lys Thr Gly Gly Gly Leu Thr Ser Leu Pro Ala Asn
 20 25 30
 Glu Ala Thr Leu Ser Ala Arg Ile Glu Arg Ala Ile Lys Thr Trp Gln
 35 40 45
 Gly Glu Leu Pro Lys Ser Glu Gln Gly Tyr Val Phe Val Leu Glu Asp
 50 55 60
 Ser Glu Thr Gly Thr Val Ala Gly Ile Cys Ala Ile Glu Val Ala Val
 65 70 75 80
 Gly Leu Asn Asp Pro Trp Tyr Asn Tyr Arg Val Gly Thr Leu Val His
 85 90 95
 Ala Ser Lys Glu Leu Asn Val Tyr Asn Ala Leu Pro Thr Leu Phe Leu
 100 105 110
 Ser Asn Asp His Thr Gly Ser Ser Glu Leu Cys Thr Leu Phe Leu Asp
 115 120 125
 Pro Asp Trp Arg Lys Glu Gly Asn Gly Tyr Leu Leu Ser Lys Ser Arg
 130 135 140
 Phe Met Phe Met Ala Ala Phe Arg Asp Lys Phe Asn Asp Lys Val Val
 145 150 155 160
 Ala Glu Met Arg Gly Val Ile Asp Glu His Gly Tyr Ser Pro Phe Trp
 165 170 175
 Gln Ser Leu Gly Lys Arg Phe Phe Ser Met Asp Phe Ser Arg Ala Asp
 180 185 190
 Phe Leu Cys Gly Thr Gly Gln Lys Ala Phe Ile Ala Glu Leu Met Pro
 195 200 205
 Lys His Pro Ile Tyr Thr His Phe Leu Ser Gln Glu Ala Gln Asp Val
 210 215 220
 Ile Gly Gln Val His Pro Gln Thr Ala Pro Ala Arg Ala Val Leu Glu
 225 230 235 240
 Lys Glu Gly Phe Arg Tyr Arg Asn Tyr Ile Asp Ile Phe Asp Gly Gly
 245 250 255
 Pro Thr Leu Glu Cys Asp Ile Asp Arg Val Arg Ala Ile Arg Lys Ser
 260 265 270
 Arg Leu Val Glu Val Ala Glu Gly Gln Pro Ala Gln Gly Asp Phe Pro
 275 280 285
 Ala Cys Leu Val Ala Asn Glu Asn Tyr His His Phe Arg Val Val Leu
 290 295 300
 Val Arg Thr Asp Pro Ala Thr Glu Arg Leu Ile Leu Thr Ala Ala Gln
 305 310 315 320
 Leu Asp Ala Leu Lys Cys His Ala Gly Asp Arg Val Arg Leu Val Arg
 325 330 335
 Leu Cys Ala Glu Glu Lys Thr Ala
 340

<210> 409
 <211> 1048
 <212> PRT
 <213> Escherichia coli

<400> 409

Met	Lys	Ile	Leu	Ser	Leu	Arg	Leu	Lys	Asn	Leu	Asn	Ser	Leu	Lys	Gly
1				5					10					15	
Glu	Trp	Lys	Ile	Asp	Phe	Thr	Arg	Glu	Pro	Phe	Ala	Ser	Asn	Gly	Leu
			20					25					30		
Phe	Ala	Ile	Thr	Gly	Pro	Thr	Gly	Ala	Gly	Lys	Thr	Thr	Leu	Leu	Asp
		35					40					45			
Ala	Ile	Cys	Leu	Ala	Leu	Tyr	His	Glu	Thr	Pro	Arg	Leu	Ser	Asn	Val
	50					55					60				
Ser	Gln	Ser	Gln	Asn	Asp	Leu	Met	Thr	Arg	Asp	Thr	Ala	Glu	Cys	Leu
65					70					75					80
Ala	Glu	Val	Glu	Phe	Glu	Val	Lys	Gly	Glu	Ala	Tyr	Arg	Ala	Phe	Trp
				85					90					95	
Ser	Gln	Asn	Arg	Ala	Arg	Asn	Gln	Pro	Asp	Gly	Asn	Leu	Gln	Val	Pro
			100					105					110		
Arg	Val	Glu	Leu	Ala	Arg	Cys	Ala	Asp	Gly	Lys	Ile	Leu	Ala	Asp	Lys
		115					120						125		
Val	Lys	Asp	Lys	Leu	Glu	Leu	Thr	Ala	Thr	Leu	Thr	Gly	Leu	Asp	Tyr
	130					135					140				
Gly	Arg	Phe	Thr	Arg	Ser	Met	Leu	Leu	Ser	Gln	Gly	Gln	Phe	Ala	Ala
145					150					155					160
Phe	Leu	Asn	Ala	Lys	Pro	Lys	Glu	Arg	Ala	Glu	Leu	Leu	Glu	Glu	Leu
				165					170					175	
Thr	Gly	Thr	Glu	Ile	Tyr	Gly	Gln	Ile	Ser	Ala	Met	Val	Phe	Glu	Gln
			180					185					190		
His	Lys	Ser	Ala	Arg	Thr	Glu	Leu	Glu	Lys	Leu	Gln	Ala	Gln	Ala	Ser
		195					200					205			
Gly	Val	Thr	Leu	Leu	Thr	Pro	Glu	Gln	Val	Gln	Ser	Leu	Thr	Ala	Ser
	210					215					220				
Leu	Gln	Val	Leu	Thr	Asp	Glu	Glu	Lys	Gln	Leu	Ile	Thr	Ala	Gln	Gln
225					230					235					240
Gln	Glu	Gln	Gln	Ser	Leu	Asn	Trp	Leu	Thr	Arg	Gln	Asp	Glu	Leu	Gln
				245						250				255	
Gln	Glu	Ala	Ser	Arg	Arg	Gln	Gln	Ala	Leu	Gln	Gln	Ala	Leu	Ala	Glu
		260						265					270		
Glu	Glu	Lys	Ala	Gln	Pro	Gln	Leu	Ala	Ala	Leu	Ser	Leu	Ala	Gln	Pro
		275					280					285			
Ala	Arg	Asn	Leu	Arg	Pro	His	Trp	Glu	Arg	Ile	Ala	Glu	His	Ser	Ala
	290					295					300				
Ala	Leu	Ala	His	Ile	Arg	Gln	Gln	Ile	Glu	Glu	Val	Asn	Thr	Arg	Leu
305					310					315					320
Gln	Ser	Thr	Met	Ala	Leu	Arg	Ala	Ser	Ile	Arg	His	His	Ala	Ala	Lys
			325						330					335	
Gln	Ser	Ala	Glu	Leu	Gln	Gln	Gln	Gln	Gln	Ser	Leu	Asn	Thr	Trp	Leu
		340					345						350		
Gln	Glu	His	Asp	Arg	Phe	Arg	Gln	Trp	Asn	Asn	Glu	Pro	Ala	Gly	Trp
		355					360					365			
Arg	Ala	Gln	Phe	Ser	Gln	Gln	Thr	Ser	Asp	Arg	Glu	His	Leu	Arg	Gln
	370					375						380			

				165					170				175			
Ala	Arg	His	Asn	Ile	Gln	Val	Asn	Gly	Ile	Ala	Pro	Gly	Tyr	Phe	Lys	
			180					185					190			
Thr	Glu	Met	Thr	Lys	Ala	Leu	Val	Glu	Asp	Glu	Ala	Phe	Thr	Ala	Trp	
		195					200					205				
Leu	Cys	Lys	Arg	Thr	Pro	Ala	Arg	Trp	Gly	Asp	Pro	Gln	Glu	Leu		
	210					215				220						
Ile	Gly	Ala	Ala	Val	Phe	Leu	Ser	Ser	Lys	Ala	Ser	Asp	Phe	Val	Asn	
225					230					235					240	
Gly	His	Leu	Leu	Phe	Val	Asp	Gly	Gly	Met	Leu	Val	Ala	Val			
				245					250							

<210> 412
 <211> 343
 <212> PRT
 <213> Escherichia coli

Met	Gln	Val	Lys	Thr	Gln	Ser	Cys	Val	Val	Ala	Gly	Lys	Lys	Thr	Val	
1				5					10					15		
Ala	Val	Thr	Glu	Gln	Thr	Ile	Asp	Trp	Asn	Asn	Asn	Gly	Thr	Leu	Val	
			20					25					30			
Gln	Ile	Thr	Arg	Gly	Gly	Ile	Cys	Gly	Ser	Asp	Leu	His	Tyr	Tyr	Gln	
		35				40						45				
Glu	Gly	Lys	Val	Gly	Asn	Phe	Met	Ile	Lys	Ala	Pro	Met	Val	Leu	Gly	
	50					55					60					
His	Glu	Val	Ile	Gly	Lys	Val	Ile	His	Ser	Asp	Ser	Ser	Glu	Leu	His	
65					70					75					80	
Glu	Gly	Gln	Thr	Val	Ala	Ile	Asn	Pro	Ser	Lys	Pro	Cys	Gly	His	Cys	
				85					90					95		
Lys	Tyr	Cys	Ile	Glu	His	Asn	Glu	Asn	Gln	Cys	Thr	Asp	Met	Arg	Phe	
			100				105						110			
Phe	Gly	Ser	Ala	Met	Tyr	Phe	Pro	His	Val	Asp	Gly	Gly	Phe	Thr	Arg	
		115					120					125				
Tyr	Lys	Met	Val	Glu	Thr	Ser	Gln	Cys	Val	Pro	Tyr	Pro	Ala	Lys	Ala	
	130					135					140					
Asp	Glu	Lys	Val	Met	Ala	Phe	Ala	Glu	Pro	Leu	Ala	Val	Ala	Ile	His	
145					150					155					160	
Ala	Ala	His	Gln	Ala	Gly	Glu	Leu	Gln	Gly	Lys	Arg	Val	Phe	Ile	Ser	
			165						170					175		
Gly	Val	Gly	Pro	Ile	Gly	Cys	Leu	Ile	Val	Ser	Ala	Val	Lys	Thr	Leu	
			180					185					190			
Gly	Ala	Ala	Glu	Ile	Val	Cys	Ala	Asp	Val	Ser	Pro	Arg	Ser	Leu	Ser	
		195					200					205				
Leu	Gly	Lys	Glu	Met	Gly	Ala	Asp	Val	Leu	Val	Asn	Pro	Gln	Asn	Asp	
	210					215					220					
Asp	Met	Asp	His	Trp	Lys	Ala	Glu	Lys	Gly	Tyr	Phe	Asp	Val	Ser	Phe	
225					230					235					240	
Glu	Val	Ser	Gly	His	Pro	Ser	Ser	Val	Asn	Thr	Cys	Leu	Glu	Val	Thr	
				245					250					255		
Arg	Ala	Arg	Gly	Val	Met	Val	Gln	Val	Gly	Met	Gly	Gly	Ala	Met	Ala	
			260					265					270			
Glu	Phe	Pro	Met	Met	Thr	Leu	Ile	Gly	Lys	Glu	Ile	Ser	Leu	Arg	Gly	
		275					280					285				
Ser	Phe	Arg	Phe	Thr	Ser	Glu	Phe	Asn	Thr	Ala	Val	Ser	Trp	Leu	Ala	
	290					295					300					

Asn Gly Val Ile Asn Pro Leu Pro Leu Leu Ser Ala Glu Tyr Pro Phe
 305 310 315 320
 Thr Asp Leu Glu Glu Ala Leu Arg Phe Ala Gly Asp Lys Thr Gln Ala
 325 330 335
 Ala Lys Val Gln Leu Val Phe
 340

<210> 413
 <211> 548
 <212> PRT
 <213> Escherichia coli

<400> 413
 Met Asp Ser Gln Arg Asn Leu Leu Val Ile Ala Leu Leu Phe Val Ser
 1 5 10 15
 Phe Met Ile Trp Gln Ala Trp Glu Gln Asp Lys Asn Pro Gln Pro Gln
 20 25 30
 Ala Gln Gln Thr Thr Gln Thr Thr Thr Thr Ala Ala Gly Ser Ala Ala
 35 40 45
 Asp Gln Gly Val Pro Ala Ser Gly Gln Gly Lys Leu Ile Ser Val Lys
 50 55 60
 Thr Asp Val Leu Asp Leu Thr Ile Asn Thr Arg Gly Gly Asp Val Glu
 65 70 75 80
 Gln Ala Leu Leu Pro Ala Tyr Pro Lys Glu Leu Asn Ser Thr Gln Pro
 85 90 95
 Phe Gln Leu Leu Glu Thr Ser Pro Gln Phe Ile Tyr Gln Ala Gln Ser
 100 105 110
 Gly Leu Thr Gly Arg Asp Gly Pro Asp Asn Pro Ala Asn Gly Pro Arg
 115 120 125
 Pro Leu Tyr Asn Val Glu Lys Asp Ala Tyr Val Leu Ala Glu Gly Gln
 130 135 140
 Asn Glu Leu Gln Val Pro Met Thr Tyr Thr Asp Ala Ala Gly Asn Thr
 145 150 155 160
 Phe Thr Lys Thr Phe Val Leu Lys Arg Gly Asp Tyr Ala Val Asn Val
 165 170 175
 Asn Tyr Asn Val Gln Asn Ala Gly Glu Lys Pro Leu Glu Ile Ser Ser
 180 185 190
 Phe Gly Gln Leu Lys Gln Ser Ile Thr Leu Pro Pro His Leu Asp Thr
 195 200 205
 Gly Ser Ser Asn Phe Ala Leu His Thr Phe Arg Gly Ala Ala Tyr Ser
 210 215 220
 Thr Pro Asp Glu Lys Tyr Glu Lys Tyr Lys Phe Asp Thr Ile Ala Asp
 225 230 235 240
 Asn Glu Asn Leu Asn Ile Ser Ser Lys Gly Gly Trp Val Ala Met Leu
 245 250 255
 Gln Gln Tyr Phe Ala Thr Ala Trp Ile Pro His Asn Asp Gly Thr Asn
 260 265 270
 Asn Phe Tyr Thr Ala Asn Leu Gly Asn Gly Ile Ala Ala Ile Gly Tyr
 275 280 285
 Lys Ser Gln Pro Val Leu Val Gln Pro Gly Gln Thr Gly Ala Met Asn
 290 295 300
 Ser Thr Leu Trp Val Gly Pro Glu Ile Gln Asp Lys Met Ala Ala Val
 305 310 315 320
 Ala Pro His Leu Asp Leu Thr Val Asp Tyr Gly Trp Leu Trp Phe Ile
 325 330 335
 Ser Gln Pro Leu Phe Lys Leu Leu Lys Trp Ile His Ser Phe Val Gly

			20					25				30			
Arg	Gly	Gln	Ser	Ala	Leu	His	Phe	Ser	Ser	Gly	Ser	Leu	Asp	Leu	Leu
		35					40					45			
Ser	His	Leu	Pro	Asp	Gly	Gln	Pro	Val	Thr	Asp	Ile	His	Ser	Gly	Leu
	50					55					60				
Glu	Ser	Leu	Arg	Gln	Gln	Ala	Pro	Ala	His	Pro	Tyr	Ser	Leu	Leu	Glu
65					70					75					80
Pro	Gln	Arg	Val	Leu	Asp	Leu	Ala	Cys	Gln	Ala	Gln	Ala	Leu	Ile	Ala
				85					90					95	
Glu	Ser	Gly	Ala	Gln	Leu	Gln	Gly	Ser	Val	Glu	Leu	Ala	His	Gln	Arg
			100					105					110		
Val	Thr	Pro	Leu	Gly	Thr	Leu	Arg	Ser	Thr	Trp	Leu	Ser	Ser	Pro	Glu
		115					120					125			
Val	Pro	Val	Trp	Pro	Leu	Pro	Ala	Lys	Lys	Ile	Cys	Val	Val	Gly	Ile
		130				135					140				
Ser	Gly	Leu	Met	Asp	Phe	Gln	Ala	His	Leu	Ala	Ala	Ala	Ser	Leu	Arg
145					150					155					160
Glu	Leu	Gly	Leu	Ala	Val	Glu	Thr	Ala	Glu	Ile	Glu	Leu	Pro	Glu	Leu
				165					170					175	
Asp	Val	Leu	Arg	Asn	Asn	Ala	Thr	Glu	Phe	Arg	Ala	Val	Asn	Ile	Ala
			180					185					190		
Arg	Phe	Leu	Asp	Asn	Glu	Glu	Asn	Trp	Pro	Leu	Leu	Leu	Asp	Ala	Leu
		195					200					205			
Ile	Pro	Val	Ala	Asn	Thr	Cys	Glu	Met	Ile	Leu	Met	Pro	Ala	Cys	Phe
	210					215					220				
Gly	Leu	Ala	Asp	Asp	Lys	Leu	Trp	Arg	Trp	Leu	Asn	Glu	Lys	Leu	Pro
225					230					235					240
Cys	Ser	Leu	Met	Leu	Leu	Pro	Thr	Leu	Pro	Pro	Ser	Val	Leu	Gly	Ile
			245						250					255	
Arg	Leu	Gln	Asn	Gln	Leu	Gln	Arg	Gln	Phe	Val	Arg	Gln	Gly	Gly	Val
			260					265					270		
Trp	Met	Pro	Gly	Asp	Glu	Val	Lys	Lys	Val	Thr	Cys	Lys	Asn	Gly	Val
		275					280					285			
Val	Asn	Glu	Ile	Trp	Thr	Arg	Asn	His	Ala	Asp	Ile	Pro	Leu	Arg	Pro
	290					295					300				
Arg	Phe	Ala	Val	Leu	Ala	Ser	Gly	Ser	Phe	Phe	Ser	Gly	Gly	Leu	Val
305					310					315					320
Ala	Glu	Arg	Asn	Gly	Ile	Arg	Glu	Pro	Ile	Leu	Gly	Leu	Asp	Val	Leu
				325					330					335	
Gln	Thr	Ala	Thr	Arg	Gly	Glu	Trp	Tyr	Lys	Gly	Asp	Phe	Phe	Ala	Pro
			340					345					350		
Gln	Pro	Trp	Gln	Gln	Phe	Gly	Val	Thr	Thr	Asp	Glu	Thr	Leu	Arg	Pro
		355													

<210> 416

<211> 396

<212> PRT

<213> Escherichia coli

<213> Escherichia coli

<400> 417

Met Gln Leu Arg Lys Pro Ala Thr Ala Ile Leu Ala Leu Ala Leu Ser
1 5 10 15
Ala Gly Leu Ala Gln Ala Asp Asp Ala Ala Pro Ala Ala Gly Ser Thr
20 25 30
Leu Asp Lys Ile Ala Lys Asn Gly Val Ile Val Val Gly His Arg Glu
35 40 45
Ser Ser Val Pro Phe Ser Tyr Tyr Asp Asn Gln Gln Lys Val Val Gly
50 55 60
Tyr Ser Gln Asp Tyr Ser Asn Ala Ile Val Glu Ala Val Lys Lys Lys
65 70 75 80
Leu Asn Lys Pro Asp Leu Gln Val Lys Leu Ile Pro Ile Thr Ser Gln
85 90 95
Asn Arg Ile Pro Leu Leu Gln Asn Gly Thr Phe Asp Phe Glu Cys Gly
100 105 110
Ser Thr Thr Asn Asn Val Glu Arg Gln Lys Gln Ala Ala Phe Ser Asp
115 120 125
Thr Ile Phe Val Val Gly Thr Arg Leu Leu Thr Lys Lys Gly Gly Asp
130 135 140
Ile Lys Asp Phe Ala Asn Leu Lys Asp Lys Ala Val Val Val Thr Ser
145 150 155 160
Gly Thr Thr Ser Glu Val Leu Leu Asn Lys Leu Asn Glu Glu Gln Lys
165 170 175
Met Asn Met Arg Ile Ile Ser Ala Lys Asp His Gly Asp Ser Phe Arg
180 185 190
Thr Leu Glu Ser Gly Arg Ala Val Ala Phe Met Met Asp Asp Ala Leu
195 200 205
Leu Ala Gly Glu Arg Ala Lys Ala Lys Lys Pro Asp Asn Trp Glu Ile
210 215 220
Val Gly Lys Pro Gln Ser Gln Glu Ala Tyr Gly Cys Met Leu Arg Lys
225 230 235 240
Asp Asp Pro Gln Phe Lys Lys Leu Met Asp Asp Thr Ile Ala Gln Val
245 250 255
Gln Thr Ser Gly Glu Ala Glu Lys Trp Phe Asp Lys Trp Phe Lys Asn
260 265 270
Pro Ile Pro Pro Lys Asn Leu Asn Met Asn Phe Glu Leu Ser Asp Glu
275 280 285
Met Lys Ala Leu Phe Lys Glu Pro Asn Asp Lys Ala Leu Asn
290 295 300

<210> 418

<211> 328

<212> PRT

<213> Escherichia coli

<400> 418

Met Asn Asn Ser Ala Phe Thr Phe Gln Thr Leu His Pro Asp Thr Ile
1 5 10 15
Met Asp Ala Leu Phe Glu His Gly Ile Arg Val Asp Ser Gly Leu Thr
20 25 30
Pro Leu Asn Ser Tyr Glu Asn Arg Val Tyr Gln Phe Gln Asp Glu Asp
35 40 45
Arg Arg Arg Phe Val Val Lys Phe Tyr Arg Pro Glu Arg Trp Thr Ala
50 55 60

115		120		125
Asp Val Phe Ile Asn Ala Gly Ile Lys Gly Glu Glu Tyr Asp Ala Ala				
130		135		140
Trp Asn Ser Phe Val Val Lys Ser Leu Val Ala Gln Gln Glu Lys Ala				
145		150		155
Ala Ala Asp Val Gln Leu Arg Gly Val Pro Ala Met Phe Val Asn Gly				160
	165		170	
Lys Tyr Gln Leu Asn Pro Gln Gly Met Asp Thr Ser Asn Met Asp Val				175
	180		185	
Phe Val Gln Gln Tyr Ala Asp Thr Val Lys Tyr Leu Ser Glu Lys Lys				190
195		200		205

<210> 420
 <211> 112
 <212> PRT
 <213> Escherichia coli

<400> 420
Met Thr Met Asn Ser Phe Glu Arg Arg Asn Lys Ile Ile Gln Leu Val
1 5 10 15
Asn Glu Gln Gly Thr Val Leu Val Gln Asp Leu Ala Gly Val Phe Ala
20 25 30
Ala Ser Glu Ala Thr Ile Arg Ala Asp Leu Arg Phe Leu Glu Gln Lys
35 40 45
Gly Val Val Thr Arg Phe His Gly Gly Ala Ala Lys Ile Met Ser Gly
50 55 60
Asn Ser Glu Thr Glu Thr Gln Glu Val Gly Phe Lys Glu Arg Phe Gln
65 70 75 80
Leu Ala Ser Ala Pro Lys Asn Arg Ile Ala Gln Ala Ala Val Lys Met
85 90 95
Ile His Glu Gly Met Thr Asp Pro Thr His Val Ile Trp Thr Gln Ala
100 105 110

<210> 421
 <211> 346
 <212> PRT
 <213> Escherichia coli

<400> 421
Met Lys Ser Val Val Asn Asp Thr Asp Gly Ile Val Arg Val Ala Glu
1 5 10 15
Ser Val Ile Pro Glu Ile Lys His Gln Asp Glu Val Arg Val Lys Ile
20 25 30
Ala Ser Ser Gly Leu Cys Gly Ser Asp Leu Pro Arg Ile Phe Lys Asn
35 40 45
Gly Ala His Tyr Tyr Pro Ile Thr Leu Gly His Glu Phe Ser Gly Tyr
50 55 60
Ile Asp Ala Val Gly Ser Gly Val Asp Asp Leu His Pro Gly Asp Ala
65 70 75 80
Val Ala Cys Val Pro Leu Leu Pro Cys Phe Thr Cys Pro Glu Cys Leu
85 90 95
Lys Gly Phe Tyr Ser Gln Cys Ala Lys Tyr Asp Phe Ile Gly Ser Arg
100 105 110
Arg Asp Gly Gly Phe Ala Glu Tyr Ile Val Val Lys Arg Lys Asn Val
115 120 125

Phe Ala Leu Pro Thr Asp Met Pro Ile Glu Asp Gly Ala Phe Ile Glu
 130 135 140
 Pro Ile Thr Val Gly Leu His Ala Phe His Leu Ala Gln Gly Cys Glu
 145 150 155 160
 Asn Lys Asn Val Ile Ile Ile Gly Ala Gly Thr Ile Gly Leu Leu Ala
 165 170 175
 Ile Gln Cys Ala Val Ala Leu Gly Ala Lys Ser Val Thr Ala Ile Asp
 180 185 190
 Ile Ser Ser Glu Lys Leu Ala Leu Ala Lys Ser Phe Gly Ala Met Gln
 195 200 205
 Thr Phe Asn Ser Ser Glu Met Ser Ala Pro Gln Met Gln Ser Val Leu
 210 215 220
 Arg Glu Leu Arg Phe Asn Gln Leu Ile Leu Glu Thr Ala Gly Val Pro
 225 230 235 240
 Gln Thr Val Glu Leu Ala Val Glu Ile Ala Gly Pro His Ala Gln Leu
 245 250 255
 Ala Leu Val Gly Thr Leu His Gln Asp Leu His Leu Thr Ser Ala Thr
 260 265 270
 Phe Gly Lys Ile Leu Arg Lys Glu Leu Thr Val Ile Gly Ser Trp Met
 275 280 285
 Asn Tyr Ser Ser Pro Trp Pro Gly Gln Glu Trp Glu Thr Ala Ser Arg
 290 295 300
 Leu Leu Thr Glu Arg Lys Leu Ser Leu Glu Pro Leu Ile Ala His Arg
 305 310 315 320
 Gly Ser Phe Glu Ser Phe Ala Gln Ala Val Arg Asp Ile Ala Arg Asn
 325 330 335
 Ala Met Pro Gly Lys Val Leu Leu Ile Pro
 340 345

<210> 422
 <211> 451
 <212> PRT
 <213> Escherichia coli

<400> 422
 Met Phe Ser Glu Val Met Arg Tyr Ile Leu Asp Leu Gly Pro Thr Val
 1 5 10 15
 Met Leu Pro Ile Val Ile Ile Ile Phe Ser Lys Ile Leu Gly Met Lys
 20 25 30
 Ala Gly Asp Cys Phe Lys Ala Gly Leu His Ile Gly Ile Gly Phe Val
 35 40 45
 Gly Ile Gly Leu Val Ile Gly Leu Met Leu Asp Ser Ile Gly Pro Ala
 50 55 60
 Ala Lys Ala Met Ala Glu Asn Phe Asp Leu Asn Leu His Val Val Asp
 65 70 75 80
 Val Gly Trp Pro Gly Ser Ser Pro Met Thr Trp Ala Ser Gln Ile Ala
 85 90 95
 Leu Val Ala Ile Pro Ile Ala Ile Leu Val Asn Val Ala Met Leu Leu
 100 105 110
 Thr Arg Met Thr Arg Val Val Asn Val Asp Ile Trp Asn Ile Trp His
 115 120 125
 Met Thr Phe Thr Gly Ala Leu Leu His Leu Ala Thr Gly Ser Trp Met
 130 135 140
 Ile Gly Met Ala Gly Val Val Ile His Ala Ala Phe Val Tyr Lys Leu
 145 150 155 160
 Gly Asp Trp Phe Ala Arg Asp Thr Arg Asn Phe Phe Glu Leu Glu Gly

<210> 424
 <211> 150
 <212> PRT
 <213> Escherichia coli

<400> 424

Met	Thr	Asn	Leu	Phe	Val	Arg	Ser	Gly	Ile	Ser	Phe	Val	Asp	Arg	Ser
1				5					10					15	
Glu	Val	Leu	Thr	His	Ile	Gly	Asn	Glu	Met	Leu	Ala	Lys	Gly	Val	Val
		20					25						30		
His	Asp	Thr	Trp	Pro	Gln	Ala	Leu	Ile	Ala	Arg	Glu	Ala	Glu	Phe	Pro
	35						40					45			
Thr	Gly	Ile	Met	Leu	Glu	Gln	His	Ala	Ile	Ala	Ile	Pro	His	Cys	Glu
	50					55					60				
Ala	Ile	His	Ala	Lys	Ser	Ser	Ala	Ile	Tyr	Leu	Leu	Arg	Pro	Thr	Asn
65				70					75						80
Lys	Val	His	Phe	Gln	Gln	Ala	Asp	Asp	Asp	Asn	Asp	Val	Ala	Val	Ser
				85				90						95	
Leu	Val	Ile	Ala	Leu	Ile	Val	Glu	Asn	Pro	Gln	Gln	Gln	Leu	Lys	Leu
			100					105					110		
Leu	Arg	Cys	Leu	Phe	Gly	Lys	Leu	Gln	Gln	Pro	Asp	Ile	Val	Glu	Thr
		115					120					125			
Leu	Ile	Thr	Leu	Pro	Glu	Thr	Gln	Leu	Lys	Glu	Tyr	Phe	Thr	Lys	Tyr
	130					135					140				
Val	Leu	Asp	Ser	Asp	Glu										
145					150										

<210> 425
 <211> 420
 <212> PRT
 <213> Escherichia coli

<400> 425

Met	Lys	Thr	Leu	Ile	Ala	Arg	His	Lys	Ala	Gly	Glu	His	Ile	Gly	Ile
1				5					10					15	
Cys	Ser	Val	Cys	Ser	Ala	His	Pro	Leu	Val	Ile	Glu	Ala	Ala	Leu	Ala
		20						25					30		
Phe	Asp	Arg	Asn	Ser	Thr	Arg	Lys	Val	Leu	Ile	Glu	Ala	Thr	Ser	Asn
	35						40					45			
Gln	Val	Asn	Gln	Phe	Gly	Gly	Tyr	Thr	Gly	Met	Thr	Pro	Ala	Asp	Phe
	50					55					60				
Arg	Glu	Phe	Val	Phe	Thr	Ile	Ala	Asp	Lys	Val	Gly	Phe	Ala	Arg	Glu
65					70				75						80
Arg	Ile	Ile	Leu	Gly	Gly	Asp	His	Leu	Gly	Pro	Asn	Cys	Trp	Gln	Gln
			85					90						95	
Glu	Asn	Ala	Asp	Ala	Ala	Met	Glu	Lys	Ser	Val	Glu	Leu	Val	Lys	Glu
		100						105					110		
Tyr	Val	Arg	Ala	Gly	Phe	Ser	Lys	Ile	His	Leu	Asp	Ala	Ser	Met	Ser
		115					120					125			
Cys	Ala	Gly	Asp	Pro	Ile	Pro	Leu	Ala	Pro	Glu	Thr	Val	Ala	Glu	Arg
	130					135					140				
Ala	Ala	Val	Leu	Cys	Phe	Ala	Ala	Glu	Ser	Val	Ala	Thr	Asp	Cys	Gln
145					150				155						160
Arg	Glu	Gln	Leu	Ser	Tyr	Val	Ile	Gly	Thr	Glu	Val	Pro	Val	Pro	Gly

Phe	Asp	Val	Ser	Val	Glu	Ala	Glu	Leu	Gly	Gln	Leu	Gly	Gly	Gln	Glu
130						135					140				
Asp	Asp	Val	Gln	Val	Asn	Glu	Ala	Asp	Ala	Leu	Tyr	Thr	Asn	Pro	Ala
145					150					155					160
Gln	Ala	Arg	Glu	Phe	Ala	Glu	Ala	Thr	Gly	Ile	Asp	Ser	Leu	Ala	Val
				165					170					175	
Ala	Ile	Gly	Thr	Ala	His	Gly	Met	Tyr	Ala	Ser	Ala	Pro	Ala	Leu	Asp
			180					185					190		
Phe	Ser	Arg	Leu	Glu	Asn	Ile	Arg	Gln	Trp	Val	Asn	Leu	Pro	Leu	Val
	195					200					205				
Leu	His	Gly	Ala	Ser	Gly	Leu	Ser	Thr	Lys	Asp	Ile	Gln	Gln	Thr	Ile
210						215					220				
Lys	Leu	Gly	Ile	Cys	Lys	Ile	Asn	Val	Ala	Thr	Glu	Leu	Lys	Asn	Ala
225					230					235					240
Phe	Ser	Gln	Ala	Leu	Lys	Asn	Tyr	Leu	Thr	Glu	His	Pro	Glu	Ala	Thr
				245					250					255	
Asp	Pro	Arg	Asp	Tyr	Leu	Gln	Ser	Ala	Lys	Ser	Ala	Met	Arg	Asp	Val
			260					265					270		
Val	Ser	Lys	Val	Ile	Ala	Asp	Cys	Gly	Cys	Glu	Gly	Arg	Ala		
	275						280						285		

<210> 427
 <211> 157
 <212> PRT
 <213> Escherichia coli

<400> 427

Met	Ser	Gln	Asn	Asp	Ile	Ile	Ile	Arg	Thr	His	Tyr	Lys	Ser	Pro	His
1				5					10					15	
Arg	Leu	His	Ile	Asp	Ser	Asp	Ile	Pro	Thr	Pro	Ser	Ser	Glu	Pro	Ile
			20					25					30		
Asn	Gln	Phe	Ala	Arg	Gln	Leu	Ile	Thr	Leu	Leu	Asp	Thr	Ser	Asp	Leu
		35				40					45				
Ser	Ser	Met	Leu	Ser	Tyr	Cys	Val	Thr	Gln	Glu	Phe	Thr	Ala	Asn	Cys
	50					55				60					
Arg	Lys	Ile	Ser	Gln	Asn	Cys	Tyr	Ser	Thr	Ala	Leu	Phe	Thr	Ile	Asn
65					70				75					80	
Phe	Ala	Thr	Ser	Pro	Ile	His	Thr	Glu	Asn	Ile	Leu	Ile	Thr	Leu	His
			85					90						95	
Tyr	Lys	Lys	Glu	Ile	Ile	Ser	Leu	Leu	Glu	Thr	Thr	Pro	Ile	Lys	
		100						105					110		
Ala	Asn	His	Leu	Arg	Ser	Ile	Leu	Asp	Tyr	Ile	Glu	Gln	Glu	Gln	Leu
	115						120					125			
Thr	Ala	Glu	Asp	Arg	Asn	His	Cys	Met	Lys	Leu	Ser	Lys	Lys	Ile	His
	130					135					140				
Arg	Glu	Lys	Asn	Tyr	Thr	Pro	Asn	Ser	Lys	Ser	Gln	Trp			
145					150						155				

<210> 428
 <211> 471
 <212> PRT
 <213> Escherichia coli

<400> 428
 Met Gln Ser Pro Ser Asp Ala Ile Phe Cys Arg His Leu Ser Leu Gln

1	5	10	15
Tyr Ala Leu Asp Ser Leu Arg Asn Gly Lys Gly Lys Val Asn Leu Ile			
	20	25	30
Lys His Tyr Ser Ser Val Glu Ser Ile Gln Gln His Val Pro Leu Val			
	35	40	45
Arg Asp Ala Glu Phe Arg Ala Leu Leu Arg His Pro Pro Ala Gly Ser			
	50	55	60
Arg Val Ile Ala Ser Lys Asp Phe Gly Phe Ala Leu Asp Ile Phe Phe			
65	70	75	80
Cys Arg Met Met Ala Asn Asn Val Ser His Met Ser Ala Ile Leu Tyr			
	85	90	95
Ile Asp Asn His Thr Leu Ser Val Arg Leu Arg Ile Lys Gln Ser Val			
	100	105	110
Tyr Gly Gln Leu Asn Tyr Val Val Ser Val Tyr Asp Pro Asn Asp Thr			
	115	120	125
Asn Val Ala Val Arg Asp Thr His Arg Thr Ala Arg Gly Phe Leu Ser			
	130	135	140
Leu Asp Lys Phe Ile Ser Ser Gly Pro Asp Ala Gln Thr Trp Ala Asp			
145	150	155	160
Arg Tyr Val Arg Asn Cys Ala Ile Ala Ile Leu Pro Leu Leu Pro Val			
	165	170	175
Gly Val Pro Gly Ala Ile Phe Ala Gly Ile Ala Ser Arg Met Pro Phe			
	180	185	190
Ala Pro Ile His Pro Ser Ala Met Leu Leu Ile Met Ala Thr Gly Gln			
	195	200	205
Ser Gln Gln Leu Ile Thr Leu Phe Lys Gln Leu Pro Ile Leu Pro Glu			
	210	215	220
Lys Glu Ile Ile Glu Ile Ile Thr Ala Gln Asn Ser Val Gly Thr Pro			
225	230	235	240
Ala Leu Phe Leu Ala Met Met Asn Gly His Thr Asp Asn Val Lys Ile			
	245	250	255
Phe Met Gln Glu Ile Gln Ser Leu Val Asp Asn His Ile Ile His Glu			
	260	265	270
Asp Asn Leu Val Lys Leu Leu Gln Thr Lys Ser Ala Asn Glu Thr Pro			
	275	280	285
Gly Leu Tyr Ile Ser Met Leu Tyr Gly Phe Asp Glu Ile Ile Asp Ile			
	290	295	300
Phe Leu Asn Ala Leu Thr Thr Pro Ile Ala Gln Glu Leu Leu Asn Lys			
305	310	315	320
Lys Leu Val Met Ser Ile Leu Ala Met Lys Ile His Asp Gly Glu Pro			
	325	330	335
Gly Leu Tyr Ala Ala Met Glu Asn Asn His Pro Leu Cys Val Thr Arg			
	340	345	350
Phe Leu Ser Lys Ile Asn Gly Ile Ala Phe Lys Tyr Lys Leu Ser Lys			
	355	360	365
Ala Asn Ile Met Asp Leu Leu Lys Gly Ala Thr Ala Gln Gly Thr Pro			
	370	375	380
Ala Leu Tyr Ile Ala Met Ser Lys Gly Asn Glu Asp Val Val Leu Ser			
385	390	395	400
Tyr Ile Ser Thr Leu Gly Ala Phe Ala Lys Lys His Ser Phe Ser Gln			
	405	410	415
His Gln Leu Phe Thr Leu Leu Ala Ala Lys Asn His Asp Asn Met Ser			
	420	425	430
Ala Val His Ile Ala Ile His His Lys His Tyr Lys Thr Val Glu Thr			
	435	440	445
Tyr Tyr Ala Ala Ile Asn Ala Ile Ser Gln Ser Leu Ser Phe Ser Ala			
	450	455	460

Asp Glu Ile Lys Thr Tyr Leu
465 470

<210> 429
<211> 128
<212> PRT
<213> Escherichia coli

<400> 429
Met Pro Ser Gly Leu Phe Met Asp Leu Leu Pro Phe Leu Leu Asp Ala
1 5 10 15
Asn Leu Ser Ala Thr Asn Pro Pro Ala Ile Pro His Trp Trp Lys Arg
20 25 30
Gln Pro Leu Ile Pro Asn Leu Leu Ser Gln Glu Leu Lys Asn Tyr Leu
35 40 45
Lys Leu Asn Val Lys Glu Lys Asn Ile Gln Ile Ala Asp Gln Val Ile
50 55 60
Ile Asp Glu Thr Ala Gly Glu Val Val Ile Gly Ala Asn Thr Arg Ile
65 70 75 80
Cys His Gly Ala Val Ile Gln Gly Pro Val Val Ile Gly Ala Asn Cys
85 90 95
Leu Ile Gly Asn Trp Ile Cys Pro Tyr Ile Ser Arg His Leu Leu Ser
100 105 110
Leu Asn Pro Leu Gln Ala Arg Cys Arg Arg Tyr Ser Arg Gly Glu Arg
115 120 125

<210> 430
<211> 398
<212> PRT
<213> Escherichia coli

<400> 430
Met Lys Thr Trp Ile Phe Ile Cys Met Ser Ile Ala Met Leu Leu Trp
1 5 10 15
Phe Leu Ser Thr Leu Arg Arg Lys Pro Ser Gln Lys Lys Gly Cys Ile
20 25 30
Asp Ala Ile Ile Pro Ala Tyr Asn Glu Gly Pro Cys Leu Ala Gln Ser
35 40 45
Leu Asp Asn Leu Leu Arg Asn Pro Tyr Phe Cys Arg Val Ile Cys Val
50 55 60
Asn Asp Gly Ser Thr Asp Asn Thr Glu Ala Val Met Ala Glu Val Lys
65 70 75 80
Arg Lys Trp Gly Asp Arg Phe Val Ala Val Thr Gln Lys Asn Thr Gly
85 90 95
Lys Gly Gly Ala Leu Met Asn Gly Leu Asn Tyr Ala Thr Cys Asp Gln
100 105 110
Val Phe Leu Ser Asp Ala Asp Thr Tyr Val Pro Pro Asp Gln Asp Gly
115 120 125
Met Gly Tyr Met Leu Ala Glu Ile Glu Arg Gly Ala Asp Ala Val Gly
130 135 140
Gly Ile Pro Ser Thr Ala Leu Lys Gly Ala Gly Leu Leu Pro His Ile
145 150 155 160
Arg Ala Thr Val Lys Leu Pro Met Ile Val Met Lys Arg Thr Leu Gln
165 170 175
Gln Leu Leu Gly Gly Ala Pro Phe Ile Ile Ser Gly Ala Cys Gly Met

				180					185				190		
Phe	Arg	Thr	Asp	Val	Leu	Arg	Lys	Phe	Gly	Phe	Ser	Asp	Arg	Thr	Lys
		195					200					205			
Val	Glu	Asp	Leu	Asp	Leu	Thr	Trp	Thr	Leu	Val	Ala	Asn	Gly	Tyr	Arg
	210					215					220				
Ile	Arg	Gln	Ala	Asn	Arg	Cys	Ile	Val	Tyr	Pro	Gln	Glu	Cys	Asn	Ser
225					230					235					240
Pro	Arg	Glu	Glu	Trp	Arg	Arg	Trp	Arg	Arg	Trp	Ile	Val	Gly	Tyr	Ala
				245					250					255	
Val	Cys	Met	Arg	Leu	His	Lys	Arg	Leu	Leu	Phe	Ser	Arg	Phe	Gly	Ile
			260					265					270		
Phe	Ser	Ile	Phe	Pro	Met	Leu	Leu	Val	Val	Leu	Tyr	Gly	Val	Gly	Ile
		275					280					285			
Tyr	Leu	Thr	Thr	Trp	Phe	Asn	Glu	Phe	Ile	Thr	Thr	Gly	Pro	His	Gly
	290					295					300				
Val	Val	Leu	Ala	Met	Phe	Pro	Leu	Ile	Trp	Val	Gly	Val	Val	Cys	Val
305					310					315					320
Ile	Gly	Ala	Phe	Ser	Ala	Trp	Phe	His	Arg	Cys	Trp	Leu	Leu	Val	Pro
				325					330					335	
Leu	Ala	Pro	Leu	Ser	Val	Val	Tyr	Val	Leu	Leu	Ala	Tyr	Ala	Ile	Trp
			340					345					350		
Ile	Ile	Tyr	Gly	Leu	Ile	Ala	Phe	Phe	Thr	Gly	Arg	Glu	Pro	Gln	Arg
		355					360					365			
Asp	Lys	Pro	Thr	Arg	Tyr	Ser	Ala	Leu	Val	Glu	Ala	Ser	Thr	Ala	Tyr
	370					375					380				
Ser	Gln	Pro	Ser	Val	Thr	Gly	Thr	Glu	Lys	Leu	Ser	Glu	Ala		
385					390					395					

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<210> 431
<211> 552
<212> PRT
<213> Escherichia coli
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<400> 431															
Met	Ile	Leu	Glu	Arg	Val	Glu	Ile	Val	Gly	Phe	Arg	Gly	Ile	Asn	Arg
1				5					10					15	
Leu	Ser	Leu	Met	Leu	Glu	Gln	Asn	Asn	Val	Leu	Ile	Gly	Glu	Asn	Ala
			20					25					30		
Trp	Gly	Lys	Ser	Ser	Leu	Leu	Asp	Ala	Leu	Thr	Leu	Leu	Leu	Ser	Pro
		35					40					45			
Glu	Ser	Asp	Leu	Tyr	His	Phe	Glu	Arg	Asp	Asp	Phe	Trp	Phe	Pro	Pro
	50					55					60				
Gly	Asp	Ile	Asn	Gly	Arg	Glu	His	His	Leu	His	Ile	Ile	Leu	Thr	Phe
65					70					75					80
Arg	Glu	Ser	Leu	Pro	Gly	Arg	His	Arg	Val	Arg	Arg	Tyr	Arg	Pro	Leu
				85					90					95	
Glu	Ala	Cys	Trp	Thr	Pro	Cys	Thr	Asp	Gly	Tyr	His	Arg	Ile	Phe	Tyr
			100					105					110		
Arg	Leu	Glu	Gly	Glu	Ser	Ala	Glu	Asp	Gly	Ser	Val	Met	Thr	Leu	Arg
		115					120					125			
Ser	Phe	Leu	Asp	Lys	Asp	Gly	His	Pro	Ile	Asp	Val	Glu	Asp	Ile	Asn
	130					135					140				
Asp	Gln	Ala	Arg	His	Leu	Val	Arg	Leu	Met	Pro	Val	Leu	Arg	Leu	Arg
145					150					155					160
Asp	Ala	Arg	Phe	Met	Arg	Arg	Ile	Arg	Asn	Gly	Thr	Val	Pro	Asn	Val
				165					170					175	

His Tyr Gly Val Val Asp Tyr Leu Ile Lys Pro Phe Gln Ala Ser Arg
 100 105 110
 Phe Glu Glu Ala Leu Thr Gly Trp Arg Gln Lys Lys Met Ala Leu Glu
 115 120 125
 Lys His Gln Tyr Tyr Asp Gln Ala Glu Leu Asp Gln Leu Ile His Gly
 130 135 140
 Ser Ser Ser Asn Glu Gln Asp Pro Arg Arg Leu Pro Lys Gly Leu Thr
 145 150 155 160
 Pro Gln Thr Leu Arg Thr Leu Cys Gln Trp Ile Asp Ala His Gln Asp
 165 170 175
 Tyr Glu Phe Ser Thr Asp Glu Leu Ala Asn Glu Val Asn Ile Ser Arg
 180 185 190
 Val Ser Cys Arg Lys Tyr Leu Ile Trp Leu Val Asn Cys His Ile Leu
 195 200 205
 Phe Thr Ser Ile His Tyr Gly Val Thr Gly Arg Pro Val Tyr Arg Tyr
 210 215 220
 Arg Ile Gln Ala Glu His Tyr Ser Leu Leu Lys Gln Tyr Cys Gln
 225 230 235

<210> 439
 <211> 543
 <212> PRT
 <213> Escherichia coli

<400> 439
 Met Arg His Ser Leu Pro Tyr Arg Met Leu Arg Lys Arg Pro Met Lys
 1 5 10 15
 Leu Ser Thr Thr Val Ile Leu Met Val Ser Ala Val Leu Phe Ser Val
 20 25 30
 Leu Leu Val Val His Leu Ile Tyr Phe Ser Gln Ile Ser Asp Met Thr
 35 40 45
 Arg Asp Gly Leu Ala Asn Lys Ala Leu Ala Val Ala Arg Thr Leu Ala
 50 55 60
 Asp Ser Pro Glu Ile Arg Gln Gly Leu Gln Lys Lys Pro Gln Glu Ser
 65 70 75 80
 Gly Ile Gln Ala Ile Ala Glu Ala Val Arg Lys Arg Asn Asp Leu Leu
 85 90 95
 Phe Ile Val Val Thr Asp Met Gln Ser Leu Arg Tyr Ser His Pro Glu
 100 105 110
 Ala Gln Arg Ile Gly Gln Pro Phe Lys Gly Asp Asp Ile Leu Lys Ala
 115 120 125
 Leu Asn Gly Glu Glu Asn Val Ala Ile Asn Arg Gly Phe Leu Ala Gln
 130 135 140
 Ala Leu Arg Val Phe Thr Pro Ile Tyr Asp Glu Asn His Lys Gln Ile
 145 150 155 160
 Gly Val Val Ala Ile Gly Leu Glu Leu Ser Arg Val Thr Gln Gln Ile
 165 170 175
 Asn Asp Ser Arg Trp Ser Ile Ile Trp Ser Val Leu Phe Gly Met Leu
 180 185 190
 Val Gly Leu Ile Gly Thr Cys Ile Leu Val Lys Val Leu Lys Lys Ile
 195 200 205
 Leu Phe Gly Leu Glu Pro Tyr Glu Ile Ser Thr Leu Phe Glu Gln Arg
 210 215 220
 Gln Ala Met Leu Gln Ser Ile Lys Glu Gly Val Val Ala Val Asp Asp
 225 230 235 240
 Arg Gly Glu Val Thr Leu Ile Asn Asp Ala Ala Gln Glu Leu Leu Asn

				245					250					255			
Tyr	Arg	Lys	Ser	Gln	Asp	Asp	Glu	Lys	Leu	Ser	Thr	Leu	Ser	His	Ser		
			260					265					270				
Trp	Ser	Gln	Val	Val	Asp	Val	Ser	Glu	Val	Leu	Arg	Asp	Gly	Thr	Pro		
		275					280					285					
Arg	Arg	Asp	Glu	Glu	Ile	Thr	Ile	Lys	Asp	Arg	Leu	Leu	Leu	Ile	Asn		
	290					295					300						
Thr	Val	Pro	Val	Arg	Ser	Asn	Gly	Val	Ile	Ile	Gly	Ala	Ile	Ser	Thr		
305					310					315					320		
Phe	Arg	Asp	Lys	Thr	Glu	Val	Arg	Lys	Leu	Met	Gln	Arg	Leu	Asp	Gly		
			325					330						335			
Leu	Val	Asn	Tyr	Ala	Asp	Ala	Leu	Arg	Glu	Arg	Ser	His	Glu	Phe	Met		
		340					345						350				
Asn	Lys	Leu	His	Val	Ile	Leu	Gly	Leu	Leu	His	Leu	Lys	Ser	Tyr	Lys		
	355					360					365						
Gln	Leu	Glu	Asp	Tyr	Ile	Leu	Lys	Thr	Ala	Asn	Asn	Tyr	Gln	Glu	Glu		
	370					375					380						
Ile	Gly	Ser	Leu	Leu	Gly	Lys	Ile	Lys	Ser	Pro	Val	Ile	Ala	Gly	Phe		
385					390				395						400		
Leu	Ile	Ser	Lys	Ile	Asn	Arg	Ala	Thr	Asp	Leu	Gly	His	Thr	Leu	Ile		
			405					410						415			
Leu	Asn	Ser	Glu	Ser	Gln	Leu	Pro	Asp	Ser	Gly	Ser	Glu	Asp	Gln	Val		
		420					425						430				
Ala	Thr	Leu	Ile	Thr	Thr	Leu	Gly	Asn	Leu	Ile	Glu	Asn	Ala	Leu	Glu		
	435						440					445					
Ala	Leu	Gly	Pro	Glu	Pro	Gly	Gly	Glu	Ile	Ser	Val	Thr	Leu	His	Tyr		
	450					455					460						
Arg	His	Gly	Trp	Leu	His	Cys	Glu	Val	Asn	Asp	Asp	Gly	Pro	Gly	Ile		
465					470				475						480		
Ala	Pro	Asp	Lys	Ile	Asp	His	Ile	Phe	Asp	Lys	Gly	Val	Ser	Thr	Lys		
			485					490						495			
Gly	Ser	Glu	Arg	Gly	Val	Gly	Leu	Ala	Leu	Val	Lys	Gln	Gln	Val	Glu		
			500				505					510					
Asn	Leu	Gly	Gly	Ser	Ile	Ala	Val	Glu	Ser	Glu	Pro	Gly	Ile	Phe	Thr		
	515					520						525					
Gln	Phe	Phe	Val	Gln	Ile	Pro	Trp	Asp	Gly	Glu	Arg	Ser	Asn	Arg			
	530					535					540						

<210> 440

<211> 328

<212> PRT

<213> Escherichia coli

<400> 440

Met	Ser	Val	Pro	Leu	Ser	Thr	Trp	Asn	Leu	Leu	Arg	Tyr	Asn	Asn	Ser		
1				5				10					15				
Tyr	Leu	Gln	Lys	Val	Thr	Met	Phe	Pro	Gln	Cys	Lys	Phe	Ser	Arg	Glu		
		20					25					30					
Phe	Leu	His	Pro	Arg	Tyr	Trp	Leu	Thr	Trp	Phe	Gly	Leu	Gly	Val	Leu		
		35				40					45						
Trp	Leu	Trp	Val	Gln	Leu	Pro	Tyr	Pro	Val	Leu	Cys	Phe	Leu	Gly	Thr		
	50				55					60							
Arg	Ile	Gly	Ala	Met	Ala	Arg	Pro	Phe	Leu	Lys	Arg	Arg	Glu	Ser	Ile		
65				70				75					80				
Ala	Arg	Lys	Asn	Leu	Glu	Leu	Cys	Phe	Pro	Gln	His	Ser	Ala	Glu	Glu		
			85					90					95				

Arg Glu Lys Met Ile Ala Glu Asn Phe Arg Ser Leu Gly Met Ala Leu
 100 105 110
 Val Glu Thr Gly Met Ala Trp Phe Trp Pro Asp Ser Arg Val Arg Lys
 115 120 125
 Trp Phe Asp Val Glu Gly Leu Asp Asn Leu Lys Arg Ala Gln Met Gln
 130 135 140
 Asn Arg Gly Val Met Val Val Gly Val His Phe Met Ser Leu Glu Leu
 145 150 155 160
 Gly Gly Arg Val Met Gly Leu Cys Gln Pro Met Met Ala Thr Tyr Arg
 165 170 175
 Pro His Asn Asn Gln Leu Met Glu Trp Val Gln Thr Arg Gly Arg Met
 180 185 190
 Arg Ser Asn Lys Ala Met Ile Gly Arg Asn Asn Leu Arg Gly Ile Val
 195 200 205
 Gly Ala Leu Lys Lys Gly Glu Ala Val Trp Phe Ala Pro Asp Gln Asp
 210 215 220
 Tyr Gly Arg Lys Gly Ser Ser Phe Ala Pro Phe Phe Ala Val Glu Asn
 225 230 235 240
 Val Ala Thr Thr Asn Gly Thr Tyr Val Leu Ser Arg Leu Ser Gly Ala
 245 250 255
 Ala Met Leu Thr Val Thr Met Val Arg Lys Ala Asp Tyr Ser Gly Tyr
 260 265 270
 Arg Leu Phe Ile Thr Pro Glu Met Glu Gly Tyr Pro Thr Asp Glu Asn
 275 280 285
 Gln Ala Ala Tyr Met Asn Lys Ile Ile Glu Lys Glu Ile Met Arg
 290 295 300
 Ala Pro Glu Gln Tyr Leu Trp Ile His Arg Arg Phe Lys Thr Arg Pro
 305 310 315 320
 Val Gly Glu Ser Ser Leu Tyr Ile
 325

<210> 441
 <211> 87
 <212> PRT
 <213> Escherichia coli

<400> 441
 Met Ala Asn Ile Lys Ser Ala Lys Lys Arg Ala Ile Gln Ser Glu Lys
 1 5 10 15
 Ala Arg Lys His Asn Ala Ser Arg Arg Ser Met Met Arg Thr Phe Ile
 20 25 30
 Lys Lys Val Tyr Ala Ala Ile Glu Ala Gly Asp Lys Ala Ala Ala Gln
 35 40 45
 Lys Ala Phe Asn Glu Met Gln Pro Ile Val Asp Arg Gln Ala Ala Lys
 50 55 60
 Gly Leu Ile His Lys Asn Lys Ala Ala Arg His Lys Ala Asn Leu Thr
 65 70 75 80
 Ala Gln Ile Asn Lys Leu Ala
 85

<210> 442
 <211> 430
 <212> PRT
 <213> Escherichia coli

<210> 443
 <211> 883
 <212> PRT
 <213> Escherichia coli

<400> 443

Met	Asn	Glu	Gln	Tyr	Ser	Ala	Leu	Arg	Ser	Asn	Val	Ser	Met	Leu	Gly
1				5					10					15	
Lys	Val	Leu	Gly	Glu	Thr	Ile	Lys	Asp	Ala	Leu	Gly	Glu	His	Ile	Leu
		20						25					30		
Glu	Arg	Val	Glu	Thr	Ile	Arg	Lys	Leu	Ser	Lys	Ser	Ser	Arg	Ala	Gly
		35					40					45			
Asn	Asp	Ala	Asn	Arg	Gln	Glu	Leu	Leu	Thr	Thr	Leu	Gln	Asn	Leu	Ser
	50					55					60				
Asn	Asp	Glu	Leu	Leu	Pro	Val	Ala	Arg	Ala	Phe	Ser	Gln	Phe	Leu	Asn
65					70					75					80
Leu	Ala	Asn	Thr	Ala	Glu	Gln	Tyr	His	Ser	Ile	Ser	Pro	Lys	Gly	Glu
				85					90					95	
Ala	Ala	Ser	Asn	Pro	Glu	Val	Ile	Ala	Arg	Thr	Leu	Arg	Lys	Leu	Lys
			100					105					110		
Asn	Gln	Pro	Glu	Leu	Ser	Glu	Asp	Thr	Ile	Lys	Lys	Ala	Val	Glu	Ser
		115					120						125		
Leu	Ser	Leu	Glu	Leu	Val	Leu	Thr	Ala	His	Pro	Thr	Glu	Ile	Thr	Arg
	130					135					140				
Arg	Thr	Leu	Ile	His	Lys	Met	Val	Glu	Val	Asn	Ala	Cys	Leu	Lys	Gln
145					150					155					160
Leu	Asp	Asn	Lys	Asp	Ile	Ala	Asp	Tyr	Glu	His	Asn	Gln	Leu	Met	Arg
			165						170					175	
Arg	Leu	Arg	Gln	Leu	Ile	Ala	Gln	Ser	Trp	His	Thr	Asp	Glu	Ile	Arg
			180					185					190		
Lys	Leu	Arg	Pro	Ser	Pro	Val	Asp	Glu	Ala	Lys	Trp	Gly	Phe	Ala	Val
		195					200					205			
Val	Glu	Asn	Ser	Leu	Trp	Gln	Gly	Val	Pro	Asn	Tyr	Leu	Arg	Glu	Leu
	210					215					220				
Asn	Glu	Gln	Leu	Glu	Glu	Asn	Leu	Gly	Tyr	Lys	Leu	Pro	Val	Glu	Phe
225					230					235					240
Val	Pro	Val	Arg	Phe	Thr	Ser	Trp	Met	Gly	Gly	Asp	Arg	Asp	Gly	Asn
				245					250					255	
Pro	Asn	Val	Thr	Ala	Asp	Ile	Thr	Arg	His	Val	Leu	Leu	Leu	Ser	Arg
			260					265						270	
Trp	Lys	Ala	Thr	Asp	Leu	Phe	Leu	Lys	Asp	Ile	Gln	Val	Leu	Val	Ser
		275					280						285		
Glu	Leu	Ser	Met	Val	Glu	Ala	Thr	Pro	Glu	Leu	Leu	Ala	Leu	Val	Gly
	290					295					300				
Glu	Glu	Gly	Ala	Ala	Glu	Pro	Tyr	Arg	Tyr	Leu	Met	Lys	Asn	Leu	Arg
305					310					315					320
Ser	Arg	Leu	Met	Ala	Thr	Gln	Ala	Trp	Leu	Glu	Ala	Arg	Leu	Lys	Gly
				325					330					335	
Glu	Glu	Leu	Pro	Lys	Pro	Glu	Gly	Leu	Leu	Thr	Gln	Asn	Glu	Glu	Leu
			340					345					350		
Trp	Glu	Pro	Leu	Tyr	Ala	Cys	Tyr	Gln	Ser	Leu	Gln	Ala	Cys	Gly	Met
		355					360						365		
Gly	Ile	Ile	Ala	Asn	Gly	Asp	Leu	Leu	Asp	Thr	Leu	Arg	Arg	Val	Lys
	370					375					380				
Cys	Phe	Gly	Val	Pro	Leu	Val	Arg	Ile	Asp	Ile	Arg	Gln	Glu	Ser	Thr
385					390					395					400
Arg	His	Thr	Glu	Ala	Leu	Gly	Glu	Leu	Thr	Arg	Tyr	Leu	Gly	Ile	Gly

Ala Ser Glu Cys Gln Met Asp Gly Ala Gly Arg Leu Leu Ile Ala Pro
85 90 95
Val Leu Arg Gln His Ala Gly Leu Thr Lys Glu Val Met Leu Val Gly
100 105 110
Gln Phe Asn Lys Phe Glu Leu Trp Asp Glu Thr Thr Trp His Gln Gln
115 120 125
Val Lys Glu Asp Ile Asp Ala Glu Gln Leu Ala Thr Gly Asp Leu Ser
130 135 140
Glu Arg Leu Gln Asp Leu Ser Leu
145 150

<210> 446
<211> 313
<212> PRT
<213> Escherichia coli

<400> 446
Met Met Glu Asn Tyr Lys His Thr Thr Val Leu Leu Asp Glu Ala Val
1 5 10 15
Asn Gly Leu Asn Ile Arg Pro Asp Gly Ile Tyr Ile Asp Gly Thr Phe
20 25 30
Gly Arg Gly Gly His Ser Arg Leu Ile Leu Ser Gln Leu Gly Glu Glu
35 40 45
Gly Arg Leu Leu Ala Ile Asp Arg Asp Pro Gln Ala Ile Ala Val Ala
50 55 60
Lys Thr Ile Asp Asp Pro Arg Phe Ser Ile Ile His Gly Pro Phe Ser
65 70 75 80
Ala Leu Gly Glu Tyr Val Ala Glu Arg Asp Leu Ile Gly Lys Ile Asp
85 90 95
Gly Ile Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Leu Asp Asp Ala
100 105 110
Glu Arg Gly Phe Ser Phe Met Arg Asp Gly Pro Leu Asp Met Arg Met
115 120 125
Asp Pro Thr Arg Gly Gln Ser Ala Ala Glu Trp Leu Gln Thr Ala Glu
130 135 140
Glu Ala Asp Ile Ala Trp Val Leu Lys Thr Tyr Gly Glu Glu Arg Phe
145 150 155 160
Ala Lys Arg Ile Ala Arg Ala Ile Val Glu Arg Asn Arg Glu Gln Pro
165 170 175
Met Thr Arg Thr Lys Glu Leu Ala Glu Val Val Ala Ala Ala Thr Pro
180 185 190
Val Lys Asp Lys Phe Lys His Pro Ala Thr Arg Thr Phe Gln Ala Val
195 200 205
Arg Ile Trp Val Asn Ser Glu Leu Glu Glu Ile Glu Gln Ala Leu Lys
210 215 220
Ser Ser Leu Asn Val Leu Ala Pro Gly Gly Arg Leu Ser Ile Ile Ser
225 230 235 240
Phe His Ser Leu Glu Asp Arg Ile Val Lys Arg Phe Met Arg Glu Asn
245 250 255
Ser Arg Gly Pro Gln Val Pro Ala Gly Leu Pro Met Thr Glu Glu Gln
260 265 270
Leu Lys Lys Leu Gly Gly Arg Gln Leu Arg Ala Leu Gly Lys Leu Met
275 280 285
Pro Gly Glu Glu Glu Val Ala Glu Asn Pro Arg Ala Arg Ser Ser Val
290 295 300
Leu Arg Ile Ala Glu Arg Thr Asn Ala

305

310

<210> 447

<211> 121

<212> PRT

<213> Escherichia coli

<400> 447

Met Ile Ser Arg Val Thr Glu Ala Leu Ser Lys Val Lys Gly Ser Met
 1 5 10 15
 Gly Ser His Glu Arg His Ala Leu Pro Gly Val Ile Gly Asp Asp Leu
 20 25 30
 Leu Arg Phe Gly Lys Leu Pro Leu Cys Leu Phe Ile Cys Ile Ile Leu
 35 40 45
 Thr Ala Val Thr Val Val Thr Thr Ala His His Thr Arg Leu Leu Thr
 50 55 60
 Ala Gln Arg Glu Gln Leu Val Leu Glu Arg Asp Ala Leu Asp Ile Glu
 65 70 75 80
 Trp Arg Asn Leu Ile Leu Glu Glu Asn Ala Leu Gly Asp His Ser Arg
 85 90 95
 Val Glu Arg Ile Ala Thr Glu Lys Leu Gln Met Gln His Val Asp Pro
 100 105 110
 Ser Gln Glu Asn Ile Val Val Gln Lys
 115 120

<210> 448

<211> 588

<212> PRT

<213> Escherichia coli

<400> 448

Met Lys Ala Ala Lys Thr Gln Lys Pro Lys Arg Gln Glu Glu His
 1 5 10 15
 Ala Asn Phe Ile Ser Trp Arg Phe Ala Leu Leu Cys Gly Cys Ile Leu
 20 25 30
 Leu Ala Leu Ala Phe Leu Leu Gly Arg Val Ala Trp Leu Gln Val Ile
 35 40 45
 Ser Pro Asp Met Leu Val Lys Glu Gly Asp Met Arg Ser Leu Arg Val
 50 55 60
 Gln Gln Val Ser Thr Ser Arg Gly Met Ile Thr Asp Arg Ser Gly Arg
 65 70 75 80
 Pro Leu Ala Val Ser Val Pro Val Lys Ala Ile Trp Ala Asp Pro Lys
 85 90 95
 Glu Val His Asp Ala Gly Gly Ile Ser Val Gly Asp Arg Trp Lys Ala
 100 105 110
 Leu Ala Asn Ala Leu Asn Ile Pro Leu Asp Gln Leu Ser Ala Arg Ile
 115 120 125
 Asn Ala Asn Pro Lys Gly Arg Phe Ile Tyr Leu Ala Arg Gln Val Asn
 130 135 140
 Pro Asp Met Ala Asp Tyr Ile Lys Lys Leu Lys Leu Pro Gly Ile His
 145 150 155 160
 Leu Arg Glu Glu Ser Arg Arg Tyr Tyr Pro Ser Gly Glu Val Thr Ala
 165 170 175
 His Leu Ile Gly Phe Thr Asn Val Asp Ser Gln Gly Ile Glu Gly Val
 180 185 190

<400> 449

Met	Ala	Asp	Arg	Asn	Leu	Arg	Asp	Leu	Leu	Ala	Pro	Trp	Val	Pro	Asp
1				5					10					15	
Ala	Pro	Ser	Arg	Ala	Leu	Arg	Glu	Met	Thr	Leu	Asp	Ser	Arg	Val	Ala
		20					25					30			
Ala	Ala	Gly	Asp	Leu	Phe	Val	Ala	Val	Val	Gly	His	Gln	Ala	Asp	Gly
		35					40					45			
Arg	Arg	Tyr	Ile	Pro	Gln	Ala	Ile	Ala	Gln	Gly	Val	Ala	Ala	Ile	Ile
	50				55						60				
Ala	Glu	Ala	Lys	Asp	Glu	Ala	Thr	Asp	Gly	Glu	Ile	Arg	Glu	Met	His
65					70					75					80
Gly	Val	Pro	Val	Ile	Tyr	Leu	Ser	Gln	Leu	Asn	Glu	Arg	Leu	Ser	Ala
				85					90					95	
Leu	Ala	Gly	Arg	Phe	Tyr	His	Glu	Pro	Ser	Asp	Asn	Leu	Arg	Leu	Val
			100					105					110		
Gly	Val	Thr	Gly	Thr	Asn	Gly	Lys	Thr	Thr	Thr	Thr	Gln	Leu	Leu	Ala
		115					120					125			
Gln	Trp	Ser	Gln	Leu	Leu	Gly	Glu	Ile	Ser	Ala	Val	Met	Gly	Thr	Val
	130					135						140			
Gly	Asn	Gly	Leu	Leu	Gly	Lys	Val	Ile	Pro	Thr	Glu	Asn	Thr	Thr	Gly
145					150					155					160
Ser	Ala	Val	Asp	Val	Gln	His	Glu	Leu	Ala	Gly	Leu	Val	Asp	Gln	Gly
			165						170					175	
Ala	Thr	Phe	Cys	Ala	Met	Glu	Val	Ser	Ser	His	Gly	Leu	Val	Gln	His
			180					185					190		
Arg	Val	Ala	Ala	Leu	Lys	Phe	Ala	Ala	Ser	Val	Phe	Thr	Asn	Leu	Ser
		195					200					205			
Arg	Asp	His	Leu	Asp	Tyr	His	Gly	Asp	Met	Glu	His	Tyr	Glu	Ala	Ala
	210				215						220				
Lys	Trp	Leu	Leu	Tyr	Ser	Glu	His	His	Cys	Gly	Gln	Ala	Ile	Ile	Asn
225					230					235					240
Ala	Asp	Asp	Glu	Val	Gly	Arg	Arg	Trp	Leu	Ala	Lys	Leu	Pro	Asp	Ala
			245						250					255	
Val	Ala	Val	Ser	Met	Glu	Asp	His	Ile	Asn	Pro	Asn	Cys	His	Gly	Arg
			260					265				270			
Trp	Leu	Lys	Ala	Thr	Glu	Val	Asn	Tyr	His	Asp	Ser	Gly	Ala	Thr	Ile
	275						280					285			
Arg	Phe	Ser	Ser	Ser	Trp	Gly	Asp	Gly	Glu	Ile	Glu	Ser	His	Leu	Met
	290					295					300				
Gly	Ala	Phe	Asn	Val	Ser	Asn	Leu	Leu	Leu	Ala	Leu	Ala	Thr	Leu	Leu
305					310					315					320
Ala	Leu	Gly	Tyr	Pro	Leu	Ala	Asp	Leu	Leu	Lys	Thr	Ala	Ala	Arg	Leu
			325						330					335	
Gln	Pro	Val	Cys	Gly	Arg	Met	Glu	Val	Phe	Thr	Ala	Pro	Gly	Lys	Pro
			340					345					350		
Thr	Val	Val	Val	Asp	Tyr	Ala	His	Thr	Pro	Asp	Ala	Leu	Glu	Lys	Ala
	355						360					365			
Leu	Gln	Ala	Ala	Arg	Leu	His	Cys	Ala	Gly	Lys	Leu	Trp	Cys	Val	Phe
	370					375					380				
Gly	Cys	Gly	Gly	Asp	Arg	Asp	Lys	Gly	Lys	Arg	Pro	Leu	Met	Gly	Ala
385					390					395					400
Ile	Ala	Glu	Glu	Phe	Ala	Asp	Val	Ala	Val	Val	Thr	Asp	Asp	Asn	Pro
				405					410					415	
Arg	Thr	Glu	Glu	Pro	Arg	Ala	Ile	Ile	Asn	Asp	Ile	Leu	Ala	Gly	Met
		420					425					430			
Leu	Asp	Ala	Gly	His	Ala	Lys	Val	Met	Glu	Gly	Arg	Ala	Glu	Ala	Val
	435						440					445			

Thr Cys Ala Val Met Gln Ala Lys Glu Asn Asp Val Val Leu Val Ala
 450 455 460
 Gly Lys Gly His Glu Asp Tyr Gln Ile Val Gly Asn Gln Arg Leu Asp
 465 470 475 480
 Tyr Ser Asp Arg Val Thr Val Ala Arg Leu Leu Gly Val Ile Ala
 485 490 495

<210> 450
 <211> 452
 <212> PRT
 <213> Escherichia coli

<400> 450
 Met Ile Ser Val Thr Leu Ser Gln Leu Thr Asp Ile Leu Asn Gly Glu
 1 5 10 15
 Leu Gln Gly Ala Asp Ile Thr Leu Asp Ala Val Thr Thr Asp Thr Arg
 20 25 30
 Lys Leu Thr Pro Gly Cys Leu Phe Val Ala Leu Lys Gly Glu Arg Phe
 35 40 45
 Asp Ala His Asp Phe Ala Asp Gln Ala Lys Ala Gly Gly Ala Gly Ala
 50 55 60
 Leu Leu Val Ser Arg Pro Leu Asp Ile Asp Leu Pro Gln Leu Ile Val
 65 70 75 80
 Lys Asp Thr Arg Leu Ala Phe Gly Glu Leu Ala Ala Trp Val Arg Gln
 85 90 95
 Gln Val Pro Ala Arg Val Val Ala Leu Thr Gly Ser Ser Gly Lys Thr
 100 105 110
 Ser Val Lys Glu Met Thr Ala Ala Ile Leu Ser Gln Cys Gly Asn Thr
 115 120 125
 Leu Tyr Thr Ala Gly Asn Leu Asn Asn Asp Ile Gly Val Pro Met Thr
 130 135 140
 Leu Leu Arg Leu Thr Pro Glu Tyr Asp Tyr Ala Val Ile Glu Leu Gly
 145 150 155 160
 Ala Asn His Gln Gly Glu Ile Ala Trp Thr Val Ser Leu Thr Arg Pro
 165 170 175
 Glu Ala Ala Leu Val Asn Asn Leu Ala Ala Ala His Leu Glu Gly Phe
 180 185 190
 Gly Ser Leu Ala Gly Val Ala Lys Ala Lys Gly Glu Ile Phe Ser Gly
 195 200 205
 Leu Pro Glu Asn Gly Ile Ala Ile Met Asn Ala Asp Asn Asn Asp Trp
 210 215 220
 Leu Asn Trp Gln Ser Val Ile Gly Ser Arg Lys Val Trp Arg Phe Ser
 225 230 235 240
 Pro Asn Ala Ala Asn Ser Asp Phe Thr Ala Thr Asn Ile His Val Thr
 245 250 255
 Ser His Gly Thr Glu Phe Thr Leu Gln Thr Pro Thr Gly Ser Val Asp
 260 265 270
 Val Leu Leu Pro Leu Pro Gly Arg His Asn Ile Ala Asn Ala Leu Ala
 275 280 285
 Ala Ala Ala Leu Ser Met Ser Val Gly Ala Thr Leu Asp Ala Ile Lys
 290 295 300
 Ala Gly Leu Ala Asn Leu Lys Ala Val Pro Gly Arg Leu Phe Pro Ile
 305 310 315 320
 Gln Leu Ala Glu Asn Gln Leu Leu Leu Asp Asp Ser Tyr Asn Ala Asn
 325 330 335
 Val Gly Ser Met Thr Ala Ala Val Gln Val Leu Ala Glu Met Pro Gly

340 345 350
 Tyr Arg Val Leu Val Val Gly Asp Met Ala Glu Leu Gly Ala Glu Ser
 355 360 365
 Glu Ala Cys His Val Gln Val Gly Glu Ala Ala Lys Ala Ala Gly Ile
 370 375 380
 Asp Arg Val Leu Ser Val Gly Lys Gln Ser His Ala Ile Ser Thr Ala
 385 390 395 400
 Ser Gly Val Gly Glu His Phe Ala Asp Lys Thr Ala Leu Ile Thr Arg
 405 410 415
 Leu Lys Leu Leu Ile Ala Glu Gln Gln Val Ile Thr Ile Leu Val Lys
 420 425 430
 Gly Ser Arg Ser Ala Ala Met Glu Glu Val Val Arg Ala Leu Gln Glu
 435 440 445
 Asn Gly Thr Cys
 450

<210> 451
 <211> 360
 <212> PRT
 <213> Escherichia coli

<400> 451
 Met Leu Val Trp Leu Ala Glu His Leu Val Lys Tyr Tyr Ser Gly Phe
 1 5 10 15
 Asn Val Phe Ser Tyr Leu Thr Phe Arg Ala Ile Val Ser Leu Leu Thr
 20 25 30
 Ala Leu Phe Ile Ser Leu Trp Met Gly Pro Arg Met Ile Ala His Leu
 35 40 45
 Gln Lys Leu Ser Phe Gly Gln Val Val Arg Asn Asp Gly Pro Glu Ser
 50 55 60
 His Phe Ser Lys Arg Gly Thr Pro Thr Met Gly Gly Ile Met Ile Leu
 65 70 75 80
 Thr Ala Ile Val Ile Ser Val Leu Leu Trp Ala Tyr Pro Ser Asn Pro
 85 90 95
 Tyr Val Trp Cys Val Leu Val Val Leu Val Gly Tyr Gly Val Ile Gly
 100 105 110
 Phe Val Asp Asp Tyr Arg Lys Val Val Arg Lys Asp Thr Lys Gly Leu
 115 120 125
 Ile Ala Arg Trp Lys Tyr Phe Trp Met Ser Val Ile Ala Leu Gly Val
 130 135 140
 Ala Phe Ala Leu Tyr Leu Ala Gly Lys Asp Thr Pro Ala Thr Gln Leu
 145 150 155 160
 Val Val Pro Phe Phe Lys Asp Val Met Pro Gln Leu Gly Leu Phe Tyr
 165 170 175
 Ile Leu Leu Ala Tyr Phe Val Ile Val Gly Thr Gly Asn Ala Val Asn
 180 185 190
 Leu Thr Asp Gly Leu Asp Gly Leu Ala Ile Met Pro Thr Val Phe Val
 195 200 205
 Ala Gly Gly Phe Ala Leu Val Ala Trp Ala Thr Gly Asn Met Asn Phe
 210 215 220
 Ala Ser Tyr Leu His Ile Pro Tyr Leu Arg His Ala Gly Glu Leu Val
 225 230 235 240
 Ile Val Cys Thr Ala Ile Val Gly Ala Gly Leu Gly Phe Leu Trp Phe
 245 250 255
 Asn Thr Tyr Pro Ala Gln Val Phe Met Gly Asp Val Gly Ser Leu Ala
 260 265 270

Leu Gly Gly Ala Leu Gly Ile Ile Ala Val Leu Leu Arg Gln Glu Phe
 275 280 285
 Leu Leu Val Ile Met Gly Gly Val Phe Val Val Glu Thr Leu Ser Val
 290 295 300
 Ile Leu Gln Val Gly Ser Phe Lys Leu Arg Gly Gln Arg Ile Phe Arg
 305 310 315 320
 Met Ala Pro Ile His His Tyr Glu Leu Lys Gly Trp Pro Glu Pro
 325 330 335
 Arg Val Ile Val Arg Phe Trp Ile Ile Ser Leu Met Leu Val Leu Ile
 340 345 350
 Gly Leu Ala Thr Leu Lys Val Arg
 355 360

<210> 452

<211> 438

<212> PRT

<213> Escherichia coli

<400> 452

Met Ala Asp Tyr Gln Gly Lys Asn Val Val Ile Ile Gly Leu Gly Leu
 1 5 10 15
 Thr Gly Leu Ser Cys Val Asp Phe Phe Leu Ala Arg Gly Val Thr Pro
 20 25 30
 Arg Val Met Asp Thr Arg Met Thr Pro Pro Gly Leu Asp Lys Leu Pro
 35 40 45
 Glu Ala Val Glu Arg His Thr Gly Ser Leu Asn Asp Glu Trp Leu Met
 50 55 60
 Ala Ala Asp Leu Ile Val Ala Ser Pro Gly Ile Ala Leu Ala His Pro
 65 70 75 80
 Ser Leu Ser Ala Ala Ala Asp Ala Gly Ile Glu Ile Val Gly Asp Ile
 85 90 95
 Glu Leu Phe Cys Arg Glu Ala Gln Ala Pro Ile Val Ala Ile Thr Gly
 100 105 110
 Ser Asn Gly Lys Ser Thr Val Thr Thr Leu Val Gly Glu Met Ala Lys
 115 120 125
 Ala Ala Gly Val Asn Val Gly Val Gly Gly Asn Ile Gly Leu Pro Ala
 130 135 140
 Leu Met Leu Leu Asp Asp Glu Cys Glu Leu Tyr Val Leu Glu Leu Ser
 145 150 155 160
 Ser Phe Gln Leu Glu Thr Thr Ser Ser Leu Gln Ala Val Ala Ala Thr
 165 170 175
 Ile Leu Asn Val Thr Glu Asp His Met Asp Arg Tyr Pro Phe Gly Leu
 180 185 190
 Gln Gln Tyr Arg Ala Ala Lys Leu Arg Ile Tyr Glu Asn Ala Lys Val
 195 200 205
 Cys Val Val Asn Ala Asp Asp Ala Leu Thr Met Pro Ile Arg Gly Ala
 210 215 220
 Asp Glu Arg Cys Val Ser Phe Gly Val Asn Met Gly Asp Tyr His Leu
 225 230 235 240
 Asn His Gln Gln Gly Glu Thr Trp Leu Arg Val Lys Gly Glu Lys Val
 245 250 255
 Leu Asn Val Lys Glu Met Lys Leu Ser Gly Gln His Asn Tyr Thr Asn
 260 265 270
 Ala Leu Ala Ala Leu Ala Leu Ala Asp Ala Ala Gly Leu Pro Arg Ala
 275 280 285
 Ser Ser Leu Lys Ala Leu Thr Thr Phe Thr Gly Leu Pro His Arg Phe

290		295		300
Glu Val Val Leu Glu His Asn Gly Val Arg Trp Ile Asn Asp Ser Lys				
305		310		320
Ala Thr Asn Val Gly Ser Thr Glu Ala Ala Leu Asn Gly Leu His Val				
	325		330	335
Asp Gly Thr Leu His Leu Leu Leu Gly Asp Gly Lys Ser Ala Asp				
	340		345	350
Phe Ser Pro Leu Ala Arg Tyr Leu Asn Gly Asp Asn Val Arg Leu Tyr				
	355		360	365
Cys Phe Gly Arg Asp Gly Ala Gln Leu Ala Ala Leu Arg Pro Glu Val				
	370		375	380
Ala Glu Gln Thr Glu Thr Met Glu Gln Ala Met Arg Leu Leu Ala Pro				
385		390		400
Arg Val Gln Pro Gly Asp Met Val Leu Leu Ser Pro Ala Cys Ala Ser				
	405		410	415
Leu Asp Gln Phe Lys Asn Phe Glu Gln Arg Gly Asn Glu Phe Ala Arg				
	420		425	430
Leu Ala Lys Glu Leu Gly				
	435			

<210> 453
 <211> 414
 <212> PRT
 <213> Escherichia coli

<400> 453
Met Arg Leu Ser Leu Pro Arg Leu Lys Met Pro Arg Leu Pro Gly Phe
1 5 10 15
Ser Ile Leu Val Trp Ile Ser Thr Ala Leu Lys Gly Trp Val Met Gly
20 25 30
Ser Arg Glu Lys Asp Thr Asp Ser Leu Ile Met Tyr Asp Arg Thr Leu
35 40 45
Leu Trp Leu Thr Phe Gly Leu Ala Ala Ile Gly Phe Ile Met Val Thr
50 55 60
Ser Ala Ser Met Pro Ile Gly Gln Arg Leu Thr Asn Asp Pro Phe Phe
65 70 75 80
Phe Ala Lys Arg Asp Gly Val Tyr Leu Ile Leu Ala Phe Ile Leu Ala
85 90 95
Ile Ile Thr Leu Arg Leu Pro Met Glu Phe Trp Gln Arg Tyr Ser Ala
100 105 110
Thr Met Leu Leu Gly Ser Ile Ile Leu Leu Met Ile Val Leu Val Val
115 120 125
Gly Ser Ser Val Lys Gly Ala Ser Arg Trp Ile Asp Leu Gly Leu Leu
130 135 140
Arg Ile Gln Pro Ala Glu Leu Thr Lys Leu Ser Leu Phe Cys Tyr Ile
145 150 155 160
Ala Asn Tyr Leu Val Arg Lys Gly Asp Glu Val Arg Asn Asn Leu Arg
165 170 175
Gly Phe Leu Lys Pro Met Gly Val Ile Leu Val Leu Ala Val Leu Leu
180 185 190
Leu Ala Gln Pro Asp Leu Gly Thr Val Val Val Leu Phe Val Thr Thr
195 200 205
Leu Ala Met Leu Phe Leu Ala Gly Ala Lys Leu Trp Gln Phe Ile Ala
210 215 220
Ile Ile Gly Met Gly Ile Ser Ala Val Val Leu Leu Ile Leu Ala Glu
225 230 235 240

210	215	220
Ser Val Glu Gln Ala Tyr Ala Glu Ala Gly Gln Pro Gln His Lys Val		
225	230	235
Thr Glu Phe Ile Asp Asp Met Ala Ala Ala Tyr Ala Trp Ala Asp Val		240
	245	250
Val Val Cys Arg Ser Gly Ala Leu Thr Val Ser Glu Ile Ala Ala Ala		255
	260	265
Gly Leu Pro Ala Leu Phe Val Pro Phe Gln His Lys Asp Arg Gln Gln		270
	275	280
Tyr Trp Asn Ala Leu Pro Leu Glu Lys Ala Gly Ala Ala Lys Ile Ile		285
	290	295
Glu Gln Pro Gln Leu Ser Val Asp Ala Val Ala Asn Thr Leu Ala Gly		300
305	310	315
Trp Ser Arg Glu Thr Leu Leu Thr Met Ala Glu Arg Ala Arg Ala Ala		320
	325	330
Ser Ile Pro Asp Ala Thr Glu Arg Val Ala Asn Glu Val Ser Arg Val		335
	340	345
Ala Arg Ala		350
355		

<210> 455
 <211> 491
 <212> PRT
 <213> Escherichia coli

<400> 455

Met Asn Thr Gln Gln Leu Ala Lys Leu Arg Ser Ile Val Pro Glu Met	
1	5
Arg Arg Val Arg His Ile His Phe Val Gly Ile Gly Gly Ala Gly Met	10
	15
	20
Gly Gly Ile Ala Glu Val Leu Ala Asn Glu Gly Tyr Gln Ile Ser Gly	25
	30
	35
Ser Asp Leu Ala Pro Asn Pro Val Thr Gln Gln Leu Met Asn Leu Gly	40
	45
	50
Ala Thr Ile Tyr Phe Asn His Arg Pro Glu Asn Val Arg Asp Ala Ser	55
65	60
	65
Val Val Val Val Ser Ser Ala Ile Ser Ala Asp Asn Pro Glu Ile Val	70
	75
	80
	85
Ala Ala His Glu Ala Arg Ile Pro Val Ile Arg Arg Ala Glu Met Leu	90
	95
	100
Ala Glu Leu Met Arg Phe Arg His Gly Ile Ala Ile Ala Gly Thr His	105
	110
	115
Gly Lys Thr Thr Thr Thr Ala Met Val Ser Ser Ile Tyr Ala Glu Ala	120
	125
	130
Gly Leu Asp Pro Thr Phe Val Asn Gly Gly Leu Val Lys Ala Ala Gly	135
145	140
	145
Val His Ala Arg Leu Gly His Gly Arg Tyr Leu Ile Ala Glu Ala Asp	150
	155
	160
	165
Glu Ser Asp Ala Ser Phe Leu His Leu Gln Pro Met Val Ala Ile Val	170
	175
	180
Thr Asn Ile Glu Ala Asp His Met Asp Thr Tyr Gln Gly Asp Phe Glu	185
	190
	195
Asn Leu Lys Gln Thr Phe Ile Asn Phe Leu His Asn Leu Pro Phe Tyr	200
	205
	210
Gly Arg Ala Val Met Cys Val Asp Asp Pro Val Ile Arg Glu Leu Leu	215
225	220
	225
	230
	235
	240

<210> 458
 <211> 475
 <212> PRT
 <213> Escherichia coli

<400> 458

Met	Asn	Thr	Ala	Leu	Ala	Gln	Gln	Ile	Ala	Asn	Glu	Gly	Gly	Val	Glu
1				5					10					15	
Ala	Trp	Met	Ile	Ala	Gln	Gln	His	Lys	Ser	Leu	Leu	Arg	Phe	Leu	Thr
		20						25					30		
Cys	Gly	Ser	Val	Asp	Asp	Gly	Lys	Ser	Thr	Leu	Ile	Gly	Arg	Leu	Leu
		35					40					45			
His	Asp	Thr	Arg	Gln	Ile	Tyr	Glu	Asp	Gln	Leu	Ser	Ser	Leu	His	Asn
	50					55					60				
Asp	Ser	Lys	Arg	His	Gly	Thr	Gln	Gly	Glu	Lys	Leu	Asp	Leu	Ala	Leu
65					70					75					80
Leu	Val	Asp	Gly	Leu	Gln	Ala	Glu	Arg	Glu	Gln	Gly	Ile	Thr	Ile	Asp
			85						90					95	
Val	Ala	Tyr	Arg	Tyr	Phe	Ser	Thr	Glu	Lys	Arg	Lys	Phe	Ile	Ile	Ala
		100						105					110		
Asp	Thr	Pro	Gly	His	Glu	Gln	Tyr	Thr	Arg	Asn	Met	Ala	Thr	Gly	Ala
	115						120					125			
Ser	Thr	Cys	Glu	Leu	Ala	Ile	Leu	Leu	Ile	Asp	Ala	Arg	Lys	Gly	Val
	130					135					140				
Leu	Asp	Gln	Thr	Arg	Arg	His	Ser	Phe	Ile	Ser	Thr	Leu	Leu	Gly	Ile
145					150					155					160
Lys	His	Leu	Val	Val	Ala	Ile	Asn	Lys	Met	Asp	Leu	Val	Asp	Tyr	Ser
			165						170					175	
Glu	Glu	Thr	Phe	Thr	Arg	Ile	Arg	Glu	Asp	Tyr	Leu	Thr	Phe	Ala	Gly
			180					185					190		
Gln	Leu	Pro	Gly	Asn	Leu	Asp	Ile	Arg	Phe	Val	Pro	Leu	Ser	Ala	Leu
	195					200						205			
Glu	Gly	Asp	Asn	Val	Ala	Ser	Gln	Ser	Glu	Ser	Met	Pro	Trp	Tyr	Ser
	210				215						220				
Gly	Pro	Thr	Leu	Leu	Glu	Val	Leu	Glu	Thr	Val	Glu	Ile	Gln	Arg	Val
225					230					235					240
Val	Asp	Ala	Gln	Pro	Met	Arg	Phe	Pro	Val	Gln	Tyr	Val	Asn	Arg	Pro
			245						250					255	
Asn	Leu	Asp	Phe	Arg	Gly	Tyr	Ala	Gly	Thr	Leu	Ala	Ser	Gly	Arg	Val
		260						265					270		
Glu	Val	Gly	Gln	Arg	Val	Lys	Val	Leu	Pro	Ser	Gly	Val	Glu	Ser	Asn
	275					280						285			
Val	Ala	Arg	Ile	Val	Thr	Phe	Asp	Gly	Asp	Arg	Glu	Glu	Ala	Phe	Ala
	290					295					300				
Gly	Glu	Ala	Ile	Thr	Leu	Val	Leu	Thr	Asp	Glu	Ile	Asp	Ile	Ser	Arg
305					310					315					320
Gly	Asp	Leu	Leu	Leu	Ala	Ala	Asp	Glu	Ala	Leu	Pro	Ala	Val	Gln	Ser
			325						330					335	
Ala	Ser	Val	Asp	Val	Val	Trp	Met	Ala	Glu	Gln	Pro	Leu	Ser	Pro	Gly
			340					345					350		
Gln	Ser	Tyr	Asp	Ile	Lys	Ile	Ala	Gly	Lys	Lys	Thr	Arg	Ala	Arg	Val
	355					360						365			
Asp	Gly	Ile	Arg	Tyr	Gln	Val	Asp	Ile	Asn	Asn	Leu	Thr	Gln	Arg	Glu
	370					375					380				
Val	Glu	Asn	Leu	Pro	Leu	Asn	Gly	Ile	Gly	Leu	Val	Asp	Leu	Thr	Phe

385		390		395		400									
Asp	Glu	Pro	Leu	Val	Leu	Asp	Arg	Tyr	Gln	Gln	Asn	Pro	Val	Thr	Gly
		405		410		415									
Gly	Leu	Ile	Phe	Ile	Asp	Arg	Leu	Ser	Asn	Val	Thr	Val	Gly	Ala	Gly
		420		425		430									
Met	Val	His	Glu	Pro	Val	Ser	Gln	Ala	Thr	Ala	Ala	Pro	Ser	Glu	Phe
		435		440		445									
Ser	Ala	Phe	Glu	Leu	Glu	Leu	Asn	Ala	Leu	Val	Arg	Arg	His	Phe	Pro
		450		455		460									
His	Trp	Gly	Ala	Arg	Asp	Leu	Leu	Gly	Asp	Lys					
465				470		475									

<210> 459
 <211> 127
 <212> PRT
 <213> Escherichia coli

<400> 459
Met Arg His Arg Lys Ser Gly Arg Gln Leu Asn Arg Asn Ser Ser His
1 5 10 15
Arg Gln Ala Met Phe Arg Asn Met Ala Gly Ser Leu Val Arg His Glu
20 25 30
Ile Ile Lys Thr Thr Leu Pro Lys Ala Lys Glu Leu Arg Arg Val Val
35 40 45
Glu Pro Leu Ile Thr Leu Ala Lys Thr Asp Ser Val Ala Asn Arg Arg
50 55 60
Leu Ala Phe Ala Arg Thr Arg Asp Asn Glu Ile Val Ala Lys Leu Phe
65 70 75 80
Asn Glu Leu Gly Pro Arg Phe Ala Ser Arg Ala Gly Gly Tyr Thr Arg
85 90 95
Ile Leu Lys Cys Gly Phe Arg Ala Gly Asp Asn Ala Pro Met Ala Tyr
100 105 110
Ile Glu Leu Val Asp Arg Ser Glu Lys Ala Glu Ala Ala Glu
115 120 125

<210> 460
 <211> 329
 <212> PRT
 <213> Escherichia coli

<400> 460
Met Gln Gly Ser Val Thr Glu Phe Leu Lys Pro Arg Leu Val Asp Ile
1 5 10 15
Glu Gln Val Ser Ser Thr His Ala Lys Val Thr Leu Glu Pro Leu Glu
20 25 30
Arg Gly Phe Gly His Thr Leu Gly Asn Ala Leu Arg Arg Ile Leu Leu
35 40 45
Ser Ser Met Pro Gly Cys Ala Val Thr Glu Val Glu Ile Asp Gly Val
50 55 60
Leu His Glu Tyr Ser Thr Lys Glu Gly Val Gln Glu Asp Ile Leu Glu
65 70 75 80
Ile Leu Leu Asn Leu Lys Gly Leu Ala Val Arg Val Gln Gly Lys Asp
85 90 95
Glu Val Ile Leu Thr Leu Asn Lys Ser Gly Ile Gly Pro Val Thr Ala
100 105 110

				165						170					175
Lys	Met	Glu	Gly	Thr	Phe	Lys	Arg	Lys	Pro	Glu	Arg	Ser	Asp	Leu	Ser
			180					185					190		
Ala	Asp	Ile	Asn	Glu	His	Leu	Ile	Val	Glu	Leu	Tyr	Ser	Lys		
		195					200					205			

<210> 462
 <211> 129
 <212> PRT
 <213> Escherichia coli

<400> 462

Met	Ala	Lys	Ala	Pro	Ile	Arg	Ala	Arg	Lys	Arg	Val	Arg	Lys	Gln	Val
1				5					10					15	
Ser	Asp	Gly	Val	Ala	His	Ile	His	Ala	Ser	Phe	Asn	Asn	Thr	Ile	Val
			20					25					30		
Thr	Ile	Thr	Asp	Arg	Gln	Gly	Asn	Ala	Leu	Gly	Trp	Ala	Thr	Ala	Gly
		35					40					45			
Gly	Ser	Gly	Phe	Arg	Gly	Ser	Arg	Lys	Ser	Thr	Pro	Phe	Ala	Ala	Gln
		50				55					60				
Val	Ala	Ala	Glu	Arg	Cys	Ala	Asp	Ala	Val	Lys	Glu	Tyr	Gly	Ile	Lys
65					70					75					80
Asn	Leu	Glu	Val	Met	Val	Lys	Gly	Pro	Gly	Pro	Gly	Arg	Glu	Ser	Thr
			85						90					95	
Ile	Arg	Ala	Leu	Asn	Ala	Ala	Gly	Phe	Arg	Ile	Thr	Asn	Ile	Thr	Asp
			100					105						110	
Val	Thr	Pro	Ile	Pro	His	Asn	Gly	Cys	Arg	Pro	Pro	Lys	Lys	Arg	Arg
		115					120					125			

Val

<210> 463
 <211> 118
 <212> PRT
 <213> Escherichia coli

<400> 463

Met	Ala	Arg	Ile	Ala	Gly	Ile	Asn	Ile	Pro	Asp	His	Lys	His	Ala	Val
1				5					10					15	
Ile	Ala	Leu	Thr	Ser	Ile	Tyr	Gly	Val	Gly	Lys	Thr	Arg	Ser	Lys	Ala
			20					25					30		
Ile	Leu	Ala	Ala	Ala	Gly	Ile	Ala	Glu	Asp	Val	Lys	Ile	Ser	Glu	Leu
		35					40					45			
Ser	Glu	Gly	Gln	Ile	Asp	Thr	Leu	Arg	Asp	Glu	Val	Ala	Lys	Phe	Val
		50				55					60				
Val	Glu	Gly	Asp	Leu	Arg	Arg	Glu	Ile	Ser	Met	Ser	Ile	Lys	Arg	Leu
65					70					75					80
Met	Asp	Leu	Gly	Cys	Tyr	Arg	Gly	Leu	Arg	His	Arg	Arg	Gly	Leu	Pro
				85					90					95	
Val	Arg	Gly	Gln	Arg	Thr	Lys	Thr	Asn	Ala	Arg	Thr	Arg	Lys	Gly	Pro
			100					105					110		

Arg Lys Pro Ile Lys Lys
 115

[illegible]

503

				405					410				415				
Ala	Gly	Met	Phe	Ile	Met	Leu	Ser	Leu	Tyr	Lys	Leu	Thr	Asp	Ala	Arg		
			420					425					430				
Val	Glu	Ala	Ile	Ser	Arg	Gln	Leu	Ile	Lys	His	Arg	Ala	Ala	Gln	Gly		
		435				440						445					
Glu	Ala	Val	Pro	Asp	Ala	Ala	Thr	Ala	Ala	Ser	His						
	450					455					460						

<210> 465
 <211> 536
 <212> PRT
 <213> Escherichia coli

<400> 465

Met	Glu	Ile	Thr	Asn	Pro	Ile	Leu	Thr	Gly	Phe	Asn	Pro	Asp	Pro	Ser		
1				5					10					15			
Leu	Cys	Arg	Gln	Gly	Glu	Asp	Tyr	Tyr	Ile	Ala	Thr	Ser	Thr	Phe	Glu		
			20					25					30				
Trp	Phe	Pro	Gly	Val	Arg	Ile	Tyr	His	Ser	Arg	Asp	Leu	Lys	Asn	Trp		
		35				40						45					
Ser	Leu	Val	Ser	Thr	Pro	Leu	Asp	Arg	Val	Ser	Met	Leu	Asp	Met	Lys		
	50					55					60						
Gly	Asn	Pro	Asp	Ser	Gly	Gly	Ile	Trp	Ala	Pro	Cys	Leu	Ser	Tyr	Ala		
65				70					75					80			
Asp	Gly	Lys	Phe	Trp	Leu	Leu	Tyr	Thr	Asp	Val	Lys	Ile	Val	Asp	Ser		
			85					90						95			
Pro	Trp	Lys	Asn	Gly	Arg	Asn	Phe	Leu	Val	Thr	Ala	Pro	Ser	Ile	Glu		
			100					105						110			
Gly	Pro	Trp	Ser	Glu	Pro	Ile	Pro	Met	Gly	Asn	Gly	Gly	Phe	Asp	Pro		
		115				120						125					
Ser	Leu	Phe	His	Asp	Asp	Asp	Gly	Arg	Lys	Tyr	Tyr	Ile	Tyr	Arg	Pro		
	130				135					140							
Trp	Gly	Pro	Arg	His	His	Ser	Asn	Pro	His	Asn	Thr	Ile	Val	Leu	Gln		
145				150					155					160			
Ala	Phe	Asp	Pro	Gln	Thr	Gly	Thr	Leu	Ser	Pro	Glu	Arg	Lys	Thr	Leu		
			165					170						175			
Phe	Thr	Gly	Thr	Pro	Leu	Cys	Tyr	Thr	Glu	Gly	Ala	His	Leu	Tyr	Arg		
		180					185						190				
His	Ala	Gly	Trp	Tyr	Tyr	Leu	Met	Ala	Ala	Glu	Gly	Gly	Thr	Ser	Tyr		
	195					200						205					
Glu	His	Ala	Val	Val	Val	Leu	Arg	Ser	Lys	Asn	Ile	Asp	Gly	Pro	Tyr		
	210					215					220						
Glu	Leu	His	Pro	Asp	Val	Thr	Met	Met	Thr	Ser	Trp	His	Leu	Pro	Glu		
225				230						235				240			
Asn	Pro	Leu	Gln	Lys	Ser	Gly	His	Gly	Ser	Leu	Leu	Gln	Thr	His	Thr		
			245					250						255			
Gly	Glu	Trp	Tyr	Met	Ala	Tyr	Leu	Thr	Ser	Arg	Pro	Leu	Arg	Leu	Pro		
		260					265						270				
Gly	Val	Pro	Leu	Leu	Ala	Ser	Gly	Gly	Arg	Gly	Tyr	Cys	Pro	Leu	Gly		
	275					280						285					
Arg	Glu	Thr	Gly	Ile	Ala	Arg	Ile	Glu	Trp	Arg	Asp	Gly	Trp	Pro	Tyr		
	290				295						300						
Val	Glu	Gly	Gly	Lys	His	Ala	Gln	Leu	Thr	Val	Lys	Gly	Pro	Gln	Val		
305				310					315					320			
Ala	Glu	Gln	Pro	Ala	Ala	Val	Pro	Gly	Asn	Trp	Arg	Asp	Asp	Phe	Asp		
			325					330						335			

Ile	Asn	Thr	Pro	Ile	Lys	Val	Ser	Ala	Glu	Pro	Asn	Gly	Ala	Arg	Leu
				245					250					255	
Val	Glu	Val	His	Gln	Pro	Leu	Ser	Glu	Lys	Ile	Asp	Asp	Asp	Pro	Gln
			260					265					270		
Leu	Leu	Pro	Ile	Thr	Leu	Asn	Ser	Ala	Met	Gln	Ser	Phe	Lys	Asp	Ala
		275					280					285			
Ala	Gln	Thr	Asp	Ala	Glu	Val	Met	Gln	His	Val	Met	Asp	Val	Arg	Ser
	290					295					300				
Gly	Met	Pro	Val	Asp	Val	Arg	Arg	His	Gln	Val	Ser	Pro	Gln	Thr	Leu
305					310					315					320

<210> 468
 <211> 494
 <212> PRT
 <213> Escherichia coli

<400> 468															
Met	Val	Ala	Ile	His	Leu	Leu	Pro	Val	Ser	Tyr	Asn	Ser	Ala	Thr	Ser
1				5					10					15	
Thr	Val	Asn	Ile	Ser	Ala	Arg	Ile	Ile	Pro	Leu	Leu	Ile	Ile	His	Gln
			20					25					30		
Arg	Tyr	Lys	Ile	Pro	Met	Pro	Lys	Val	Gln	Ala	Asp	Gly	Leu	Pro	Leu
		35					40					45			
Pro	Gln	Arg	Tyr	Gly	Ala	Ile	Leu	Thr	Ile	Val	Ile	Gly	Ile	Ser	Met
	50					55					60				
Ala	Val	Leu	Asp	Gly	Ala	Ile	Ala	Asn	Val	Ala	Leu	Pro	Thr	Ile	Ala
65					70				75						80
Thr	Asp	Leu	His	Ala	Thr	Pro	Ala	Ser	Ser	Ile	Trp	Val	Val	Asn	Ala
				85					90					95	
Tyr	Gln	Ile	Ala	Ile	Val	Ile	Ser	Leu	Leu	Ser	Phe	Ser	Phe	Leu	Gly
			100					105					110		
Asp	Met	Phe	Gly	Tyr	Arg	Arg	Ile	Tyr	Lys	Cys	Gly	Leu	Val	Val	Phe
		115					120					125			
Leu	Leu	Ser	Ser	Leu	Phe	Cys	Ala	Leu	Ser	Asp	Ser	Leu	Gln	Met	Leu
	130					135					140				
Thr	Leu	Ala	Arg	Val	Ile	Gln	Gly	Phe	Gly	Gly	Ala	Ala	Leu	Met	Ser
145					150					155					160
Val	Asn	Thr	Ala	Leu	Ile	Arg	Leu	Ile	Tyr	Pro	Gln	Arg	Phe	Leu	Gly
			165						170					175	
Arg	Gly	Met	Gly	Ile	Asn	Ser	Phe	Ile	Val	Ala	Val	Ser	Ser	Ala	Ala
			180					185					190		
Gly	Pro	Thr	Ile	Ala	Ala	Ala	Ile	Leu	Ser	Ile	Ala	Ser	Trp	Lys	Trp
		195					200					205			
Leu	Phe	Leu	Ile	Asn	Val	Pro	Leu	Gly	Ile	Ile	Ala	Leu	Leu	Leu	Ala
	210					215					220				
Met	Arg	Phe	Leu	Pro	Pro	Asn	Gly	Ser	Arg	Ala	Ser	Lys	Pro	Arg	Phe
225					230					235					240
Asp	Leu	Pro	Ser	Ala	Val	Met	Asn	Ala	Leu	Thr	Phe	Gly	Leu	Leu	Ile
				245					250				255		
Thr	Ala	Leu	Ser	Gly	Phe	Ala	Gln	Gly	Gln	Ser	Leu	Thr	Leu	Ile	Ala
			260					265					270		
Ala	Glu	Leu	Val	Val	Met	Val	Val	Val	Gly	Ile	Phe	Phe	Ile	Arg	Arg
		275						280				285			
Gln	Leu	Ser	Leu	Pro	Val	Pro	Leu	Leu	Pro	Val	Asp	Leu	Leu	Arg	Ile
	290					295					300				
Pro	Leu	Phe	Ser	Leu	Ser	Ile	Cys	Thr	Ser	Val	Cys	Ser	Phe	Cys	Ala

006TET-0941269

Glu Glu Glu Ile Val Glu Arg Gly Met Lys Leu Ile Ala Asp Tyr Glu
 210 215 220
 Leu Ser Ala Leu Leu Val Thr Arg Ser Glu Gln Gly Met Ser Leu Leu
 225 230 235 240
 Gln Pro Gly Lys Ala Pro Leu His Met Pro Thr Gln Ala Gln Glu Val
 245 250 255
 Tyr Asp Val Thr Gly Ala Gly Asp Thr Val Ile Gly Val Leu Ala Ala
 260 265 270
 Thr Leu Ala Ala Gly Asn Ser Leu Glu Glu Ala Cys Phe Phe Ala Asn
 275 280 285
 Ala Ala Ala Gly Val Val Val Gly Lys Leu Gly Thr Ser Thr Val Ser
 290 295 300
 Pro Ile Glu Leu Glu Asn Ala Val Arg Gly Arg Ala Asp Thr Gly Phe
 305 310 315 320
 Gly Val Met Thr Glu Glu Glu Leu Lys Leu Ala Val Ala Ala Ala Arg
 325 330 335
 Lys Arg Gly Glu Lys Val Val Met Thr Asn Gly Val Phe Asp Ile Leu
 340 345 350
 His Ala Gly His Val Ser Tyr Leu Ala Asn Ala Arg Lys Leu Gly Asp
 355 360 365
 Arg Leu Ile Val Ala Val Asn Ser Asp Ala Ser Thr Lys Arg Leu Lys
 370 375 380
 Gly Asp Ser Arg Pro Val Asn Pro Leu Glu Gln Arg Met Ile Val Leu
 385 390 395 400
 Gly Ala Leu Glu Ala Val Asp Trp Val Val Ser Phe Glu Glu Asp Thr
 405 410 415
 Pro Gln Arg Leu Ile Ala Gly Ile Leu Pro Asp Leu Leu Val Lys Gly
 420 425 430
 Gly Asp Tyr Lys Pro Glu Glu Ile Ala Gly Ser Lys Glu Val Trp Ala
 435 440 445
 Asn Gly Gly Glu Val Leu Val Leu Asn Phe Glu Asp Gly Cys Ser Thr
 450 455 460
 Thr Asn Ile Ile Lys Lys Ile Gln Gln Asp Lys Lys Gly
 465 470 475

<210> 470

<211> 946

<212> PRT

<213> Escherichia coli

<400> 470

Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
 1 5 10 15
 Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
 20 25 30
 Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
 35 40 45
 His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
 50 55 60
 Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
 65 70 75 80
 Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
 85 90 95
 Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
 100 105 110
 Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val

<210> 472
 <211> 207
 <212> PRT
 <213> Escherichia coli

<400> 472

Met	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Leu	Lys	Asp	Ala	Gly	Ile	Ser	Leu
1			5						10					15	
Thr	Asp	His	Gln	Lys	Asn	Gln	Leu	Ile	Ala	Tyr	Val	Asn	Met	Leu	His
			20					25					30		
Lys	Trp	Asn	Lys	Ala	Tyr	Asn	Leu	Thr	Ser	Val	Arg	Asp	Pro	Asn	Glu
		35					40					45			
Met	Leu	Val	Arg	His	Ile	Leu	Asp	Ser	Ile	Val	Val	Ala	Pro	Tyr	Leu
	50					55					60				
Gln	Gly	Glu	Arg	Phe	Ile	Asp	Val	Gly	Thr	Gly	Pro	Gly	Leu	Pro	Gly
65					70				75						80
Ile	Pro	Leu	Ser	Ile	Val	Arg	Pro	Glu	Ala	His	Phe	Thr	Leu	Leu	Asp
			85						90					95	
Ser	Leu	Gly	Lys	Arg	Val	Arg	Phe	Leu	Arg	Gln	Val	Gln	His	Glu	Leu
			100					105					110		
Lys	Leu	Glu	Asn	Ile	Glu	Pro	Val	Gln	Ser	Arg	Val	Glu	Glu	Phe	Pro
		115					120					125			
Ser	Glu	Pro	Pro	Phe	Asp	Gly	Val	Ile	Ser	Arg	Ala	Phe	Ala	Ser	Leu
	130					135					140				
Asn	Asp	Met	Val	Ser	Trp	Cys	His	His	Leu	Pro	Gly	Glu	Gln	Gly	Arg
145					150					155					160
Phe	Tyr	Ala	Leu	Lys	Gly	Gln	Met	Pro	Glu	Asp	Glu	Ile	Ala	Leu	Leu
				165					170						175
Pro	Glu	Glu	Tyr	Gln	Val	Glu	Ser	Val	Val	Lys	Leu	Gln	Val	Pro	Ala
			180					185					190		
Leu	Asp	Gly	Glu	Arg	His	Leu	Val	Val	Ile	Lys	Ala	Asn	Lys	Ile	
		195					200						205		

<210> 473
 <211> 629
 <212> PRT
 <213> Escherichia coli

<400> 473

Met	Phe	Tyr	Pro	Asp	Pro	Phe	Asp	Val	Ile	Ile	Ile	Gly	Gly	Gly	His
1				5					10					15	
Ala	Gly	Thr	Glu	Ala	Ala	Met	Ala	Ala	Ala	Arg	Met	Gly	Gln	Gln	Thr
			20					25					30		
Leu	Leu	Leu	Thr	His	Asn	Ile	Asp	Thr	Leu	Gly	Gln	Met	Ser	Cys	Asn
		35					40					45			
Pro	Ala	Ile	Gly	Gly	Ile	Gly	Lys	Gly	His	Leu	Val	Lys	Glu	Val	Asp
	50					55					60				
Ala	Leu	Gly	Gly	Leu	Met	Ala	Lys	Ala	Ile	Asp	Gln	Ala	Gly	Ile	Gln
65					70				75						80
Phe	Arg	Ile	Leu	Asn	Ala	Ser	Lys	Gly	Pro	Ala	Val	Arg	Ala	Thr	Arg
				85					90					95	
Ala	Gln	Ala	Asp	Arg	Val	Leu	Tyr	Arg	Gln	Ala	Val	Arg	Thr	Ala	Leu
			100					105					110		
Glu	Asn	Gln	Pro	Asn	Leu	Met	Ile	Phe	Gln	Gln	Ala	Val	Glu	Asp	Leu
		115					120					125			
Ile	Val	Glu	Asn	Asp	Arg	Val	Val	Gly	Ala	Val	Thr	Gln	Met	Gly	Leu

His Lys Pro Ala Ser Ile Gly Gln Ala Ser Arg Ile Ser Gly Val Thr
 595 600 605
 Pro Ala Ala Ile Ser Ile Leu Leu Val Trp Leu Lys Lys Gln Gly Met
 610 615 620
 Leu Arg Arg Ser Ala
 625

<210> 474
 <211> 147
 <212> PRT
 <213> Escherichia coli

<400> 474
 Met Ala Asp Ile Thr Leu Ile Ser Gly Ser Thr Leu Gly Gly Ala Glu
 1 5 10 15
 Tyr Val Ala Glu His Leu Ala Glu Lys Leu Glu Glu Ala Gly Phe Thr
 20 25 30
 Thr Glu Thr Leu His Gly Pro Leu Leu Glu Asp Leu Pro Ala Ser Gly
 35 40 45
 Ile Trp Leu Val Ile Ser Ser Thr His Gly Ala Gly Asp Ile Pro Asp
 50 55 60
 Asn Leu Ser Pro Phe Tyr Glu Ala Leu Gln Glu Gln Lys Pro Asp Leu
 65 70 75 80
 Ser Ala Val Arg Phe Gly Ala Ile Gly Ile Gly Ser Arg Glu Tyr Asp
 85 90 95
 Thr Phe Cys Gly Ala Ile Asp Lys Leu Glu Ala Glu Leu Lys Asn Ser
 100 105 110
 Gly Ala Lys Gln Thr Gly Glu Thr Leu Lys Ile Asn Ile Leu Asp His
 115 120 125
 Asp Ile Pro Glu Asp Pro Ala Glu Glu Trp Leu Gly Ser Trp Val Asn
 130 135 140
 Leu Leu Lys
 145

<210> 475
 <211> 151
 <212> PRT
 <213> Escherichia coli

<400> 475
 Met Gly Gln Arg Asn Val Ser Leu Met Glu Lys Lys Met Lys Lys Gly
 1 5 10 15
 Thr Val Leu Asn Ser Asp Ile Ser Ser Val Ile Ser Arg Leu Gly His
 20 25 30
 Thr Asp Thr Leu Val Val Cys Asp Ala Gly Leu Pro Ile Pro Lys Ser
 35 40 45
 Thr Thr Arg Ile Asp Met Ala Leu Thr Gln Gly Val Pro Ser Phe Met
 50 55 60
 Gln Val Leu Gly Val Val Thr Asn Glu Met Gln Val Glu Ala Ala Ile
 65 70 75 80
 Ile Ala Glu Glu Ile Lys His His Asn Pro Gln Leu His Glu Thr Leu
 85 90 95
 Leu Thr His Leu Glu Gln Leu Gln Lys His Gln Gly Asn Thr Ile Glu
 100 105 110
 Ile Arg Tyr Thr Thr His Glu Gln Phe Lys Gln Gln Thr Ala Glu Ser

115	120	125
Gln Ala Val Ile Arg Ser	Gly Glu Cys Ser Pro	Tyr Ala Asn Ile Ile
130	135	140
Leu Cys Ala Gly Val Thr	Phe	
145	150	

<210> 476
 <211> 501
 <212> PRT
 <213> Escherichia coli

<400> 476

Met	Glu	Ala	Leu	Leu	Gln	Leu	Lys	Gly	Ile	Asp	Lys	Ala	Phe	Pro	Gly
1				5					10					15	
Val	Lys	Ala	Leu	Ser	Gly	Ala	Ala	Leu	Asn	Val	Tyr	Pro	Gly	Arg	Val
			20					25					30		
Met	Ala	Leu	Val	Gly	Glu	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Met	Met	Lys
		35				40					45				
Val	Leu	Thr	Gly	Ile	Tyr	Thr	Arg	Asp	Ala	Gly	Thr	Leu	Leu	Trp	Leu
	50					55					60				
Gly	Lys	Glu	Thr	Thr	Phe	Thr	Gly	Pro	Lys	Ser	Ser	Gln	Glu	Ala	Gly
65					70				75					80	
Ile	Gly	Ile	Ile	His	Gln	Glu	Leu	Asn	Leu	Ile	Pro	Gln	Leu	Thr	Ile
				85				90					95		
Ala	Glu	Asn	Ile	Phe	Leu	Gly	Arg	Glu	Phe	Val	Asn	Arg	Phe	Gly	Lys
			100					105					110		
Ile	Asp	Trp	Lys	Thr	Met	Tyr	Ala	Glu	Ala	Asp	Lys	Leu	Leu	Ala	Lys
		115				120					125				
Leu	Asn	Leu	Arg	Phe	Lys	Ser	Asp	Lys	Leu	Val	Gly	Asp	Leu	Ser	Ile
	130					135					140				
Gly	Asp	Gln	Gln	Met	Val	Glu	Ile	Ala	Lys	Val	Leu	Ser	Phe	Glu	Ser
145					150					155				160	
Lys	Val	Ile	Ile	Met	Asp	Glu	Pro	Thr	Asp	Ala	Leu	Thr	Asp	Thr	Glu
				165					170					175	
Thr	Glu	Ser	Leu	Phe	Arg	Val	Ile	Arg	Glu	Leu	Lys	Ser	Gln	Gly	Arg
			180					185					190		
Gly	Ile	Val	Tyr	Ile	Ser	His	Arg	Met	Lys	Glu	Ile	Phe	Glu	Ile	Cys
		195				200						205			
Asp	Asp	Val	Thr	Val	Phe	Arg	Asp	Gly	Gln	Phe	Ile	Ala	Glu	Arg	Glu
	210					215					220				
Val	Ala	Ser	Leu	Thr	Glu	Asp	Ser	Leu	Ile	Glu	Met	Met	Val	Gly	Arg
225					230					235				240	
Lys	Leu	Glu	Asp	Gln	Tyr	Pro	His	Leu	Asp	Lys	Ala	Pro	Gly	Asp	Ile
			245						250					255	
Arg	Leu	Lys	Val	Asp	Asn	Leu	Cys	Gly	Pro	Gly	Val	Asn	Asp	Val	Ser
			260					265					270		
Phe	Thr	Leu	Arg	Lys	Gly	Glu	Ile	Leu	Gly	Val	Ser	Gly	Leu	Met	Gly
		275					280					285			
Ala	Gly	Arg	Thr	Glu	Leu	Met	Lys	Val	Leu	Tyr	Gly	Ala	Leu	Pro	Arg
	290					295					300				
Thr	Ser	Gly	Tyr	Val	Thr	Leu	Asp	Gly	His	Glu	Val	Val	Thr	Arg	Ser
305					310					315				320	
Pro	Gln	Asp	Gly	Leu	Ala	Asn	Gly	Ile	Val	Tyr	Ile	Ser	Glu	Asp	Arg
			325						330					335	
Lys	Arg	Asp	Gly	Leu	Val	Leu	Gly	Met	Ser	Val	Lys	Glu	Asn	Met	Ser
			340					345					350		

Leu Thr Ala Leu Arg Tyr Phe Ser Arg Ala Gly Gly Ser Leu Lys His
 355 360 365
 Ala Asp Glu Gln Gln Ala Val Ser Asp Phe Ile Arg Leu Phe Asn Val
 370 375 380
 Lys Thr Pro Ser Met Glu Gln Ala Ile Gly Leu Leu Ser Gly Gly Asn
 385 390 395 400
 Gln Gln Lys Val Ala Ile Ala Arg Gly Leu Met Thr Arg Pro Lys Val
 405 410 415
 Leu Ile Leu Asp Glu Pro Thr Arg Gly Val Asp Val Gly Ala Lys Lys
 420 425 430
 Glu Ile Tyr Gln Leu Ile Asn Gln Phe Lys Ala Asp Gly Leu Ser Ile
 435 440 445
 Ile Leu Val Ser Ser Glu Met Pro Glu Val Leu Gly Met Ser Asp Arg
 450 455 460
 Ile Ile Val Met His Glu Gly His Leu Ser Gly Glu Phe Thr Arg Glu
 465 470 475 480
 Gln Ala Thr Gln Glu Val Leu Met Ala Ala Ala Val Gly Lys Leu Asn
 485 490 495
 Arg Val Asn Gln Glu
 500

<210> 477
 <211> 321
 <212> PRT
 <213> Escherichia coli

<400> 477
 Met Thr Thr Gln Thr Val Ser Gly Arg Arg Tyr Phe Thr Lys Ala Trp
 1 5 10 15
 Leu Met Glu Gln Lys Ser Leu Ile Ala Leu Leu Val Leu Ile Ala Ile
 20 25 30
 Val Ser Thr Leu Ser Pro Asn Phe Phe Thr Ile Asn Asn Leu Phe Asn
 35 40 45
 Ile Leu Gln Gln Thr Ser Val Asn Ala Ile Met Ala Val Gly Met Thr
 50 55 60
 Leu Val Ile Leu Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Leu Leu
 65 70 75 80
 Ala Leu Thr Gly Ala Val Ala Ala Ser Ile Val Gly Ile Glu Val Asn
 85 90 95
 Ala Leu Val Ala Val Ala Ala Ala Leu Ala Leu Gly Ala Ala Ile Gly
 100 105 110
 Ala Val Thr Gly Val Ile Val Ala Lys Gly Arg Val Gln Ala Phe Ile
 115 120 125
 Ala Thr Leu Val Met Met Leu Leu Arg Gly Val Thr Met Val Tyr
 130 135 140
 Thr Asn Gly Ser Pro Val Asn Thr Gly Phe Thr Glu Asn Ala Asp Leu
 145 150 155 160
 Phe Gly Trp Phe Gly Ile Gly Arg Pro Leu Gly Val Pro Thr Pro Val
 165 170 175
 Trp Ile Met Gly Ile Val Phe Leu Ala Ala Trp Tyr Met Leu His His
 180 185 190
 Thr Arg Leu Gly Arg Tyr Ile Tyr Ala Leu Gly Gly Asn Glu Ala Ala
 195 200 205
 Thr Arg Leu Ser Gly Ile Asn Val Asn Lys Ile Lys Ile Ile Val Tyr
 210 215 220
 Ser Leu Cys Gly Leu Leu Ala Ser Leu Ala Gly Ile Ile Glu Val Ala

225		230		235		240									
Arg	Leu	Ser	Ser	Ala	Gln	Pro	Thr	Ala	Gly	Thr	Gly	Tyr	Glu	Leu	Asp
				245					250					255	
Ala	Ile	Ala	Ala	Val	Val	Leu	Gly	Gly	Thr	Ser	Leu	Ala	Gly	Gly	Lys
			260					265					270		
Gly	Arg	Ile	Val	Gly	Thr	Leu	Ile	Gly	Ala	Leu	Ile	Leu	Gly	Phe	Leu
		275					280					285			
Asn	Asn	Gly	Leu	Asn	Leu	Leu	Gly	Val	Ser	Ser	Tyr	Tyr	Gln	Met	Ile
	290					295					300				
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Gln															

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 <212> PRT
 <213> Escherichia coli

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35 40 45
Gln Lys Glu Ala Asp Lys Leu Gly Tyr Asn Leu Val Val Leu Asp Ser
50 55 60
Gln Asn Asn Pro Ala Lys Glu Leu Ala Asn Val Gln Asp Leu Thr Val
65 70 75 80
Arg Gly Thr Lys Ile Leu Leu Ile Asn Pro Thr Asp Ser Asp Ala Val
85 90 95
Gly Asn Ala Val Lys Met Ala Asn Gln Ala Asn Ile Pro Val Ile Thr
100 105 110
Leu Asp Arg Gln Ala Thr Lys Gly Glu Val Val Ser His Ile Ala Ser
115 120 125
Asp Asn Val Leu Gly Gly Lys Ile Ala Gly Asp Tyr Ile Ala Lys Lys
130 135 140
Ala Gly Glu Gly Ala Lys Val Ile Glu Leu Gln Gly Ile Ala Gly Thr
145 150 155 160
Ser Ala Ala Arg Glu Arg Gly Glu Gly Phe Gln Gln Ala Val Ala Ala
165 170 175
His Lys Phe Asn Val Leu Ala Ser Gln Pro Ala Asp Phe Asp Arg Ile
180 185 190
Lys Gly Leu Asn Val Met Gln Asn Leu Leu Thr Ala His Pro Asp Val
195 200 205
Gln Ala Val Phe Ala Gln Asn Asp Glu Met Ala Leu Gly Ala Leu Arg
210 215 220
Ala Leu Gln Thr Ala Gly Lys Ser Asp Val Met Val Val Gly Phe Asp
225 230 235 240
Gly Thr Pro Asp Gly Glu Lys Ala Val Asn Asp Gly Lys Leu Ala Ala
245 250 255
Thr Ile Ala Gln Leu Pro Asp Gln Ile Gly Ala Lys Gly Val Glu Thr
260 265 270
Ala Asp Lys Val Leu Lys Gly Glu Lys Val Gln Ala Lys Tyr Pro Val
275 280 285

Asp Leu Lys Leu Val Val Lys Gln
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<210> 479
<211> 309
<212> PRT
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His Ile Leu Asn Leu Gln Ser Phe Pro Thr Pro Gly Glu Thr Val Thr
20 25 30
Gly Asn His Tyr Gln Val Ala Phe Gly Gly Lys Gly Ala Asn Gln Ala
35 40 45
Val Ala Ala Gly Arg Ser Gly Ala Asn Ile Ala Phe Ile Ala Cys Thr
50 55 60
Gly Asp Asp Ser Ile Gly Glu Ser Val Arg Gln Gln Leu Ala Thr Asp
65 70 75 80
Asn Ile Asp Ile Thr Pro Val Ser Val Ile Lys Gly Glu Ser Thr Gly
85 90 95
Val Ala Leu Ile Phe Val Asn Gly Glu Gly Glu Asn Val Ile Gly Ile
100 105 110
His Ala Gly Ala Asn Ala Ala Leu Ser Pro Ala Leu Val Glu Ala Gln
115 120 125
Arg Glu Arg Ile Ala Asn Ala Ser Ala Leu Leu Met Gln Leu Glu Ser
130 135 140
Pro Leu Glu Ser Val Met Ala Ala Ala Lys Ile Ala His Gln Asn Lys
145 150 155 160
Thr Ile Val Ala Leu Asn Pro Ala Pro Ala Arg Glu Leu Pro Asp Glu
165 170 175
Leu Leu Ala Leu Val Asp Ile Ile Thr Pro Asn Glu Thr Glu Ala Glu
180 185 190
Lys Leu Thr Gly Ile Arg Val Glu Asn Asp Glu Asp Ala Ala Lys Ala
195 200 205
Ala Gln Val Leu His Glu Lys Gly Ile Arg Thr Val Leu Ile Thr Leu
210 215 220
Gly Ser Arg Gly Val Trp Ala Ser Val Asn Gly Glu Gly Gln Arg Val
225 230 235 240
Pro Gly Phe Arg Val Gln Ala Val Asp Thr Ile Ala Ala Gly Asp Thr
245 250 255
Phe Asn Gly Ala Leu Ile Thr Ala Leu Glu Glu Lys Pro Leu Pro
260 265 270
Glu Ala Ile Arg Phe Ala His Ala Ala Ala Ala Ile Ala Val Thr Arg
275 280 285
Lys Gly Ala Gln Pro Ser Val Pro Trp Arg Glu Glu Ile Asp Ala Phe
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Leu Asp Arg Gln Arg
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<213> Artificial Sequence

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